

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCCTCT	ATATGGAACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGAGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACACT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAAGTGAAT	TTGAAGGTTT	AGGTTCCGTT	GTTTCAAG		1689

20

2) INFORMATION FOR SEQ ID NO: 1047

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGACAGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTT	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCCTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAATGAT	GACCTTTTCT	CAAGGGTTCG	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
55	TTTGGACAAG	GGATTTCAGC	GACCCAGACG	CAAATGATTC	GTGCCTTCAC	900
	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCGGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAAGTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGA	AGGGCAGTGG	CTATGAAAGA	1350
	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAAC	GTTAAATCAG	GTAACCAATC	1400
5	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTCCACC	TGGCGATTG	1450
	GCGGAAGCCT	TACGTGCAAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGACACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

15

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1682 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGACTG	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACTAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTAAGTGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550

AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
GGCTGGAAAA	AAGAGACTGC	TGAAACCTTT	GCTAAATGGT	TGGATATTGA	1650
GTTGGAATTT	GAAGGTTTCAG	GTTCCGTCGT	TC		1682

5

2) INFORMATION FOR SEQ ID NO: 1049

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1241 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R690

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

GCAGCGTTGC	GTGATACCGT	TGAAAAAACC	ATTAAAAACT	GTTTGGATTT	50
TGAAAGGAGA	CAGGAGCATG	AATAGAATAA	AAGTTGCAAT	ACTGTTTGGG	100
25 GGTGCTCAG	AGGAGCATGA	CGTATCGGTA	AAATCTGCAA	TAGAGATAGC	150
CGCTAACATT	AATAAAGAAA	AATACGAGCC	GTTATACATT	GGAATTACGA	200
AATCTGGTGT	ATGGAAAATG	TGCGAAAAAC	CTTGCGCGGA	ATGGGAAAAC	250
GACAATTGCT	ATTCAGCTGT	ACTCTCGCCG	GATAAAAAAA	TGCACGGATT	300
ACTTGTTAAA	AAGAACCATG	AATATGAAAT	CAACCATGTT	GATGTAGCAT	350
30 TTTTCAGCTTT	GCATGGCAAG	TCAGGTGAAG	ATGGATCCAT	ACAAGGTCTG	400
TTTGAATTGT	CCGGTATCCC	TTTTGTAGGC	TGCGATATTC	AAAGCTCAGC	450
AATTTGTATG	GACAAATCGT	TGACATACAT	CGTTGCGAAA	AATGCTGGGA	500
TAGCTACTCC	CGCCTTTTGG	GTTATTAATA	AAGATGATAG	GCCGGTGGCA	550
GCTACGTTTA	CCTATCCTGT	TTTTGTAAAG	CCGGCGCGTT	CAGGCTCATC	600
35 CTTCGGTGTG	AAAAAAGTCA	ATAGCGCGGA	CGAATTGGAC	TACGCAATTG	650
AATCGGCAAG	ACAATATGAC	AGCAAAATCT	TAATTGAGCA	GGCTGTTTCG	700
GGCTGTGAGG	TCGGTTGTGC	GGTATTGGGA	AACAGTGCCG	CGTTAGTCTG	750
TGGCGAGGTG	GACCAAATCA	GGCTGCAGTA	CGGAATCTTT	CGTATTCATC	800
AGGAAGTCGA	GCCGGAAAAA	GGCTCTGAAA	ACGCAGTTAT	AACCGTTCCC	850
40 GCAGACCTTT	CAGCAGAGGA	GCGAGGACGG	ATACAGGAAA	CGGCAAAAAA	900
AATATATAAA	GCGCTCGGCT	GTAGAGGTCT	AGCCCGTGTG	GATATGTTTT	950
TACAAGATAA	CGGCCGCATT	GTA CTGAACG	AAGTCAATAC	TCTGCCCGGT	1000
TTCACGTCAT	ACAGTCGTTA	TCCCCGTATG	ATGGCCGCTG	CAGGTATTGC	1050
ACTTCCCGAA	CTGATTGACC	GCTTGATCGT	ATTAGCGTTA	AAGGGGTGAT	1100
45 AAGCATGGAA	ATAGGATTTA	CTTTTTTTAGA	TGAAATAGTA	CACGGTGTTT	1150
GTTGGGACGC	TAAATATGCC	ACTTGGGATA	ATTCACCGG	AAAACCGGTT	1200
GACGGTTATG	AAGTAAATCG	CATTGTAGGG	ACATACGAAT	T	1241

50

2) INFORMATION FOR SEQ ID NO: 1050

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1249 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
10	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
15	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
20	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
25	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
30	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCAACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCG	1249

35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1272 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

50	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAAACTG	50
	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	100
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	150
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	200
55	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	250
	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	300
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	350
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	400
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	450
60	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	500

	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	550
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	600
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	650
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	700
5	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	750
	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	800
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	850
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	900
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	950
10	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1000
	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1050
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1100
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTAGAT	GAAATAGTAC	1150
	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1200
15	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAATT	1250
	GGCTTGAATC	GCTTTTTTGA	GG			1272

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

35	TCCCCCGGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
40	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
45	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
50	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
55	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	1200
60	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTA		1237

2) INFORMATION FOR SEQ ID NO: 1053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

20	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	TTGAAAAAAC	50
	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	GAATAGAATA	100
	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	ACGTATCGGT	150
	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	AAATACGAGC	200
	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	GTGCGAAAAA	250
25	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	TACTCTCGCC	300
	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	GAATATGAAA	350
	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	GTCAGGTGAA	400
	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	CTTTTGTAGG	450
	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	TTGACATACA	500
30	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	GGTTATTAAT	550
	AAAGATGATA	GGCCGGTGGC	AGCTACGTTT	ACCTATCCTG	TTTTTGTTAA	600
	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	AATAGCGCGG	650
	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	CAGCAAAATC	700
	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	CGGTATTGGG	750
35	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	AGGCTGCAGT	800
	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGGAAAA	AGGCTCTGAA	850
	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	AGCGAGGACG	900
	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	TGTAGAGGTC	950
	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	TGTACTGAAC	1000
40	GAAGTCAATA	CTCTGCCCGG	TTTCACGTCA	TACAGTCGTT	ATCCCCGTAT	1050
	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	CGCTTGATCG	1100
	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	ACTTTTTTAG	1150
	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	CACTTGGGAT	1200
	AATTTACCGG	GAAAACCGGT	TGACGGGTAT	GAAAGTAAAT	CGCATTGTAG	1250
45	GGACATTCGA	ATT				1263

2) INFORMATION FOR SEQ ID NO: 1054

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

5	CGGCCTATTA	TNCCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	50
	AAAAACTGTT	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAG	100
	TTGCAATACT	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	150
	TCTGCAATAG	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	200
	ATACATTGGA	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	250
10	GCGCGGAATG	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	300
	AAAAAAATGC	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	350
	CCATGTTGAT	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	400
	GATCCATACA	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	450
	GATATTCAAA	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	500
15	TGCGAAAAAT	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	550
	ATGATAGGCC	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	600
	GCGCGTTCAG	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	650
	ATTGGACTAC	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	700
	TTGAGCAGGC	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	750
20	AGTGCCGCGT	TAGTTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	800
	AATCTTTTCGT	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	850
	CAGTTATAAC	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	900
	CAGGAAACGG	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	950
	CCGTGTGGAT	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	1000
25	TCAATACTCT	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	1050
	GCCGCTGCAG	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	1100
	AGCGTTAAAG	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	1150
	AATAGTACAC	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	1200
30	TCACCGGAAA	ACCGGTTGAC	GATTATAAGT	AA		1232

2) INFORMATION FOR SEQ ID NO: 1055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

50	TACCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	AAAAACTGTT	50
	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAG	TTGCAATACT	100
	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	TCTGCAATAG	150
	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	ATACATTGGA	200
	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	GCGCGGAATG	250
	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	AAAAAAATGC	300
55	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	CCATGTTGAT	350
	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	GATCCATACA	400
	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	GATATTCAAA	450
	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	TGCGAAAAAT	500
	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	ATGATAGGCC	550
60	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	GCGCGTTCAG	600

	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	AATAGTACAC	1150
	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTTAGAA				1218

15

2) INFORMATION FOR SEQ ID NO: 1056

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1265 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R688

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGTTTGCTCA	GAGGAGCATG	150
	ACGTATCCGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGCG	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTGTTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGGAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCGG	TTTCACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTAT	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTACCGG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

60

2) INFORMATION FOR SEQ ID NO: 1057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
GCTGCAGTAC	GGAATCTTTC	GTATTTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	1200
CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
ATTGTAGGGA	CATACGAAT				1269

2) INFORMATION FOR SEQ ID NO: 1058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCAATGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCAG	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	GTGCTTGTGA	TGCGATTCTT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GCGTCTGGCT	CGAATCGATT	TTTTTCGTCAC	950
	CAATCAAGGA	CGGATTTTAT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCAATGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCAG	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTCGTCAC	950
5	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
	AACACATTAC	AATTGATCAA	TAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	CCCCCGCAC	TTAGTG				1166

10

2) INFORMATION FOR SEQ ID NO: 1060

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

	AACATGAAAA	AAATCGCCTT	ATTTTTGGAG	GCAATTCACC	GGAATACACC	50
30	GTTTCTTTAG	CTTCAGCAAC	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	100
	CTATGACTAC	GACCTCTCTT	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	150
	GGTACTTGTA	TACAGGAGAA	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	200
	TTGGATACGA	AACATAAACA	GAAAATACAG	CCGCTATTTC	AAGGAAACGG	250
	CTTTTGGCTA	AGTGAAGAGC	AGCAAACGTT	GGTACCTGAT	GTTTATTTC	300
35	CCATTATGCA	TGGCAAATAC	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	350
	GAATTGATGA	AGCTGCCTTA	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	400
	ATGTATGAAC	AAATGGCTGC	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	450
	AAAGTGCTCC	TACGATTCTC	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	500
	ATCGAAGCTT	TTATCCAGAC	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	550
40	TGAAGCGGGC	TCCTCAAAAG	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	600
	TCGCTTCTGC	CTTAAAAGAA	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	650
	CAAAAAAATA	TTGCCGGTGT	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	700
	CTCTTTGACT	GTCGGTGCTT	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	750
	TCGATTTTGA	AGAAAAGTAC	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	800
45	GCGCCATTGC	CTGAAACGAT	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	850
	GCTCTATCGT	AGTCTTGGTC	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	900
	TCACGGAGCG	AGGAGAACTA	TACTTGAATG	AAATCAATAC	TATGCCGGGC	950
	TTTACGAGTC	ACTCCCGCTA	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	1000
	CTATCAAGAA	CTACTACAAA	AACTGCTT			1028

50

2) INFORMATION FOR SEQ ID NO: 1061

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

```

10  AATATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAGTACGCC      50
    GTTCTTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
    CGATGACTAT GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
    GGTATTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
    TTGGATACGA AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
    CTTTTGGCTA AGTGAAGAGC AACAAACGTT GGTTCCTGAT GTTTTATTTT      300
15  CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
    GAATTGATGA AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
    ATGTATGAAC AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
    AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
    ATCGAAGCTT TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20  TGAAGCGGGC TCCTCAAAGG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
    TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTCAGC AGTGCTCCTA      650
    CAAAAAATAA TTGCCGGTGT TGAGATCGGT TCGGGTATTT TGGGCAACGA      700
    CTCTTTGACT GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
    TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25  GCACCATTCG CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
    GCTCTATCGT AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTG      900
    TCACGGATCA AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
    TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
30  CTATCAAGAA CTACTACAAA AACTGCTTGT      1030

```

2) INFORMATION FOR SEQ ID NO: 1062

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1031 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

```

50  AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
    CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
    CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
    TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
    TGTGATACGA GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
    GGCTTTTGGC TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
55  TCCCATATAT CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
    TTGAATTGAT GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
    TTATGTATGA ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
    ACAAAGTGCT CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
    AAATCGAAGC TTTTATCCAG ACCCATGGCT TCCCAGTTTT CTTTAAGCCT      550
60  AATGAAGCGG GCTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

```

```

AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC 650
TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC 700
GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTCATTAG TAGACGGCTT 750
TTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCCTCC 800
5 CTGCGCCATT GCCTGAAACG ATTGAAACCA AGGTCAAAGA ACAAGCTCAG 850
CTGCTCTATC GTAGTCTTGG TCTTAAAGGT CTTGCTCGCA TCGACTTTTT 900
TGTCACGGAG CGAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG 950
GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCGGCTTA 1000
10 TCCTATCAAG AACTACTACA AAAACTGCTT G 1031

```

2) INFORMATION FOR SEQ ID NO: 1063

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

```

AACATGAAAA AAATCGCCAT TATTTTTTGA GGCAATTCAC CGGAATACAC 50
30 CGTTTCTTTA GCTTCAGCAA CTAGCGCAAT CGAAGCACTC CAATCATCTC 100
CCTATGACTA CGACCTCTCT TTGATCGGGA TCGCCCCAGA TGCTATGGAT 150
TGGTACTTGT ATACAGGAGA ACTGGAAAAC ATCCGACAAG ACACGTGGTT 200
GTTGGATACG AAACATAAAC AGAAAATACA GCCGCTATTT GAAGGAAACG 250
GCTTTTGGCT AAGTGAAGAG CAGCAAACGT TAGTACCTGA TATTTTATTT 300
35 CCCATTATGC ATGGCAAATA CGGGGAAGAT GGCAGTATCC AAGGATTGTT 350
TGAATTGATG AAACATACCTT ATGTAGGTTG CGGGGTGGCA GGTTCGCTT 400
TATGTATGAA CAAATGGCTG CTGCATCAAG CTGCAGCAGC CATTGGCGTA 450
CAAAGTGCTC CTACGATTCT CTTGACAAAT CAAGCCAACC AGCAAGAACA 500
AATCGAAGCT TTTATCCAGA CCCATGGCTT CCCAGTTTTC TTTAAGCCTA 550
40 ATGAAGCGGG CTCTTCAAAA GGGATCACTA AAGTCACCTG CGTTGAAGAA 600
ATCGCTTCTG CCTTAAAAAA AGCCTTTACT TATTGTTCCG CAGTGCTCCT 650
ACAAAAAAAT ATTGCCGGTG TTGAGATCGG TTGCGGTATT TTGGGCAACG 700
ACTCTTTGAC TGTCGGTGCT TGTGACGCCA TTTCATTAGT AGACGGCTTT 750
TTCGATTTTG AAGAAAAGTA CCAGCTGATC AGCGCCAAAA TCACCGTCCC 800
45 TGCGCCATTG CCTGAAACGA TTGAAACCAA GGTCAAAGAA CAAGCTCAGC 850
TGCTCTATCG TAGTCTTGGT CTTAAAGGTC TTGCTCGCAT CGACTTTTTT 900
GTCACGGATC AAGGAGAACT ATACTTGAAT GAAATCAATA CTATGCCGGG 950
CTTTACGAGT CACTCCCGTT ATCCTGCCAT GATGGCAGCG GTCGGCTTAT 1000
50 CCTATCAAGA ACTACTACAA AAACTGCTTG 1030

```

2) INFORMATION FOR SEQ ID NO: 1064

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

10	AAACATGAAA	AAAATCGCCA	TTATTTTGG	AGGCAATTCA	CCGGAATACA	50
	CCGTTTCTTT	AGCTTCAGCA	ACTAGCGCAA	TCGAAGCACT	CCAATCATCT	100
	CCCTATGACT	ACGACCTCTC	TTTGATCGGG	ATCGCCCCAG	ATGCTATGGA	150
	TTGGTACTTG	TATACAGGAG	AACTGGAAAA	CATCCGACAA	GACACGTGGT	200
	TGTTGGATAC	GAAACAGAAA	CAGAAAATAC	AGCCGCTATT	CGAAGGAAAC	250
	GGCTTTTGGT	TAAGTGAAGA	GCAGCAAACG	TTGGTACCTG	ATGTTTTATT	300
15	TCCCATTATG	CATGGCAAAT	ACGGGGAAGA	TGGCAGTATC	CAAGGATTGT	350
	TTGAATTGAT	GAAGCTACCT	TATGTAGGCT	GCGGGGTGGC	AGGTTCTGCC	400
	TTATGTATGA	ACAAATGGTT	GCTGCATCAA	GCTGCAGCAG	CCATTGGCGT	450
	ACAAAGTGCT	CCTACGATTC	TCTTGACAAA	TCACGCCAAC	CAGCAAGAAC	500
	AAATCGAAGC	TTTTATCCAG	ACCCATGGCT	TTCCAGTTTT	CTTTAAGCCT	550
20	AATGAAGCGG	GTTCTCAAA	AGGGATCACT	AAAGTCACCT	GCGTTGAAGA	600
	AATCGCTTCT	GCCTTAAAG	AAGCCTTTAC	TTATTGTTCC	GCAGTGCTCC	650
	TACAAAAAAA	TATTGCCGGT	GTTGAGATCG	GTTGCGGTAT	TTTGGGCAAC	700
	GACTCTTTGA	CTGTCGGTGC	TTGTGACGCC	ATTCATTAG	TAGACGGCTT	750
	TTTCGATTTT	GAAGAAAAGT	ACCAGCTGAT	CAGCGCCAAA	ATCACCGTCC	800
25	CTGCGCCATT	GCCTGAAACG	ATTGAAACTA	AGGTCAAAGA	ACAAGCTCAG	850
	CTGCTCTATC	GTAGTCTTGG	ACTTAAAGGT	CTTGCTCGCA	TCGACTTTTT	900
	TGTCACGGAT	CAAGGAGAAC	TATACTTGAA	TGAAATCAAT	ACTATGCCGG	950
	GCTTTACGAG	TCACTCCCGC	TATCCTGCCA	TGATGGCAGC	GGTCGGGTTA	1000
30	TCCTATCAAG	AACTACTACA	AAAACACTTT	GT		1032

2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

50	AAAAACATGA	AAAAAATCGC	CATTATTTTT	GGAGGCAATT	CACCGGAATA	50
	CACCGTTTCT	TTAGCTTCAG	CAACTAGCGC	AATCGAAGCA	CTCCAATCAT	100
	CTCCCTATGA	CTACGACCTC	TCTTTGATCG	GGATCGCCCC	AGATGCTATG	150
	GATTGGTACT	TGTATACAGG	AGAACTGGAA	AACATCCGAC	AAGACACGTG	200
	GTTGTTGGAT	ACGAAACATA	AACAGAAAAT	ACAGCCGCTA	TTCGAAGGAA	250
	ACGGCTTTTG	GCTAAGTGAA	GAGCAGCAAA	CGTTGGTACC	TGATGTTTTA	300
55	TTTCCCATTA	TGCATGGCAA	ATACGGGGAA	GATGGCAGTA	TCCAAGGATT	350
	GTTTGAATTG	ATGAAGCTGC	CTTATGTAGG	CTGCGGGGTG	GCAAGTTCTG	400
	CCTTATGTAT	GAACAAATGG	CTGCTGCATC	AAGCTGCAGC	AGCCATTGGC	450
	GTACAAAGTG	CTCCTACGAT	TCTCTTGACA	AATCAAGCCA	ACCAGCAAGA	500
	ACAAATCGAA	GCTTTTATCC	AGACCCATGG	CTTTCCAGTT	TTCTTTAAGC	550
60	CTAATGAAGC	GGGCTCCTCA	AAAGGGATCA	CTAAAGTCAC	CTGCGTTGAA	600

	GAAATCGCTT	CTGCCTTAAA	AGAAGCCTTT	ACTTATTGTT	CCGCAGTGCT	650
	CCTACAAAAA	AATATTGCCG	GTGTTGAGAT	CGGTTGCGGT	ATTTTGGGCA	700
	ACGACTCTTT	GACTGTCGGT	GCTTGTGACG	CCATTTTCATT	AGTAGACGGC	750
	TTTTTCGATT	TTGAAGAAAA	GTACCAGCTG	ATCAGCGCCA	AAATCACCGT	800
5	CCCTGCGCCA	TTGCCTGAAA	CGATTGAAAC	CAAGGTCAAA	GAACAAGCTC	850
	AGCTGCTCTA	TCGTAGTCTT	GGTCTTAAAG	GTCTTGCTCG	CATCGACTTT	900
	TTTGTACCGG	ATCAAGGAGA	ACTATACTTG	AATGAAATCA	ATACTATGCC	950
	GGGCTTTACG	AGTCACTCCC	GCTATCCTGC	CATGATGGCA	GCGGTCGGCT	1000
10	TATCCTATCA	AGAACTACTA	CAAAAACCTGC	TTGT		1034

2) INFORMATION FOR SEQ ID NO: 1066

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

	CATGAAAAAA	ATCGCCATTA	TTTTTGGAGG	CAATTCACCG	GAATACACCG	50
30	TTTCTTTAGC	CTCAGCAACT	AGCGCAATCG	AAGCACTCCA	ATCATCTCCC	100
	TATGATTACG	ACCTCTCTTT	GATCGGGATC	GCCCCAGATG	CTATGGATTG	150
	GTACTTGTAT	ACAGGAGAAC	TGGAAAACAT	CCGACAAGAC	ACGTGGTTGT	200
	TGGATACGAA	ACATACACAG	AAAATCCAGC	CACTTTTTGA	AGGAAACGGC	250
	TTTTGGATAA	GTGAAGCGCA	GCAAACGTTG	GTACCTGATG	TTTTATTTCC	300
35	CATTATGCAT	GGTAAATACG	GGGAAGATGG	CAGTATCCAA	GGATTGTTTG	350
	AATTGATGAA	GCTGCCTTAT	GTAGGCTGTG	GGGTGGCAGC	CTCTGCCTTA	400
	TGTATGAACA	AATGGTTATT	GCATCAAGCA	GCAGCAGCGA	TTGGCGTACA	450
	AAGCGCTCCT	ACGATTCTCT	TGACAAATCA	AGCCAACCAG	CAAAGACAAA	500
	TCGAAGCCTT	TATCCAGACC	CATGGCTTTC	CAGTTTTCTT	TAAGCCTAAT	550
40	GAAGCGGGCT	CCTCAAAAGG	GATCACAAAA	GTAACCTGTG	TTGAAGAAAT	600
	CGCTCCTGCC	TTGAAGGAAG	CCTTCGCTTA	TTGTTCCGCA	GTGCTCTTAC	650
	AAAAAAATAT	CGCTGGCGTT	GAGATTGGTT	GCGGTATCTT	AGGCAACGAC	700
	TCTTTGACTG	TCGGTGCTTG	TGACGCTATT	TCATTAGTAG	ACGGCTTTTT	750
	CGATTTTGAA	GAAAAGTACC	AGTTGATCAG	CGCCAAAATC	ACCGTTCCTG	800
45	CGCCATTGCC	TGAAACGATT	GAAACCAAAG	TCAAAGAACA	AGCTCAGCTG	850
	CTCTATCACA	GTCTTGCTCT	TAAAGGACTT	GCTCGCATCG	ACTTTTTTGT	900
	CACGGATCAA	GGAGAACTAT	ACTTGAATGA	AATCAATACT	ATGCCGGGCT	950
	TTACGAGTCA	CTCCCGCTAT	CCTGCCATGA	TGGCAGCGGT	CGGCTTATCC	1000
50	TATCAAGAAT	TA				1012

2) INFORMATION FOR SEQ ID NO: 1067

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

```

10 CTTACGCTTT ATCGATTAGA CACGGGNAGC TTGTCCAATG GGRAGCCGAT      50
   TTGATTTTAT GGATGAACGC TCTCATCATG CGGCAAATGG AATATCATGC      100
   AATGAAGCGC AAAATCGCAG ACGTTTGCGC TCCATCATGG AAAACAGTGG      150
   GTTTGAAGCA TATAGCCTCG AATGGTGGCA CTATGTATTA AGAGACGAAC      200
   CATACCCCAA TAGCTATTTT GATTTCCCGG TTAAATAAAC TTTTAACCGT      250
   TGCACGGACA AACTATATAA GCTAACTCTT TCGGCAGGAA ACCCGACGTA      300
15 TGTAAGTGGT TCTTAGGGAA TTTATATATA GTAGATAGTA TTGAAGATGT      350
   AAGGCAGAGC GATATTGCGG TCATTATCTG CGTGCGCTGC GGCAAGATAG      400
   CCTGATAATA AGACTGATCG CATAGAGGGG TGGTATTTCA CACCGCCCAT      450
   TGTCAACAGG CAGTTCAGCC TCGTTAAATT CAGCATGGGT ATCACTTATG      500
   AAAATTTCATC TACATTGGTG ATAATAGTAA ATCCAGTAGG GCGAAATAAT      550
20 TGACTGTAAT TTACGGGGCA AAACGGCACA ATCTCAAACG AGATTGTGCC      600
   GTTTAAGGGG AAGATTCTAG AAATATTTCA TACTTCCAAC TATATAGTTA      650
   AGGAGGAGAC TGAAAATGAA GAAGTTGTTT TTTTATTGTG TATTGTTATT      700
   CTTAATATAC TTAGGTTATT G                                721

```

25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 668 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R492

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

```

   ATTTTTAAGG ATGAACGCTC TTCATCATGC GGCAAATGGA ATATCATGCA      50
   ATGAAGCGCA AAATCGCAGA CGTTTGCGCT CCATCATGGA AAACAGTGGG      100
45 TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC TATGTATTAA GAGACGAACC      150
   ATACCCCAAT AGCTATTTTG ATTTCCCGGT TAAATAAACT TTAAACCGTT      200
   GCACGGACAA ACTATATAAG CTAACCTCTT CGGCAGGAAA CCCGACGTAT      250
   GTAAGTGGTT CTTAGGGAAT TTATATATAG TAGATAGTAT TGAAGATGTA      300
   AGGCAGAGCG ATATTGCGGT CATTATCTGC GTGCGCTGCG GCAAGATAGC      350
50 CTGATAATAA GACTGATCGC ATAGAGGGGT GGTATTTTAC ACCGCCCAT      400
   GTCAACAGGC AGTTCAGCCT CGTTAAATTC AGCATGGGTA TCACTTATGA      450
   AAATTTCATCT ACATTGGTGA TAATAGTAAA TCCAGTAGGG CGAAATAATT      500
   GACTGTAATT TACGGGGCAA AACGGCACA TCTCAAACGA GATTGTGCCG      550
   TTTAAGGGGA AGATTCTAGA AATATTTTCA ACTTCCAAC ATATAGTTAA      600
55 GGAGGAGACT GAAAATGAAG AAGTTGTTTT TTTTATTGTT ATTGTTATTC      650
   TTAATATACT TAGGTTAT

```

60 2) INFORMATION FOR SEQ ID NO: 1069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

```

15  CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT      50
    GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC      100
    GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT      150
    CCATCATGGA AACACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC      200
20  TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT      250
    TAAATAAACT TTTAACCGTT GCACGGACAA ACTATATAAG CTAACCTCTT      300
    CGGCAGGAAA CCCGACGTAT GTAAC TGGT CTTAGGGAAT TTATATATAG      350
    TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC      400
    GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT      450
25  GGTATTTTAC ACCGCCCAT GTCAACAGGC AGTTCAGCCT CGTTAAATTC      500
    AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA      550
    TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA      600
    TCTCAAACGA GATTGTGCCG TTTAAGGGGA AGATTCTAGA AATATTTCAT      650
    ACTTCCAAC TATATAGTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT      700
30  TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTTAAT      750
    GAAANCCTGA                                     760
  
```

2) INFORMATION FOR SEQ ID NO: 1070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

```

50  AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT      50
    GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGTAAC      100
    AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC      150
    AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA      200
55  TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT      250
    GTATTAAGAG ACGAACCATA CCCC AATAGC TATTTTGATT TCCCCGTTAA      300
    ATAAACTTTT AACCGTTGCA CGGACAAACT ATATAAGCTA ACTCTTTCGG      350
    CAGGAAACCC GACGTATGTA ACTGGTTCTT AGGGAATTTA TATATAGTAG      400
    ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG      450
60  CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT      500
  
```

ATTTACACACC	GCCCATTGTC	AACAGGCAGT	TCAGCCTCGT	TAAATTCAGC	550
ATGGGTATCA	CTTATGAAAA	TTCATCTACA	TTGGTGATAA	TAGTAAATCC	600
AGTAGGGCGA	AATAATTGAC	TGTAATTTAC	GGGGCAAAAC	GGCACAATCT	650
CAAACGAGAT	TGTGCCGTTT	AAGGGGAAGA	TTCTAGAAAT	ATTTCATACT	700
5 TCCAACATA	TAGTTAAGGA	GGAGACTGAA	AATGAAGAAG	TTGTTTTTTT	750
TTATTGTTAT	TGTTATTCTT	AATATACTTA	GGTTATGACT	ACGTTAATGA	800
A					801

10

2) INFORMATION FOR SEQ ID NO: 1071

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 711 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R684

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

TTGTACCAAT	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	50
GCGGCAAAATG	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	100
CTCCATCATG	GAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	150
30 ACTATGTATT	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	200
GTTAAATAAA	CTTTTAACCG	TTGCACGGAC	AACTATATA	AGCTAACTCT	250
TTCGGCAGGA	AACCCGACGT	ATGTAACGG	TTCTTAGGGA	ATTTATATAT	300
AGTAGATAGT	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	350
GCGTGCGCTG	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	400
35 GTGGTATTTT	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	450
TCAGCATGGG	TATCACTTAT	GAAAATTCAT	CTACATTGGT	GATAATAGTA	500
AATCCAGTAG	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	550
AATCTCAAAC	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	600
ATACTTCCAA	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	650
40 TTTTTTATTG	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	700
ATGAAGCACT	G				711

45 2) INFORMATION FOR SEQ ID NO: 1072

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072

60

	GCCATTGATC	TTACGCTTTA	TCGATTAGAC	ACGGGTNAGC	TTGTACCAAT	50
	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	GCGGCAAATG	100
	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	CTCCATCATG	150
	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	ACTATGTATT	200
5	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	GTTAAATAAA	250
	CTTTTAACCG	TTGCACGGAC	AAACTATATA	AGCTAACTCT	TTCGGCAGGA	300
	AACCCGACGT	ATGTAACCTG	TTCTTAGGGA	ATTTATATAT	AGTAGATAGT	350
	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	GCGTGCGCTG	400
	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	GTGGTATTTC	450
10	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	TCAGCATGGG	500
	TATCACTTAT	GAAAATTCAT	CTACATTGGT	GATAATAGTA	AATCCAGTAG	550
	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	AATCTCAAAC	600
	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	ATACTTCCAA	650
	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	TTTTTTTATTG	700
15	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	ATGAAGCACT	750
	G					751

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

35	ATTTGATTTT	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	50
	GCAATGAAGC	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	100
	GGGTTTGAAG	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	150
	ACCATACCCC	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	200
40	GTTGCACGGA	CAAACTATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	250
	TATGTAACTG	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	300
	GTAAGGCAGA	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	350
	AGCCTGATAA	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	400
	ATTGTCAACA	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	450
45	TGAAAATTCA	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	500
	ATTGACTGTA	ATTTACGGGG	CAAAACGGCA	CAATCTCAA	CGAGATTGTG	550
	CCGTTTAAGG	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	600
	TAAGGAGGAG	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	650
	TTCTTAATAT	ACTTAGGTTA	TGACTACGTT	AATGA		685

50

2) INFORMATION FOR SEQ ID NO: 1074

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

	ATCGATTAGA	CACGGGTGAG	CTTGTACCAA	TGGGGAGCCG	ATTTGATTTT	50
10	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	GCAATGAAGC	100
	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	GGGTTTGAAG	150
	CATATAGCCT	CGAATGGTGG	CACATATGTAT	TAAGAGACGA	ACCATACCCC	200
	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	GTTGCACGGA	250
	CAAACTATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	TATGTAACTG	300
15	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	GTAAGGCAGA	350
	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	AGCCTGATAA	400
	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	ATTGTCAACA	450
	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	TGAAAATTCA	500
	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	ATTGACTGTA	550
20	ATTTACGGGG	CAAAACGGCA	CAATCTCAAA	CGAGATTGTG	CCGTTTAAGG	600
	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	TAAGGAGGAG	650
	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	TTCTTAATAT	700
	ACTTAGGTTA	TGACTACGTT	AATGAAGCAC	TG		732

25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 670 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

	TCTCATCATG	CGGCAAATGG	AATATCATGC	AATGAAGCGC	AAAATCGCAG	50
	ACGTTTGC	TCCATCATGG	AAAACAGTGG	GTTTGAAGCA	TATAGCCTCG	100
45	AATGGTGGCA	CTATGTATTA	AGAGACGAAC	CATACCCCAA	TAGCTATTTT	150
	GATTTCCCCG	TTAAATAAAC	TTTTAACCGT	TGCACGGACA	AACTATATAA	200
	GCTAACTCTT	TCGGCAGGAA	ACCCGACGTA	TGTAACGGT	TCTTAGGGAA	250
	TTTATATATA	GTAAGATAGT	TTGAAGATGT	AAGGCAGAGC	GATATTGCGG	300
	TCATTATCTG	CGTGCGCTGC	GGCAAGATAG	CCTGATAATA	AGACTGATCG	350
50	CATAGAGGGG	TGGTATTTCA	CACCGCCCAT	TGTCAACAGG	CAGTTCAGCC	400
	TCGTAAAT	CAGCATGGGT	ATCACTTATG	AAAATTCATC	TACATTGGTG	450
	ATAATAGTAA	ATCCAGTAGG	GCGAAATAAT	TGACTGTAAT	TTACGGGGCA	500
	AAACGGCACA	ATCTCAAACG	AGATTGTGCC	GTTTAAGGGG	AAGATTCTAG	550
	AAATATTTCA	TACTTCCAAC	TATATAGTTA	AGGAGGAGAC	TGAAAATGAA	600
55	GAAGTTGTTT	TTTTTATTGT	TATTGTTATT	CTTAATATAC	TTAGGTTATG	650
	ACTACGTAA	TGAAGCACTG				670

60 2) INFORMATION FOR SEQ ID NO: 1076

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: Z36901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

```

ATGAAAATAA TAATTTT TAG AGTGCTAACT TTTTCTTTG TTATCTTTTC      50
TGTTAATGTG GTTGCGAAGG AATTACCTT AGATTCTCG ACAGCAAAGA      100
CGTATGTAGA TTCGCTGAAT GTCATTGCT CTGCAATAGG TACTCCATTA      150
20 CAGACTATTT CATCAGGAGG TACGTCTTTA CTGATGATTG ATAGTGGCAC      200
AGGGGATAAT TTGTTTGCAG TTGATGTCAG AGGGATAGAT CCAGAGGAAG      250
GGCGGTTTAA TAATCTACGG CTTATTGTTG AACGAAATAA TTTATATGTG      300
ACAGGATTTG TTAACAGGAC AAATAATGTT TTTTATCGCT TTGCTGATTT      350
TTCACATGTT ACCTTTCCTG GTACAACTGC GGTTACATTG TCTGGTGACA      400
25 GTAGCTATAC CACGTTACAG CGTGTTGCGG GGATCAGTCG TACGGGGATG      450
CAGATAAATC GCCATTCGTT GACTACTTCT TATCTGGATT TAATGTCGCA      500
TAGCGGAACC TCACTGACGC AGTCTGTGGC AAGAGCGATG TTACGGTTTG      550
TTACTGTGAC AGCTGAAGCT TTACGTTTTC GGCAAATTCA GAGGGGATTT      600
CGTACAACAC TTGATGATCT CAGTGGGCGT TCTTATGTAA TGACTGCTGA      650
30 AGATGTTGAT CTTACGTTGA ACTGGGGAAG GTTGAGTAGT GTCCTGCCTG      700
ACTATCATGG ACAAGACTCT GTTCGTGTTG GAAGAATTTC TTTTGGAAGT      750
GTTAATGCAA TTCTGGGTAG CGTGGCATT AACTGAATT GTCATCATCA      800
TGCATCGCGA GTTGCCAGAA TTGTACCTAA TGAGTTTCCT TCTATGTGCC      850
CGGTAGATGG AAGAGTGCGT GGGATTACGC ACAATAAAAT ATTGTGGGAC      900
35 TCATCCACTC TGGGGGCAAT TTTGATACGC AGGGCTATTA GCAGTTGA      948

```

2) INFORMATION FOR SEQ ID NO: 1077

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

```

CACCTGTATA TGAAGTGTAT ATTATTTAAA TGGGTACTGT GCCTGTTACT      50
GGGTTTTTCT TCGGTATCCT ATTCCCGGGA GTTTACGATA GACTTTTCGA      100
CCCAACAAAG TTATGTCTCT TCGTTAAATA GTATACGGAC AGAGATATCG      150
ACCCCTCTTG AACATATATC TCAGGGGACC ACATCGGTGT CTGTTATTAA      200
60 CCACACCCCA CCGGGCAGTT ATTTTGCTGT GGATATACGA GGGCTTGATG      250

```

	TCTATCAGGC	GCGTTTTGAC	CATCTTCGGC	TGATTATTGA	GCAAAATAAT	300
	TTATATGTGG	CCGGGTTCGT	TAATACGGCA	ACAAATACTT	TCTACCGTTT	350
	TTCAGATTTT	ACACATATAT	CAGTGCCCGA	TGTGACAACG	GTTTCCATGA	400
	CAACGGACAG	CAGTTATACC	ACTCTGCAAC	GTGTCGCAGC	GCTGGAACGT	450
5	TCCGGAATGC	AAATCAGTCG	TCACTCACTG	GTTTCATCAT	ATCTGGCGTT	500
	AATGGAGTTC	AGTGGTAATA	CAATGACCAG	AGATGCATCC	AGAGCAGTTC	550
	TGCGTTTTGT	CACTGTCACA	GCAGAAGCCT	TACGCTTCAG	GCAGATACAG	600
	AGAGAATTTT	GTCAGGCACT	GTCTGAAACT	GCTCCTGTGT	ATACCATGAC	650
	GCCGGGAGAC	GTGGACCTCA	CTCTGAACTG	GGGGCGAATC	AGCAATGTGC	700
10	TTCCGGAGTA	TCGGGGAGAG	GATGGTGTCA	GAGTGGGGAG	AATATCCTTT	750
	AATAATATAT	CAGCGATACT	GGGTACTGTG	GCCGTTATAC	TGAATTGCCA	800
	TCATCAGGGG	GCGCGTTCTG	TTCGCGCCGT	GAATGAAGAG	AGTCAACCAG	850
	AATGTCAGAT	AACTGGCGAC	AGGCCCGTTA	TAAAAATAAA	CAATACATTA	900
	TGGGAAAGTA	ATACAGCTGC	AGCGTTTCTG	AACAGAAAGT	CACAGTTTTT	950
15	ATATACAACG	GGTAAATAAA	GGAGTTAAGT	ATGAAGAAGA	TGTTTATGGC	1000
	GGTTTTATTT	GCATTAGTTT	CTGTTAATGC	AATGGCGGCG	GATTGTGCTA	1050
	AAGGTAAAAT	TGAGTTTTTC	AAGTATAATG	AGGATGACAC	ATTTACAGTG	1100
	AAGGTTGACG	GGAAAGAATA	CTGGACCAGT	CGCTGGAATC	TGCAACCGTT	1150
	ACTGCAAAGT	GCTCAGCTGA	CAGGAATGAC	TGTCACAATC	AAATCCAGTA	1200
20	CCTGTGAATC	AGGCTCCGGA	TTTGCTGAAG	TGCAGTTTAA	TAATGACTGA	1250
	GGCATAACC					1259

25 2) INFORMATION FOR SEQ ID NO: 1078

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1079

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55

2) INFORMATION FOR SEQ ID NO: 1080

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 25 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

10 TATAGCTACT GTCACCAGAC AATGT 25

2) INFORMATION FOR SEQ ID NO: 1081

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA 20

2) INFORMATION FOR SEQ ID NO: 1082

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40 TTGARCRAAA TAATTTATAT GTG 23

45 2) INFORMATION FOR SEQ ID NO: 1083

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT 20

60

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

CTACTCCCGC CTTTGGGTT

20

2) INFORMATION FOR SEQ ID NO: 1087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

5 2) INFORMATION FOR SEQ ID NO: 1088

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20

TCGGCAAGAC AATATGACAG C

21

2) INFORMATION FOR SEQ ID NO: 1093

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: CSsa-165

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	AAAGGAAATG	250
AATCATGAAA	CAATTAACTA	AGCCTTTATA	CTTTTACCTA	TTACTTTTTA	300
TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

50

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAACAG GTACTTCTAA CTA .

23

2) INFORMATION FOR SEQ ID NO: 1095

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

TCTTCAAAAT CGAAAAAGCC GTC

23

2) INFORMATION FOR SEQ ID NO: 1099

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

TCAAAAGGGA TCACWAAAGT MAC

23

2) INFORMATION FOR SEQ ID NO: 1100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

GTAAAKCCCG GCATRGTRTT GATTTC

26

2) INFORMATION FOR SEQ ID NO: 1101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

GACGGYTTTT TYGATTTTGA AGA

23

2) INFORMATION FOR SEQ ID NO: 1102

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

2) INFORMATION FOR SEQ ID NO: 1103

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

2) INFORMATION FOR SEQ ID NO: 1104

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

2) INFORMATION FOR SEQ ID NO: 1105

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

CTCCTACGAT TCTCTTGAYA AATCA

2) INFORMATION FOR SEQ ID NO: 1106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

CAACCGATCT CAACACCGGC AAT

23

2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

CTCATTTGAC TTCCTCCTTT GCT

23

2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

GTAAGAATCG GAAAAGCGGA AGG

23

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

2) INFORMATION FOR SEQ ID NO: 1110

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

CTTTTCCGG CTCGWYTTCC TGATG

25

2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

GGCTGYGATA TTCAAAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

40

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

55

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

60

2) INFORMATION FOR SEQ ID NO: 1117

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 801 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: 94
(C) ACCESSION NUMBER: U94526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

AAATTCGATC CGCACTACAT CGGAATTACA AAAAACGGTG TATGGAAGCT 50
ATGCAAGAAG CCATGTACGG AATGGGAAGC CGACAGTCTC CCCGCCATAC 100
TCTCCCCGGA TAGGAAAACG CATGGGCTGC TTGTCATGAA AGAAAGCGAA 150
20 TACGAAACAC GGC GTATTGA TGTGGCTTTC CCGGTTTTGC ATGGCAAATG 200
CGGGGAGGAT GGTGCGATAC AGGGGCTGTT TGTATTGTCT GGTATCCCCT 250
ATGTGGGCTG TGATATTCAA AGCTCCGCAG CTTGCATGGA CAAATCACTG 300
GCCTACATTC TTACAAAAAA TGCGGGCATC GCCGTTCCCG AATTTCAAAT 350
GATTGATAAA GGTGACAAGC CGGAGGCGGG TGC GCTTACC TACCCTGTCT 400
25 TTGTGAAGCC GGCACGGTCA GGTTCGTCCT TTGGCGTAAC CAAAGTAAAC 450
GGTACGGAAG AACTTAACGC TGCGATAGAA GCGGCAGGAC AATATGATGG 500
AAAAATCTTA ATTGAGCAAG CGATTTTCGGG CTGTGAGGTC GGGTGTGCGG 550
TCATGGGGAA CGAGGATGAT TTGATTGTCG GCGAAGTGGA TCAAATCCGG 600
CTGAGCCACG GTATCTTCCG CATCCATCAG GAAAACGAGC CGGAAAAAGG 650
30 CTCAGAAAAT GCGATGATTA CAGTTCCCGC AGACATTCCG GTCGAGGAAC 700
GAAATCGGGT GCAGGAAACG GCAAAGAAAG TATATCGGGT GCTTGGATGC 750
AGAGGGCTTG CCCGTGTTGA TCTTTTTTTT CAGGAGGATG GCGGCATCGT 800
T 801

35

2) INFORMATION FOR SEQ ID NO: 1118

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

TTTTTCWGAGC CTTTTTCCGG CTCG 24
50

2) INFORMATION FOR SEQ ID NO: 1119

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC

25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG

24

2) INFORMATION FOR SEQ ID NO: 1121

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

35

TGTTTGWATT GTCYGGYATC CC

22

2) INFORMATION FOR SEQ ID NO: 1122

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCATTG CTACGTGG

18

2) INFORMATION FOR SEQ ID NO: 1123

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

60

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

10 TTTCGGGCTG TGAGGTCGGB TG 22

2) INFORMATION FOR SEQ ID NO: 1124

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTTGRTCC ACYTCGCCRA CA 22

2) INFORMATION FOR SEQ ID NO: 1125

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40 ACTCACAAC TGGATGGATG 20

45 2) INFORMATION FOR SEQ ID NO: 1126

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

60 TTATGGTTGT GCTGGTTGAG G 21

2) INFORMATION FOR SEQ ID NO: 1127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

2) INFORMATION FOR SEQ ID NO: 1128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

2) INFORMATION FOR SEQ ID NO: 1129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

ATGATGACHG AMATGATGAA AAC

23

2) INFORMATION FOR SEQ ID NO: 1130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130

5 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

20

35

2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

50

2) INFORMATION FOR SEQ ID NO: 1134

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAACCTT CCT

23

2) INFORMATION FOR SEQ ID NO: 1135

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

CATTATGCAA ACGCCATTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T

21

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTTGAY GAA

23

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

	ATGAAAAAAA	TTGCCGTTTT	ATTTGGAGGG	AATTCTCCAG	AATACTCAGT	50
	GTCAC TAACC	TCAGCAGCAA	GTGTGATCCA	AGCTATTGAC	CCGCTGAAAT	100
15	ATGAAGTAAT	GACCATTTGGC	ATCGCACCAA	CAATGGATTG	GTATTGGTAT	150
	CAAGGAAACC	TCGCGAATGT	TCGCAATGAT	ACTTGGCTAG	AAGATCACAA	200
	AAACTGTCAC	CAGCTGACTT	TTTCTAGCCA	AGGATTTATA	TTAGGAGAAA	250
	AACGAATCGT	CCCTGATGTC	CTCTTTCCAG	TCTTGCATGG	GAAGTATGGC	300
	GAGGATGGCT	GTATCCAAGG	ACTGCTTGAA	CTAATGAACC	TGCCTTATGT	350
20	TGGTTGCCAT	GTGCTGCTCT	CCGCATTATG	TATGAACAAA	TGGCTCTTGC	400
	ATCAACTTGC	TGATACCATG	CGAATCGCTA	GTGCTCCAC	TTTGCTTTTA	450
	TCCCGCTATG	AAAACGATCC	TGCCACAATC	GATCGTTTTA	TTCAAGACCA	500
	TGGATTCCCG	ATCTTTATCA	AGCCGAATGA	AGCCGGTTCT	TCAAAAGGGA	550
	TCACAAAAGT	AACTGACAAA	ACAGCGCTCC	AATCTGCATT	AACGACTGCT	600
25	TTTGCTTACG	GTTCTACTGT	GTTGATCCAA	AAGGCGATAG	CGGGTATTGA	650
	AATTGGCTGC	GGCATCTTAG	GAAATGAGCA	ATTGACGATT	GGTGCTTG TG	700
	ATGCGATTTT	TCTTGTCGAC	GGTTTTTTTG	ATTTTGAAGA	GAAATACCAA	750
	TTAATCAGCG	CCACGATCAC	TGTCCCAGCA	CCATTGCCTC	TCGCGCTTGA	800
	ATCACAGATC	AAGGAGCAGG	CACAGCTGCT	TTATCGAAAC	TTGGGATTGA	850
30	CGGGTCTGGC	TCGAATCGAT	TTTTTCGTCA	CCAATCAAGG	AGCGATTTAT	900
	TTAAACGAAA	TCAACACCAT	GCCGGGATTT	ACTGGGCACT	CCCGCTACCC	950
	AGCTATGATG	GCGGAAGTCG	GGTTATCCTA	CGAAATATTA	GTAGAGCAAT	1000
	TGATTGCACT	GGCAGAGGAG	GACAAACGAT	GA		1032

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1768 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 50 (C) ACCESSION NUMBER: X56895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

	GATATCGTTA	CGCTTCATGT	GCCGCTCAAT	ACGGATACGC	ACTATATTAT	50
55	CAGCCACGAA	CAAATACAGA	GAATGAAGCA	AGGAGCATT	CTTATCAATA	100
	CTGGGCGCGG	TCCACTTGTA	GATACCTATG	AGTTGGTTAA	AGCATTAGAA	150
	AACGGGAAAC	TGGGCGGTGC	CGCATTGGAT	GTATTGGAAG	GAGAGGAAGA	200
	GTTTTTCTAC	TCTGATTGCA	CCCAAAAACC	AATTGATAAT	CAATTTT TAC	250
	TTAAACTTCA	AAGAATGCCT	AACGTGATAA	TCACACCGCA	TACGGCCTAT	300
60	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAAACTG	350

	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	400
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	450
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	500
	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	550
5	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	600
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	650
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	700
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	750
	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	800
10	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	850
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	900
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	950
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	1000
	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	1050
15	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	1100
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	1150
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	1200
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	1250
	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1300
20	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1350
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1400
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTAGAT	GAAATAGTAC	1450
	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1500
	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAGTT	1550
25	GGCTGAATCG	CTTTTGAAGG	CAAAAGAACT	GGCTGCTACC	CAAGGGTACG	1600
	GATTGCTTCT	ATGGGACGGT	TACCGTCCTA	AGCGTGCTGT	AAACTGTTTT	1650
	ATGCAATGGG	CTGCACAGCC	GGAAAATAAC	CTGACAAAGG	AAAGTTATTA	1700
	TCCCAATATT	GACCGAACTG	AGATGATTTT	AAAAGGATAC	GTGGCTTCAA	1750
	AATCAAGCCA	TAGCCGCG				1768
30						

2) INFORMATION FOR SEQ ID NO: 1140

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1086 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
- 45 (C) ACCESSION NUMBER: L29638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

	GTAAGAATCG	GAAAAGCGGA	AGGAAGAAAA	ACATGAAAAA	AATCGCCATT	50
50	ATTTTTTGAG	GCAATTCACC	GGAATACACC	GTTTCTTTAG	CTTCAGCAAC	100
	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	CTATGACTAC	GACCTCTCTT	150
	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	GGTACTTGTA	TACAGGAGAA	200
	CTGGAAAAACA	TCCGACAAGA	CACGTGGTTG	TTGGATACGA	AACATAAACA	250
	GAAAATACAG	CCGCTATTTC	AAGGAAACGG	CTTTTGGCTA	AGTGAAGAGC	300
55	AGCAAACGTT	GGTACCTGAT	GTTTTATTTC	CCATTATGCA	TGGCAAATAC	350
	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	GAATTGATGA	AGCTGCCTTA	400
	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	ATGTATGAAC	AAATGGCTGC	450
	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	AAAGTGCTCC	TACGATTCTC	500
	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	ATCGAAGCTT	TTATCCAGAC	550
60	CCATGGCTTC	CCAGTTTTTCT	TTAAGCCTAA	TGAAGCGGGC	TCCTCAAAAG	600

	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	TCGCTTCTGC	CTTAAAAGAA	650
	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	CAAAAAAATA	TTGCCGGTGT	700
	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	CTCTTTGACT	GTCGGTGCTT	750
	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	TCGATTTTGA	AGAAAAGTAC	800
5	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	GCGCCATTGC	CTGAAACGAT	850
	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	GCTCTATCGT	AGTCTTGCTC	900
	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	TCACGGAGCG	AGGAGAACTA	950
	TACTTGAATG	AAATCAATAC	TATGCCGGGC	TTTACGAGTC	ACTCCCGCTA	1000
	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	CTATCAAGAA	CTACTACAAA	1050
10	AACTGCTTGT	CTTAGCAAAG	GAGGAAGTCA	AATGAG		1086

2) INFORMATION FOR SEQ ID NO: 1141

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 25 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: extracted from M97297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

30	ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
	TGCATTCCAT	GCTCTTTCGC	CTCGCTTTGG	CGTTATGGCA	ACGATAATTA	100
	ACGCCAACGT	GTCGGAATCC	AACGCCAAAT	CCGCGCCTTT	CAATCAATGT	150
	ATCAGTGTGG	GACATAAATC	AGAGATTTCC	GCCTCTATTC	TTCTTGCGCT	200
	GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
35	ATATAGATAC	AACTGCTGCT	AAGAGAATTG	GCATCACTGT	CGACAATGTG	300
	GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTTCTTAT	350
	GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
	TCAGGTTGGA	CAGCGACCGT	GGCAAGGTAC	TCAGCGACAT	GACAGTTGGT	450
	GTGGTGGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
40	ATTTGGATGT	AAAGTGTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
	ACTATGTACC	GTTTGATGAG	TTGCTGCAAA	ATAGCGATAT	CGTTACGCTT	600
	CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
	ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
	TTGTAGATAC	CTATGAGTTG	GTTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
45	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
50	TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
	TGCTATTTCAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
55	CTTTGCATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
60	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550

	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
5	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCC	TGTGGATATG	TTTTTACAAG	1850
	ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
10	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGGAAAACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
	GAAGGCAAAA	GAAGTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	GCTGTAAACT	GTTTTATGCA	ATGGGCTGCA	2250
15	CAGCCGGAAA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAAAG	GATACGTGGC	TTCAAAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
20	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
	CGGCAGGAAA	CCCGACGTAT	GTAACGTGTT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
25	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCAT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACCTTATGA	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	2900
	TCCAGTAGGG	CGAAATAAAT	GACTGTAAAT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTAT	3000
30	ACTTCCAAC	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAAAT	ATGATCAAAA	3150
	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
35	AGTAAATATC	CTGTTCCGCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
40	TACCAGCAGG	TTATAGTGAG	CATAATTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAAATGGA	ACGAGCCCCT	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTCGCTA	TGTTGGTTTA	3700
	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
45	GGATTACCTA	AAAGAAGAAA	AAACCATTTC	TGTTAGTGTA	AATGGGGAAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTTACTA	AAAATACCAC	CATTCATGTG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAAGG	AGGTAA	3946

50

2) INFORMATION FOR SEQ ID NO: 1142

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

2) INFORMATION FOR SEQ ID NO: 1143

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

TGTYTTCCAA GGTTTCAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40

GACTTTGTTT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

20

2) INFORMATION FOR SEQ ID NO: 1151

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

20

2) INFORMATION FOR SEQ ID NO: 1152

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

2) INFORMATION FOR SEQ ID NO: 1153

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

CTCGTATGTC CCTACAATGC

20

2) INFORMATION FOR SEQ ID NO: 1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

GTTTGAAGCA TATAGCCTCG

20

2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

CAGTGCTTCA TTAACGTAGT C

21

2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

GTTGAAATGC ATCACGAACA ATT

23

2) INFORMATION FOR SEQ ID NO: 1157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

5

2) INFORMATION FOR SEQ ID NO: 1158

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

20 AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

35

TGAAGGTTTG CCAGGTGA

18

40 2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

50

CGTTTCTGTT AAAGAAATTA GAAG

24

55

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

GTTGGTTTCA ACGTTAAGAA C

21

2) INFORMATION FOR SEQ ID NO: 1164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

GGTTTCAACG TCAAGAAC

18

2) INFORMATION FOR SEQ ID NO: 1165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

2) INFORMATION FOR SEQ ID NO: 1166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

2) INFORMATION FOR SEQ ID NO: 1167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

2) INFORMATION FOR SEQ ID NO: 1168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

GAACAATTGG TTGAAGGTGT

2) INFORMATION FOR SEQ ID NO: 1169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: SP-665
 (C) ACCESSION NUMBER: AF139883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

20	ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
	CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
	ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
	ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
25	TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
	TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
	ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
	TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
	ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
30	GCTTGGTTAG	CGATTTCAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
	GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
	AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
	CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
	CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
35	CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
	GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
	TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
	AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
	AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
40	TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
	TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACCTGGAGC	TCGTCACCAA	1050
	GCAAGTAAAC	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
	CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
	ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
45	TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
	TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
	TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
	GGTCTTGTTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
	TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
50	CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
	TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
	TGTCGGAAC	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
	TGATGAAAAC	AGTCTTGACT	TATGGAAC	GGCGTGGAGC	CTATCTTCCT	1650
	TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
55	AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
	TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCTG	1800
	AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCTAGTTG	CAGCTAAAGT	1850
	TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
	GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950
60	GGAGCTCGCC	CAATATGGAC	TGAACCCTCT	ACTCAACAAT	CCTCAACAGC	2000

TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

5

2) INFORMATION FOR SEQ ID NO: 1170

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

40 2) INFORMATION FOR SEQ ID NO: 1172

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1560 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: 64147
(C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

GATCCTCTAA	ATGATTCTCA	GGTGGCTGTT	ATTGCCTCTA	TTTCAAAGGA	50
GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	GGATAGAAAG	GTTTTGGAAA	100
CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	CCAGTGAAAA	AGCTGGTCTC	150
60 CCAGCGGAAG	AAGCAGAAGC	CTATCTTAA	AAAGGCTATT	CTCTAAATGA	200

641

	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
5	TCAATTGAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCTAT	450
	GCAGTCGCCC	TTAACCCTAA	AACAGGTGCT	GTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTGAGGA	AATCAGACCT	TGACAGACCA	650
10	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCTTGG	TATCCTGCCT	700
	TTTCTAGACC	AATGCCGATT	ACGGCGGTTT	AGGCTCTAGA	GTATTCATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCCTAGGT	CTTATGGGGC	AGACCTATCA	800
	ACCCAATATG	TTTGTGCGCA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
15	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	AAAGAGTATA	GCTTTGCTAA	950
	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAACCTATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	ATGGTGTTTCG	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	GATAAGGGAG	GAATGAGTGA	1100
	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
20	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
	ACTAGTGAAT	TGACAACTGG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAAATGGTGT	1400
25	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

30

2) INFORMATION FOR SEQ ID NO: 1173

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2007 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: CS109
 45 (C) ACCESSION NUMBER: Z49096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
50	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
55	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGTCTA	350
	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAACCTC	400
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGCATTA	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGAACTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
60	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600

	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
5	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	850
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
10	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	1100
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
15	AGTTGGGACG	GACCTCTAT	ATGGAAGTAT	GTATAATCAC	TACACAGGAA	1350
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1400
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
20	GGAGAATTTG	CCACCCCAAT	CTTGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTAAGTGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
25	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1850
	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
30	TAATATG					2007

2) INFORMATION FOR SEQ ID NO: 1174

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTCGC

18

2) INFORMATION FOR SEQ ID NO: 1175

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

5 2) INFORMATION FOR SEQ ID NO: 1176

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20 2) INFORMATION FOR SEQ ID NO: 1177

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

20

35 2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2456 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC8325
(C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

ATGAACTGAT	TATACTTAAC	ATTAAAAAAG	ATGATAACAC	CTTCTACACC	50
55 TCCATATCAC	AAAAAATTAT	AACATTATTT	TGACATAAAT	ACTACATTTG	100
TAATATACTA	CAAATGTAGT	CTTATATAAG	GAGGATATTG	ATGAAAAAGA	150
TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	GTTTGGTATA	200
TATTTTATG	CTTCAAAAGA	TAAAGAAATT	AATAATACTA	TTGATGCAAT	250
TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	TATATTTCTA	300
60 AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	AAAAATATAT	350

	AATAGTTT	AG	CGT	TAA	AG	TATA	AA	CATT	CAG	GAT	CG	TAA	AAAA	AAAA	400
	AGTATCT	AAA	AA	TAAAA	AA	C	GAG	TAG	AT	G	TCA	AT	ATA	AAAA	450
	ACTACG	GTA	CA	TTG	AT	CG	AA	CGT	T	CA	AT	T	T	T	500
	GGTATG	TG	GA	AG	T	AG	AT	TG	GG	AT	CA	T	AG	C	550
5	GAAAG	AC	CA	AG	C	A	T	A	C	A	T	A	T	A	600
	TTTTAG	AC	CG	AA	CA	AT	GT	G	A	AT	TG	CC	A	T	650
	TTAGGC	AT	CG	TT	CA	AA	GA	A	TG	T	CT	TA	AA	A	700
	TAAAGA	ACT	A	AG	T	A	T	T	CT	G	A	A	C	A	750
	TTGGGT	AC	AA	G	A	T	A	C	T	A	T	A	T	A	800
10	GATGA	A	T	A	T	T	A	A	G	T	A	T	T	T	850
	AACAG	AA	AG	T	C	G	T	A	A	T	A	T	C	T	900
	GTTAT	G	T	T	G	T	C	C	A	T	T	A	A	C	950
	GGCTA	T	A	A	A	G	A	T	G	C	A	G	T	A	1000
	CGATA	A	A	A	A	G	A	T	G	G	C	T	A	T	1050
15	ATAAT	A	G	C	A	A	T	C	G	C	A	T	A	A	1100
	GGCAA	A	G	A	T	A	A	C	T	A	A	C	T	A	1150
	TAACA	A	C	A	T	G	A	T	A	T	A	T	A	T	1200
	CAGGT	G	A	A	T	A	T	A	T	A	T	A	T	A	1250
	TTTAT	G	T	A	T	G	A	T	A	T	A	T	A	T	1300
20	AAAAG	A	A	A	C	C	T	G	C	T	C	A	C	A	1350
	CTCAA	A	A	A	A	A	T	A	A	C	A	G	A	T	1400
	GATAA	A	A	A	C	A	A	G	T	T	A	A	A	A	1450
	TTGGG	G	T	G	G	T	A	C	A	A	C	G	T	T	1500
	ACTTA	A	A	A	C	A	A	G	C	A	T	A	G	A	1550
25	GCACT	C	G	A	T	G	A	A	T	T	G	A	A	A	1600
	TGTTG	G	T	G	T	G	A	A	T	T	T	G	A	A	1650
	CAAAC	A	A	A	A	A	A	T	T	A	T	A	T	A	1700
	CAAGG	T	G	A	A	A	T	A	T	A	T	A	T	A	1750
	ATTAG	A	A	A	A	A	T	A	T	A	T	A	T	A	1800
30	AAAAC	A	A	A	A	A	G	T	T	G	G	A	A	A	1850
	TTAA	A	T	G	A	T	G	A	T	A	T	A	T	A	1900
	TTAT	A	G	A	T	C	T	A	T	G	C	A	A	A	1950
	AAAT	G	A	A	A	C	A	A	G	T	G	G	A	A	2000
	GATA	A	A	G	A	T	A	T	A	T	A	T	A	T	2050
35	AGATA	A	A	G	A	G	A	A	G	T	A	T	A	T	2100
	ATGAG	C	T	A	T	A	T	A	T	A	T	A	T	A	2150
	AACAG	T	G	A	A	G	A	A	G	T	A	T	A	T	2200
	TATTA	A	T	A	A	T	A	A	G	T	A	T	A	T	2250
	TTGT	A	T	G	T	T	G	A	C	A	C	A	T	A	2300
40	TTTCT	T	A	T	T	T	T	T	C	A	T	A	T	A	2350
	AGTTT	A	A	T	A	A	T	A	A	T	A	T	A	T	2400
	TCCGT	A	T	T	T	A	T	A	T	A	T	A	T	A	2450
	GCAT	G	C												2456

45

2) INFORMATION FOR SEQ ID NO: 1179

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

ATTGTTGAC GGGTGACTTT

60

20

2) INFORMATION FOR SEQ ID NO: 1180

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
10 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180
15 TCCACCGTTG CCAATCGCA 19

2) INFORMATION FOR SEQ ID NO: 1181

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181
30 AGCAGCTTAC TAGATGCCGT 20

2) INFORMATION FOR SEQ ID NO: 1182

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182
AACTGCAAGA GATCCTTTGG 20

2) INFORMATION FOR SEQ ID NO: 1183

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2535 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: 175
 (C) ACCESSION NUMBER: M18729

5

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
10	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTTTATG	100
	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
15	GTTGTAAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCTGA	350
	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGA	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
20	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
	AGCTTTGAAG	ACCTTCATTT	ATTGGATTG	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCTTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
25	CTCAGGTAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTTTTATG	1000
	ACATTGAGCG	CTTGGCTAGT	CGTGTTTCTT	TTGGCAAAAC	CAATCCAAAG	1050
30	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	AGTGTGCCAC	GGATTCGTGC	1100
	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTTGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	CAGAGAAGGG	ACTAGCTGGA	1300
35	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCAGCTC	1350
	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTC	1400
	GCAACTGGGA	AATGTGCCAG	CCCAC'TTTTT	CCGCAAGGCG	ACGCTGAAAA	1450
	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	CCCGTATCGA	GGGAGATATG	1500
	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	GAATACGAAA	TATTTATGCG	1550
40	CATTCGTGAA	GAGGTCGGCA	AGTACATCCA	GCGTTTACAA	GCTCTAGCCC	1600
	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	GTCTGGCGGT	TGTGGCTGAA	1650
	ACCCAGCATT	TGATTTCGACC	TGAGTTTGGT	GACGATTCAC	AAATTGATAT	1700
	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAAA	GGTTATGGGG	GCTCAGACCT	1750
	ATATTCCAAA	TACGATTTCAG	ATGGCAGAAG	ATACCAGTAT	TCAATTGGTT	1800
45	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	TATATGCGTC	AGTTAGCCAT	1850
	GACGGCGGTT	ATGGCCAGC	TGGGTTCCTA	TGTTCTGTCT	GAAAGCGCCC	1900
	ATTTACCGAT	TTTTGATGCG	ATTTTACCC	GTATCGGAGC	AGCAGATGAC	1950
	TTGGTTTCGG	GTCAGTCAAC	CTTTATGGTG	GAGATGATGG	AGGCCAATAA	2000
	TGCCATTTTCG	CATGCGACCA	AGAACTCTCT	CATTCTCTTT	GATGAATTGG	2050
50	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	CTCTTGCTCA	GTCCATCATC	2100
	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	ACCTCTTTTG	CGACCCACTA	2150
	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	ACAACACTTG	GTCAATGTCC	2200
	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	TCACCTTCCT	TCACAAGATT	2250
	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	ATCCATGTTG	CCAAGATTGC	2300
55	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	GGATAAGATT	TTGACTCAGC	2350
	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	CCATGAGACA	AACTAGTGCT	2400
	GTCACTGAAC	AGATTTCACT	CTTTGATAGG	GCAGAAGAGC	ATCCTATCCT	2450
	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	TATGACACCT	ATGCAGGTTA	2500
60	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	TATAA		2535

2) INFORMATION FOR SEQ ID NO: 1184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGCG	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TTG			623

2) INFORMATION FOR SEQ ID NO: 1185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
55	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
60	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550

CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC T 621

5

2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

20 (xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

25 TGACGGGTGA CTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350
 GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
 30 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCCT TCTTGGATTC 450
 ATCGCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
 CAGGTCTTTC TCGACCATT TTTGAGCGT AGTGACTTGA CAGACAGTCT 550
 CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC TT 622

35

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

55 TGACGGGTGA CTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCGGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 60 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350

GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGATTTC	450
ATCGCCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
5 CAAGGGTGTT	TATGACATTG	AGCGCTTGCG	TAGTCGTGTT	TCTTTTGGCA	600
AAACCAATCC	AAAGGATCTC	TT			622

10 2) INFORMATION FOR SEQ ID NO: 1188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

25	GGGTGACTTT	TATGTAACGG	GGCTATTGGA	TTTCACGTTG	GTTTGTGGGG	50
	AAATTCGCAA	TCTCAAGGCT	AGAGAAGTGG	TGCTGGGTTA	TGACTTGTCT	100
	GAGGAAGAAG	AACAAATCCT	CAGTCGTCAG	ATGAATCTGG	TGCTTTCTTA	150
	TGAGAAGGAA	GGCTTTGAGG	ACCTTCATTT	ACTGGATCCA	CGACTGGCAG	200
30	CTGTGGAGCA	AGCGGCAGCT	AGTAAGCTCC	TCCAGTATGT	TCACCGGACC	250
	CAGATGCGGG	AATTGAACCA	CCTCAAACCA	GTTATCCGCT	ATGAAATCAA	300
	AGATTTCTTA	CAGATGGACT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	350
	AGAATGCCCG	TTCAGGCAAG	AAGCAAGGCA	GTCTTTTCTG	GCTTTTAGAT	400
	GAAACCAAGA	CGGCTATGGG	AATGCGTCTC	TTGCGTTCTT	GGATTCATCG	450
35	TCCTTTGATT	GATAAGGAGC	GAATCGTCCA	GCGTCAAGAG	GTGGTGCAGG	500
	TCTTTCTTGA	CCACTTCTTT	GAGCGTAGTG	ATTTAACGGA	CAGTCTTAAG	550
	GGTGTTTATG	ATATCGAACG	CTTGGCTAGT	CGGGTTTCTT	TTGGCAAGA	599

40

2) INFORMATION FOR SEQ ID NO: 1189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

GGTGACGGGT	GACTTTTATG	TGACAGGTCT	TTTGGATTTT	ACGCTGGTTT	50
GTGGGGAAAT	CCGCAATCTC	AAGGCTCGAG	AAGTGGTGCT	GGGTTATGAC	100
TTGTCTGAGG	AAGAAGAACA	GATCCTTAGT	CGTCAGATGA	ATCTGGTACT	150
60 TTCTATGAA	AAAGAAGGCT	TTGAAGACCT	TCATTTACTG	GATTCACGAT	200

	TGGCAGCTGT	GGAGCAAGCG	GCATCTAGTA	AACTGCTTCA	GTATGTTTCAT	250
	CGGACTCAGA	TGAGGGAATT	GAACCACCTC	AAGCCTGTTA	TCCGCTATGA	300
	AATCAAAGAT	TTTTTGCAGA	TGGATTATGC	GACCAAGGCT	AGTCTGGATT	350
	TGGTTGAGAA	TGCCCCGTTCA	GGCAAGAAGC	AAGGTAGTCT	TTTTTGGCTT	400
5	TTGGATGAAA	CCAAAACAGC	TATGGGAATG	CGTCTCTTGC	GGTCTTGGAT	450
	TCATCGCCCC	CTGATTGATA	AGGAACGAAT	TGTCCAACGC	CAAGAAGTTG	500
	TGCAGGTCTT	TCTCGACCAT	TTCTTTGAGC	GTAGTGATTT	GACAGACAGT	550
	CTCAAGGGTG	TTTATGACAT	TGAGCGCTTG	GCTAGTCGTG	TTTCTTTTGG	600
	CAAAACCAAT	CCAAAGGATC	TCTT			624

10

2) INFORMATION FOR SEQ ID NO: 1190

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGT	CTTGGTCTGC	50
30	GGGGAAATCC	GCAATTTGAA	AGCTAGGGGA	GTGGTGCTGG	GCTATGCCTT	100
	GCCAGAAGCT	GAGGAGCAGG	TTTTGGCTGG	ACAGATGAAC	CTTTTACTGT	150
	CCTATGTGGA	GAAGGTTTTG	GAGGATGTTC	AGCTGCTGGG	CGAGGAGCTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCAGGGAAA	CTGCTGGAGT	ATGTGCACCG	250
	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCTCAG	CATTATGAAA	300
35	TCAAGGACTT	CCTGCAAATG	GACTATGCCA	CCAAGGCGAG	TCTGGATTTG	350
	ACAGAAAATG	CTCGCTCGGG	CAAGAAGCAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACT	AAGACGGCCA	TGGGCGGCCG	CATGCTGCGC	TCTTGATCC	450
	AGCGTCCGCT	GATTGATGAA	GCGCGAATTA	GCCAGCGACA	GAATGTCGTT	500
	GAGGTTTTTC	TGGATCATTT	CTTTGAGCGG	AGTGATTTGA	CGGAGAGCCT	550
40	CAAGGGGGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGC	599

2) INFORMATION FOR SEQ ID NO: 1191

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

60	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGC	CCTGGTCTGC	50
----	------------	------------	------------	------------	------------	----

	GGGGAAATCC	GTAATTTGAA	GGCTAGGGAA	GTGGTGCTGG	GCTATGCTTT	100
	GCCAGAAGCT	GAGGAGCAGG	TCTTGGCTGG	ACAGATGAAT	CTTTTGCTGT	150
	CCTATGTACA	GACGGCCTTG	GACGATGTCC	AGCTGCTGGG	CGAGGAACTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCGGGGAAA	TTGCTAGAGT	ATGTGCACCG	250
5	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCCAG	CATTATGAAA	300
	TCAAGGACTT	TCTGCAAATG	GATTATGCTA	CCAAGGCGAG	TCTGGATTTG	350
	ACAGAAAATG	CTCGCTCGGG	TAAGAAACAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACC	AAGACGGCCA	TGGGCGGCCG	TATGCTGCGC	TCTTGGATCC	450
	AGCGTCCGTT	GATTGATGAA	GTGCGAATTA	GCCAGCGGCA	GAATGTCGTC	500
10	GAGGTTTTTC	TGGAACATTT	CTTTGAGCGG	AGTGATTTGA	CGGAGAGCCT	550
	CAAGGGAGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGCA	600
	AGACCAATCC	AAAGGATCTC	TT			622

15

2) INFORMATION FOR SEQ ID NO: 1192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

30

2) INFORMATION FOR SEQ ID NO: 1193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

45

2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

60

CATTTC AAGT AATACAACAG AATC

24

5 2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTTC AAGT AACACAAC TG AATC

24

20 2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTC AA GTAATACAAC AGAA

24

35 2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

50 2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

	AACGGGCGTC	TCGATAGAAA	AACACGTGAA	AATCCCAATG	ATTATAAACA	50
10	ATCAATATAC	GATTTTGCTG	AAGCTGTAAC	AAAAGGTATT	AAGGAACAAA	100
	CAAATAAAAA	TTAATAGGCA	ACTTAACCAG	AATCGTTAAA	ACTATATGAC	150
	GATTCTGGTT	TTTTAAATTC	AAAAAGTTTT	CTAAAAAATT	TACTTGCTTC	200
	TTTAAAGTAT	AGGTATGAAA	TACAATTGAT	TAAAATAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAATAA	GCCTTTATAC	TTTTACCTAT	TACTTTTTAT	300
15	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAKGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT	A		381

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC

25

35 2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

40 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAAA GCTGT

25

50 2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

GTGTTGAAAT GTTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

GGIGARMGIG GIAAYGARAT G

21

2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

655

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

TCAAAAAGTT TTCTAAAAAA TTTAC

25

2) INFORMATION FOR SEQ ID NO: 1209

656

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA

2) INFORMATION FOR SEQ ID NO: 1210

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

2) INFORMATION FOR SEQ ID NO: 1211

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

2) INFORMATION FOR SEQ ID NO: 1212

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

CCICIRGIG GIGAIACIGC WCC

2) INFORMATION FOR SEQ ID NO: 1213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

AARGGIGGIA CIGCIGCIAT HCCIGG

26

2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

GGTAAAACAG GTACCTCTAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: D471
- (C) ACCESSION NUMBER: X65717

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

AACAAAATAA	AAGAACTTAC	CTATTTTCCA	TCCAAAATGT	TTAGCAATCA	50
TCATCTGCAA	GGCAACGTAT	TGCATGGCAT	TGATGTGATG	AGCAACTAAT	100
ATGTCATTAG	AACGTTGCGT	CAAACTAGCA	TCTAAATAAA	GATCGAAATG	150
CAGTTATCAA	AAATGCAAGC	TCCTATCGGC	CCTTGTTTTA	ATTATTACTC	200
ACATTGCCTT	AATGTATTTA	CTTGCTTATT	ATTAACTTTT	TTGCTAAGTT	250
AGTAGCGTCA	GTTATTCATT	GAAAGGACAT	TATTATGAAA	ATTCTTGTA	300
CAGGCTTTGA	TCCCTTTGGC	GGCGAAGCTA	TTAATCCTGC	CCTTGAAGCT	350
ATCAAGAAAT	TGCCAGCAAC	CATTCATGGA	GCAGAAATCA	AATGTATTGA	400

	AGTTCCAACG	GTTTTTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
	AAAGCTTTCA	ACCTGATGCA	GTCCTTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
	ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
	TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
5	GTAAAGCAGC	TTATTTTTC	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
	ATTCATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAATACAG	CTGGTACCTT	700
	TGTTTGCAAT	CATTTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
	GTCCAAATGC	CAAAGCTGGG	TTTATGCATA	TTCCCTTTAT	GATGGAACAG	800
	GTTGTTGATA	AACCTAATAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
10	AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTTCAAA	GATCGTTCGG	900
	ATTTAAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
	TATTTTAAAA	AAACAGAGAT	ATGAATAAC	TCTGTTTTTT	TTGTGCTAAA	1000
	AATGAAAGAC	CTAGGGAAAC	TTTTCATCGG	TCTTTCTCAA	TTGTCATCTT	1050
	AATCTAATAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
15	AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAACAT	TAAGGTCAGG	1150
	GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TAACAAAGGA	CTAATATCAT	1200
	AGGTGGCTAC	CACCTTTCCA	GAATCAGGTT	GGAGTTTGAC	AATAGTATTG	1250
	GTTTGCCAAA	TATTGGCATA	GAGATAACCA	TCTACATACT	CTAATTCGTT	1300
	AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

2) INFORMATION FOR SEQ ID NO: 1216

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1217

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50

CAAATGCCAT TTCAAGTAAC ACAAC

25

55 2) INFORMATION FOR SEQ ID NO: 1218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

10

2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

55 GAYACICCCIG GICAYGTIGA YTT

23

60

2) INFORMATION FOR SEQ ID NO: 1222

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222

ATYGAYACIC CIGGICAYGT IGAYTT

26

2) INFORMATION FOR SEQ ID NO: 1223

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223

AYITCIARRT GIARYTCRCC CATICC

26

2) INFORMATION FOR SEQ ID NO: 1224

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224

CCIGYIHTIY TIGARCCAT IATG

24

2) INFORMATION FOR SEQ ID NO: 1225

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225

TAICCRAACA TYTCISMIAR IGGIAC

26

2) INFORMATION FOR SEQ ID NO: 1226

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226
15 GTIRMRTAIC CRAACATYTC 20

2) INFORMATION FOR SEQ ID NO: 1227

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227
30 GTICCIYTIK CIGARATGTT YGGITA 26

2) INFORMATION FOR SEQ ID NO: 1228

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228
GTICCIYTIK CIGARATGTT YGGITAYGC 29

2) INFORMATION FOR SEQ ID NO: 1229

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCI GT IATCAT

26

5 2) INFORMATION FOR SEQ ID NO: 1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC 150
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA 350
 TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTCAG CCGCAGTCTG 400
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTGCGTTC 450
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTTAACCA 500
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550
 GTGCTGAAGA ACATTTACC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700
 35 AATCCGACAG TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750
 GAAGAAGTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850
 GTGTTACAGC GATGCTGGAT GCGGTAATTG ATTACCTGCC ATCCCCGGTT 900
 GACGTACCTG CGATCAACGG TATCCTGGAC GACGGTAAAG ACACTCCGGC 950
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000
 TCGCTACCGA CCCGTTTGTT GGTAACCTGA CCTTCTTCCG TGTTTACTCC 1050
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100
 TGAGCGTTTC GGTGCTATCG TTCAGATGCA CGCTAACAAA CGTGAAGAGA 1150
 TCAAAGAAGT TCGCGCGGGC GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200
 45 GTAACCACTG GTGACACCCT GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450
 50 AGCGTGAATT CAACGTTGAA GCGAAGCTAG GTAAACCGCA GGTGTGTTAC 1500
 CGTGAAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550
 ACAGTCTGGT GGTCGTGGTC AGTATGGTCA TGTTGTTATC GACATGTACC 1600
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTTG ATAAAGGTAT 1700
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750
 TGGGTATTTC TCTGCACTTC GGTCTTACC ATGACGTTGA CTCCTCTGAA 1800
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTAAAGAAG GCTTTAAGAA 1850
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG ACTTGAGCCG TCGTCGTGGT 1950
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GCGGTTAAGA TCCACGCTGA 2000

AGTACCGCTG	TCTGAAATGT	TCGGATACGC	AACTCAGCTG	CGTTCTCTGA	2050
CCAAAGGTCG	TGCATCATAC	ACTATGGAAT	TCCTGAAGTA	TGATGAAGCG	2100
CCGAGTAACG	TTGCTCAGGC	CGTAATTGAA	GCCCGTGGTA	AATAA	2145

5

2) INFORMATION FOR SEQ ID NO: 1231

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

2) INFORMATION FOR SEQ ID NO: 1232

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

2) INFORMATION FOR SEQ ID NO: 1233

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

55 2) INFORMATION FOR SEQ ID NO: 1234

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
60 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

10

2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

25

2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 34 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTCG CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

55

GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

60

2) INFORMATION FOR SEQ ID NO: 1238

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC

38

2) INFORMATION FOR SEQ ID NO: 1239

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC

33

2) INFORMATION FOR SEQ ID NO: 1240

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC

38

2) INFORMATION FOR SEQ ID NO: 1241

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC

35

2) INFORMATION FOR SEQ ID NO: 1242

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 600 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (E) STRAIN: BM4147-1
 (F) ACCESSION NUMBER: U39790
- 15 (xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

20	TTCTTAGAGA	CATTGAATAT	GCCTTATGTC	GGCGCAGGCG	TATTGACCAG	50
	TGCATGTGCC	ATGGATAAAA	TCATGACCAA	GTATATTTTA	CAAGCTGCTG	100
	GTGTGCCGCA	AGTTCCTTAT	GTACCAGTAC	TTAAGAATCA	ATGGAAAGAA	150
	AATCCTAAAA	AAGTATTTGA	TCAATGTGAA	GGTTCTTTGC	TTTATCCGAT	200
	GTTTGTCAAA	CCTGCGAATA	TGGGTTCTAG	TGTCGGCATT	ACAAAGGCAG	250
25	AAAACCGAGA	AGAGCTGCAA	AATGCTTTAG	CAACAGCCTA	TCAGTATGAT	300
	TCTCGAGCAA	TCGTTGAACA	AGGAATTGAA	GCGCGCGAAA	TCGAAGTTGC	350
	TGTATTAGGA	AATGAAGATG	TTCGGACGAC	TTTGCCTGGC	GAAGTCGTAA	400
	AAGACGTAGC	ATTCTATGAT	TATGAAGCCA	AATATATCAA	TAATAAAATC	450
	GAAATGCAGA	TTCCAGCCGA	AGTGCCGGAA	GAAGTTTATC	AAAAAGCGCA	500
30	AGAGTACGCG	AAGTTAGCTT	ACACGATGTT	AGGTGGAAGC	GGATTGAGCC	550
	GGTGCGATTT	CTTTTTGACA	AATAAAAATG	AATTATTCCT	GAATGAATTA	600

35 2) INFORMATION FOR SEQ ID NO: 1243

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

50 (xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

50	GGTACCAAAG	AAAAAAACGA	ACGCCACAAC	CAACAGCCTC	TAAAGCAACA	50
	CCTGCTTCTG	AAATTGAGGG	AGATTTAGCA	AATGTCAATG	AGATTCTTTT	100
	GGTTCACGAT	GATCGTGTCG	GGTCAGCAAC	GATGGGAATG	AAAGTCTTAG	150
	AAGAAATTTT	AGATAAAGAG	AAAATTTCAA	TGCCGATTCG	AAAAATTAAT	200
55	ATTAATGAAT	TAACCAACA	AACACAGGCT	TTAATTGTCA	CAAAAGCTGA	250
	ACTAACGGAA	CAAGCACGTA	AAAAGCACC	GAAAGCGACA	CACTTATCAG	300
	TAAAAAGTTA	TGGTTAATCC	CCAAAAATAT	GAAACAGTGG	GTTTCGCTCT	350
	TAAAAGAAAG	TGCCTAGAGA	GGAAGAAAAC	AATGGAAAAT	CTTACGAATA	400
	TTTCAATTGA	ATTAAATCAA	CAGTTTAATA	CAAAAGAAGA	AGCTATTTCG	450
60	TTTTCCGGCC	AGAAACTAGT	CGAGGCAGGC	TGTGTTGAGC	CCGCTTATAT	500

	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAAGAAG	CCAAAAAATT	AGTGAAAAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
	AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
5	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
10	TTAAAAGAAC	GTAAAAGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
	ACAAATTAAC	GTTGAAAATG	TGACCGGGTT	AAATAACATG	ACAGAACCAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCGCTGGAT	ATTATCGCTT	1200
15	GTGAAAATAT	GATTGGTGGT	TCAACCTTTT	TAGCAGAAGA	AGTGGCCATA	1250
	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCCTGATGC	1300
	GGCAGTTGAT	CGGATTGTTC	CATTACAAAA	ACATAAAGAT	CCACTTTTGT	1350
	TTCAAGTTGA	GCCTTTTTGT	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAGTTAGA	AGGCGTCATT	ACTTGTCGAT	TAGAGCCGTA	1450
20	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAAATCAGT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAAATAAAT	ATATTTTCAGA	TGCTATTACA	1700
25	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCGCAAG	AACGGTTTAT	1750
	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCT	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAGATCCAG	AAACGGTTAA	AAATATTAAA	1950
30	CAAAACGTAG	AACCTGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACTTTGGG	2100
	AGGTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTAAA	CTTAAACTTG	2150
	TTCATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
35	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
	GAACTTGGTG	AAGAAGGGGG	GATCC			2275

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

55	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTGCGGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATT	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
60	CCAGCCAAAA	CGATATTTTT	ATAATCATT	CGTGAAAAAG	GTTTCCCTTC	250

ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

2) INFORMATION FOR SEQ ID NO: 1245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCCAC	AGATGGACTT	150
GTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
ACTTAGATGG	TGAGGTTCCCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
CAAGCACCTG	CATTCGAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATAACCAC	GAAATGAGCG	550
ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGCCCGT	750
ATGCCATCTG	CGGTAGGTTA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800
ATTACAAGAG	CGTATTACAT	CTACAAATAA	AGGGTCTATC	ACGTC	845

2) INFORMATION FOR SEQ ID NO: 1246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 11986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

TGCACTTCAT	TTAGGTGATG	ACACAGTTCG	TACAGTTGCA	ATGTCTTCCA	50
------------	------------	------------	------------	------------	----

	CAGATGGACT	TGTTTCGTGGC	ACAGAAGTAG	AAGATACTGG	TAAAGCAATC	100
	TCTGTACCA	TTGGTGATGT	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	150
	TGATGCAATT	GACTTAGATG	GTGATGTTCC	TGCGGATGTA	CGTCGTGATC	200
	CAATTCACCG	TCAAGCGCCT	GCATTCGAAG	AGTTATCTAC	TAAAGTAGAA	250
5	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	300
	GGGTGGTAAG	ATTGGTCTAT	TCGGTGGTGC	CGGCGTAGGT	AAAACAGTAT	350
	TAATTCAGGA	ATTAATTAAT	AACATCGCAC	AAGAGCACGG	TGGTATCTCT	400
	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAAGGTAACG	ACTTATACCA	450
	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	500
10	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCATT	AACAGGTTTA	550
	ACAATGGCTG	AACATTTCCG	TGATGAGCAA	GGACAAGACG	TACTATTGTT	600
	CATCGATAAC	ATCTTCCGTT	TCACGCAAGC	GGGTTCTGAA	GTATCTGCCC	650
	TTCTTG					656

15

2) INFORMATION FOR SEQ ID NO: 1247

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

	CGAAACGGA	AGTATTA	ACTTA	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTTCGT		100
35	GGCACAGAAG	TAGAAGATAC	TGGTAAACCA	ATCTCTGTAC	CAGTTGGTGA		150
	TGTAACACTT	GGTCGCGTAT	TTAACGTATT	AGGTGATGCA	ATTGACTTAG		200
	ATGGTGAGGT	TCCTGCAGAT	GTACATCGTG	ATCCAATTCA	CCGTCAAGCA		250
	CCTGCATTTCG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AACTGGTAT		300
	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC		350
40	TATTCGGTGG	TGCCGGCGTA	GGTAAACAG	TATTAATTCA	GGAATTAATT		400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTTCG	CTGGTGTAGG		450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG		500
	GCGTAATCAA	GAAAACTGCG	ATGGTATTTCG	GACAAATGAA	CGAGCCACCT		550
	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT		600
45	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC		650
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA		700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA		750
	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT	A		791

50

2) INFORMATION FOR SEQ ID NO: 1248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: BGSC 4AC1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

15	ATCTACAATG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAAGCATGAA	50
	CTTAACATTT	GAAGTTGCAC	TTCATTTAGG	TGATGATACA	GTTCGTACAG	100
	TTGCGATGTC	TTCCACAGAT	GGACTTGTTT	GTGGCACAGA	AGTAGAAGAT	150
	ACTGGTAAAG	CAATCTCTGT	ACCAAGTTGGT	GATGCAACAC	TTGGACGTGT	200
	ATTCAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAA	CTTCCTGCGG	250
20	ATGTACACCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAAC	AGTATTAATT	CAGGAGTTAA	TCAATAACAT	CGCACAAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
25	TAATGACTTA	TACCACGAAA	TGAGCGATTC	TGGCGTAATC	AAGAAAACCTG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
	GCATTAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTTCATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
30	CCAACACTTG	CAACAGAAAT	GGGTCAATTA	CAAGAGCGTA	TTACATCTAC	800
	AAATAAAGGG	TCTATCACGT	CTATC			825

35 2) INFORMATION FOR SEQ ID NO: 1249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

50	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAAGTATTAA	50
	CTTAACATTT	GAAGTTGCAC	TTCATTTAGG	TGATGATACA	GTTCGTACAG	100
	TTGCGATGTC	TTCCACAGAT	GGACTTGTTT	GTGGCACAGA	AGTAGAAGAT	150

	ACTGGTAAAC	CAATCTCTGT	ACCAGTTGGT	GATGTAACAC	TTGGTCGCGT	200
	ATTTAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAG	GTTCTGTCAG	250
	ATGTACATCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
5	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAC	AGTATTAATT	CAGGAATTAA	TTAACAACAT	CGCACAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
	TAATGACTTA	TACCACGAAA	TGAGCGATTC	TGGCGTAATC	AAGAAAAC TG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
10	GCATTAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTTCATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
	CCAACACTTG	CAACAGAAAT	GGGTC			775

15

2) INFORMATION FOR SEQ ID NO: 1250

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10204

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

	CCAGCAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAGC	50
	GAGCATCAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	GATGACACAG	100
35	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTTCG	TGGCACAGAA	150
	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	ATGTAACACT	200
	TGGTCGCGTA	TTCAACGTAT	TAGGTGATGC	AATTGACTTA	GATGGTGATG	250
	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	ACCTGCATTC	300
	GAAGAACTAT	CTACAAGAAT	AGAAATTCTT	GAAACTGGTA	TTAAAGTAGT	350
40	AGATTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACG	GTATTAATTC	AGGAATTAAT	TAACAACATC	450
	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	GTGAGCGTAC	500
	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	GGCGTAATTA	550
	AGAAAAC TGC	GATGGTATTT	GGACAAATGA	ACGAGCCACC	TGGAGCACGT	600
45	CAACGTGTTG	CATTAACAGG	TTTAACAATG	GCTGAACATT	TCCGTGATGA	650
	GCAAGGACAA	GACGTACTAT	TGTTTCATCGA	TAACATCTTC	CGTTTCACGC	700
	AAGCAGGTTT	TGAAGTATCT	GCCCTTCTTG	GTCGTATGCC	ATCTGCGGTA	750
	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	AAGAGCGTAT	800
50	TACATCTACA	AATAAAGGGT	CTATCACGTC	TA		832

2) INFORMATION FOR SEQ ID NO: 1251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

```

15 AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT      50
   AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC      100
   AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG      150
   ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC      200
20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCCCTGC      250
   AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT      300
   TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA      350
   CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTTC GTGGTGCCGG      400
   CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATTAACAAC ATCGCACAAAG      450
25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG      500
   GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC      550
   TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG      600
   TTGCATTAAC AGGTTTAACA ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA      650
   CAAGACGTAC TTCTGTTTCA CGATAACATC TTCCGTTTCA CGCAAGCGGG      700
30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTTACC      750
   AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT      800
   AC                                                                802

```

2) INFORMATION FOR SEQ ID NO: 1252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

```

AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT      50
AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC      100

```

	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	GAAGTAGAAG	150
	ATACTGGTAA	ACCAATCTCT	GTACCAGTTG	GTGATGTAAC	ACTTGGTCGC	200
	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	AGGTTCTCTC	250
	AGATGTACAT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	TTCGAAGAAT	300
5	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	AGTAGACTTA	350
	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCG	GTGGTGCCGG	400
	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATTAACAAC	ATCGCACAAAG	450
	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	TCAAGAAAAC	550
10	TGCGATGGTA	TTCCGACAAA	TGAACGAGCC	ACCTGGAGCA	CGTCAACGTG	600
	TTGCATTAAC	AGGCTTAACA	ATGGCTGAGC	ATTTCCGTGA	TGAGCAAGGA	650
	CAAGACGTAC	TTCTGTTCAT	CGATAACATC	TTCCGTTTCA	CGCAAGCGGG	700
	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	GTAGGTTACC	750
	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	TATTACATCT	800
15	ACAAATAAAG	GGTCTATCAC	GTC			823

2) INFORMATION FOR SEQ ID NO: 1253

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

35	CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	CATGAACCTTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCGTGG	CACAGAAGTA	150
	GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTTGGTGATG	CAACACTTGG	200
	ACGTGTATTTC	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAACCTC	250
40	CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
	CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AATTAATCAA	TAACATCGCA	450
	CAAGAGCATG	GTGGTATCTC	TGTATTCGCT	GGTGTAGGTG	AGCGTACTCG	500
45	TGAGGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
50	TACCAACCGA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATT	798

2) INFORMATION FOR SEQ ID NO: 1254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	ACACAGTTCG	TACAGTTGCA	50
ATGTCTTCCA	CAGATGGACT	TGTTTCGTGGC	ACAGAAGTAG	AAGATACTGG	100
TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	AACACTTGGT	CGTGTATTTA	150
ACGTATTAGG	TGATGCAATT	GACTTAGATG	GTGAGGTTCC	TGCGGATGTA	200
CGTCGTGATC	CAATTCACCG	TCAAGCACCT	GCATTCGAAG	AATTATCTAC	250
TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	300
CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	TCGGTGGTGC	CGGTGTAGGT	350
AAAACGGTAT	TAATTCAGGA	ATTAATCAAT	AACATCGCAC	AAGAACACGG	400
TGGTATCTCT	GATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAGGGTAATG	450
ACTTATACCA	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	500
GTATTCGGAC	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCGTT	550
AACAGGTTTA	ACAATGGCTG	AGCATTTCGG	TGATGAGCAA	GGACAAGACG	600
TACTTCTGTT	CATCGATAAT	ATCTTCCGTT	TCACGCAAGC	AGGTTCTGAA	650
GTATCTGCC	TTCTTGCCG	TATGCCATCT	GCGGTAGGTT	ACCAACCAAC	700
ACTTGCAACA	GAAATGGGTC	AATTACAAGA	GCGTATTACA	TCTACAAATA	750
AAGGGTCTAT	CACGTCT				767

2) INFORMATION FOR SEQ ID NO: 1255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: C-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

GAAATGCGTG	AATCATTTTT	AGATTATGCG	ATGAGTGTTA	TCGTTGCTCG	50
TGCATTGCCA	GATGTTTCGTG	ACGGTTTAAA	ACCAGTACAT	CGTCGTATAC	100

	TATATGGATT	AAATGAACAA	GGTATGACAC	CGGATAAATC	ATATAAAAAA	150
	TCAGCACGTA	TCGTTGGTGA	CGTAATGGGT	AAATATCACC	CTCATGGTGA	200
	CTTATCTATT	TATGAAGCAA	TGGTACGTAT	GGCTCAAGAT	TTCAGTTATC	250
	GTTATCCGCT	TGTTGATGGC	CAAGGTAAC	TTGGTTCAAT	GGATGGAGAT	300
5	GGCGCAGCAG	CAATGCGTTA	TACTGAAGCG	CGTATGACTA	AAATCACACT	350
	TGAACTGTTA	CGTGATATTA	ATAAAGATAC	AATAGATTTT	ATCGATAACT	400
	ATGATGGTAA	TGAAAGAGAG	CCGTCAGTCT	TACCTGCTCG	ATTCCCTAAC	450
	TTATTAGCCA	ATGGTGCATC	AGGTATCGCG	GTAGGTATGG	CAACGAATAT	500
	TCCACCACAT	AACTTAACAG	AATTAATCAA	TGGTGTACTT	AGCTTAAGTA	550
10	AGAACCCTGA	TATTTCAATT	GCTGAGTTAA	TGGAGGATAT	TGAAGGTCCT	600
	GATTTCCCAA	CTGCTGGACT	TATTTTAGGT	AAGAGTGGTA	TTAGACGTGC	650
	ATATGAAACA	GGTCGTGGTT	CAATTCAAAT	GCGTTCTCGT	GCAGTTATTG	700
	AAGAACGTGG	AGNCGGACGT	CAACGTATTG	TTGTCACTGA	AATTCCTTTC	750
	CAAGTGAATA	AGGCTCGTAT	GATTGAAAAA	ATTGCAGAGC	TCGTTCTGTA	800
15	CAAGAAAATT	GACGGTATCA	CTGATTTACG	TGATGAAACA	AGTTTACGTA	850
	CTGGTGTGCG	TGTCGTTATT	GATGTGCGTA	AGGATGCAAA	TGCTAGTGTC	900
	ATTTTAAATA	ACTTATACAA	ACAAACACCT	CTTCAAACAT	CATTTGGTGT	950
	GAATATGATT	GCACTTGTA	ATGGTAGACC	GAAGCTTATT	AATTTAAAG	1000
	AAGCGTTGGT	ACATTATTTA	GAGCATCAAA	AGACAGTTGT	TAGAAGACGT	1050
20	ACGCAATACA	ACTTACGTAA	AGCTAAAGAT	CGTGCCACA	TTTTAGAAGG	1100
	ATTACGTATC	GCACTTGACC	ATATCGATGA	AATTATTTC	ACGATTCGTG	1150
	AGTCAGATAC	AGATAAAGTT	GCAA			1174

25

2) INFORMATION FOR SEQ ID NO: 1256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAGCAAGCAT	50
	TAACTTAACA	TTTGAAGTTG	CACTTCATTT	AGGTGATGAC	ACAGTTCGTA	100
	CAGTTGCAAT	GTCTTCCACA	GATGGACTTG	TTCGTGGCAC	AGAAGTAGAA	150
45	GATACTGGTA	AAGCAATCTC	TGTACCAGTT	GGTGATGTAA	CACTTGGTGC	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGA	GATGTTCTTG	250
	CGGATGTACG	TCGTGATCCA	ATTCACCGTC	AAGCGCCTGC	ATTCGAAGAG	300
	TTATCTACTA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
	ACTTGCTCCT	TACATTAAGG	GTGGTAAGAT	CGGTCTATTC	GGTGGTGCCG	400
50	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTAATCGTGA	500
	AGGTAACGAC	TTATACCACG	AAATGAGCGA	TTCTGGCGTA	ATTAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGAGC	ACGTCAACGT	600

GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCTGT	ATGAGCAAGG	650
GCAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
GTTCTGAAGT	ATCTGCCCTT	CTTGGTCGTA	TGCCATCTGC	GGTAGGTTAC	750
CAGCCAACAC	TTGCAACAGA	AATGGGTCAA			780

5

2) INFORMATION FOR SEQ ID NO: 1257

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 7700

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	ACGAAAACGG	50
25 AACAAGCATT	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGACA	100
CAGTTCGTAC	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
ACTTGGTCGT	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
AGGTTTCCTGC	GGATGTACGT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
30 TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGTCTATTCG	400
GTGGTGCCGG	TGTAGGTAAA	ACGGTATTAA	TTCAGGAATT	AATCAATAAC	450
ATCGCACAAAG	AACACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	500
TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
35 TTAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
CGTCAACGTG	TTGCGTTAAC	AGGTTTAAACA	ATGGCTGAGC	ATTTCCGTGA	650
TGAGCAAGGA	CAAGATGTAC	TTCTGTTTAT	CGATAATATC	TTCCGTTTCA	700
CGCAAGCAGG	TTCTGAAGTA	TCTGCCCTTC	TTGGCCGTAT	GCCATCTGCG	750
GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
40 TATTACATCT	ACAAATA				817

2) INFORMATION FOR SEQ ID NO: 1258

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

	CCAGAAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	TATTAAGTTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCTGTG	CACAGAAGTA	150
10	GAAGATACTG	GTAAACCAAT	CTCTGTACCA	GTTGGTGATG	TAACACTTGG	200
	TCGCGTATTT	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAGGTTT	250
	CTGCAGATGT	ACATCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTGCGA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
15	CCGGCGTAGG	TAAACAGTA	TTAATTCAGG	AATTAATTAA	CAACATCGCA	450
	CAAGAGCACG	GTGGTATCTC	TGTATTCTGCT	GGTGTAGGTG	AGCGTACTCG	500
	TGAGGGTAAT	GAATTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCTGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
20	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
	TACCAACCAA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATTAC	800
	ATCTACAAAT	AAAGGGTCTA	TCACGTCTA			829

25

2) INFORMATION FOR SEQ ID NO: 1259

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 844 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

	TGGCGGAAAG	CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	50
45	ACGAAAACGG	TGAAGTTAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	100
	GATGATACAG	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTTCG	150
	TGGCACAGAA	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	200
	ATGCAACACT	TGGTCGCGTA	TTTAACGTAT	TAGGTGATGC	TATTGACTTA	250
	GATGGTGAGG	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	300
50	ACCTGCATTC	GAAGAATTAT	CTACTAAAGT	AGAAATTCTT	GAAACTGGTA	350
	TTAAAGTAGT	AGACTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGC	400
	CTATTCGGTG	GTGCCGGTGT	AGGTAAAACA	GTATTAATTC	AGGAGTTAAT	450
	CAACAACATC	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	500

	GTGAGCGTAC	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	550
	GGCGTAATTA	AGAAAAGTGC	GATGGTATTC	GGACAAATGA	ACGAGCCACC	600
	TGGAGCACGT	CAACGTGTTG	CATTAACAGG	CTTAACAATG	GCTGAATATT	650
	TCCGTGATGA	GCAAGGACAA	GACGTACTTC	TGTTTCATCGA	TAATATCTTC	700
5	CGTTTCACGC	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GCCGTATGCC	750
	ATCTGCGGTA	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	800
	AAGAGCGTAT	TACATCTACA	AATAAAGGGT	CTATCACGTC	TATC	844

10

2) INFORMATION FOR SEQ ID NO: 1260

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 840 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 49064

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

	AAGCTACCAG	AAATCTACAA	CGCCCTTACG	GTAAAACAGA	GCAACGAAAA	50
	CGGAACAAGC	ATTAAGTTAA	CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	100
	ACACAGTTCG	TACAGTTGCA	ATGTCTTCCA	CAGATGGACT	TGTTCTGTCG	150
30	ACAGAAAGTAG	AAGATACTGG	TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	200
	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	TGATGCAATT	GACTTAGATG	250
	GTGAGGTTCC	TGCGGATGTA	CGCCGTGATC	CAATTCACCG	TCAAGCACCT	300
	GCAATCGAAG	AATTATCTAC	TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	350
	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	400
35	TCGGTGGTGC	CGGTGTAGGT	AAAACAGTAT	TAATTCAGGA	ATTAATCAAC	450
	AACATCGCAC	AAGAACACGG	TGGTATCTCT	GTATTCGCTG	GTGTAGGTGA	500
	GCGTACTCGT	GAGGGTAATG	ACTTATACCA	CGAAATGAGC	GATTCAGGCG	550
	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	AAATGAACGA	GCCACCTGGA	600
	GCGCGTCAAC	GTGTTGCGTT	AACAGGTTTA	ACAATGGCTG	AGCATTTCGG	650
40	TGATGAGCAA	GGACAAGACG	TTCTTCTGTT	CATCGATAAT	ATCTTCCGTT	700
	TCACGCAAGC	AGGTTCTGAA	GTATCTGCCC	TTCTTGGTCG	TATGCCATCT	750
	GCGGTAGGTT	ACCAACCAAC	ACTTGCAACA	GAAATGGGTC	AATTACAAGA	800
	GCGTATTACA	TCTACAAATA	AAGGGTCTAT	CACGTCTATC		840

45

2) INFORMATION FOR SEQ ID NO: 1261

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 839 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

```

10 GCGGAAAGCT ACCAGAAATC TACAATGCCC TTACGGTAAA ACAAAGCAAC      50
   GAAAACGGAA GCATGAACCT AACATTTGAA GTTGCACTTC ATTTAGGTGA      100
   TGATACAGTT CGTACAGTTG CGATGTCTTC CACAGATGGA CTTGTTCGTG      150
   GCACAGAAGT AGAAGATACT GGTAAGCAA TCTCTGTACC AGTTGGTGAT      200
   GCAACACTTG GACGTGTATT CAACGTATTA GGTGATGCAA TTGACTTAGA      250
15 TGGTGAACCT CCTGCGGATG TACACCGTGA TCCAATTCAC CGTCAAGCAC      300
   CTGCATTTCGA AGAATTATCT ACTAAAGTAG AAATTCTTGA AACTGGTATT      350
   AAAGTAGTAG ACTTACTTGC TCCTTACATT AAGGGTGGTA AGATCGGCCT      400
   ATTCGGTGGT GCCGGCGTAG GTAAACAGT ATTAATTCAG GAGTTAATCA      450
   ATAACATCGC ACAAGAGCAC GGTGGTATCT CTGTATTCGC TGGTGTAGGT      500
20 GAGCGTACTC GTGAGGGTAA TGACTTATAC CACGAAATGA GCGATTCTGG      550
   CGTAATCAAG AAAACTGCGA TGGTATTCGG ACAAATGAAC GAGCCACCTG      600
   GAGCACGTCA ACGTGTTGCA TTAACAGGTT TAACAATGGC TGAGCATTTC      650
   CGTGATGAGC AAGGACAAGA CGTACTTCTG TTCATCGATA ACATCTTCCG      700
   TTTACGCAA GCGGGTCTG AAGTATCTGC CCTTCTTGGT CGTATGCCAT      750
25 CTGCGGTAGG TTACCAACCA ACACTTGCAA CAGAAATGGG TCAATTACAA      800
   GAGCGTATTA CATCTACAAA TAAAGGTCT ATCACGTCT      839

```

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

```

45 AAGCTACCAG AAATCTACAA TGCCCTTACG GTAAAACAAA GCAACGAAAA      50
   CGGAAGCATG AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA      100
   CAGTTCGTAC AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA      150
   GAAGTAGAAG ATACTGGTAA AGCAATCTCT GTACCAGTTG GTGATGCAAC      200
50 ACTTGGACGT GTATTCAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG      250
   AACTTCCTGC GGATGTACAC CGTGATCCAA TTCACCGTCA AGCACCTGCA      300
   TTCGAAGAAT TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT      350
   AGTAGACTTA CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTCG      400

```

	GTGGTGCCGG	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATCAATAAC	450
	ATCGCACAAAG	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	500
	TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
	TCAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
5	CGTCAACGTG	TTGCATTAAC	AGGTTTAACA	ATGGCTGAGC	ATTTCCGTGA	650
	TGAGCAAGGA	CAAGACGTAC	TTCTGTTTCAT	CGATAACATC	TTCCGTTTCA	700
	CGCAAGCGGG	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
	TATTACATCT	ACAAATAAAG	GGTCTATCAC	GTC		833

2) INFORMATION FOR SEQ ID NO: 1263

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 25 (B) STRAIN: BGSC 4Q1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

	CGAAAACGGA	AGCATGAACT	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
30	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTCTG	100
	GGCACAGAAG	TAGAAGATAC	TGGTAAAGCA	ATTTCTGTAC	CAGTTGGTGA	150
	TGTAACACTT	GGACGTGTAT	TCAACGTATT	AGGTGATGCA	ATTGACTTAG	200
	ATGGTGAACT	TCCTGCGGAT	GTACACCGTG	ATCCAATTCA	CCGTCAAGCA	250
	CCTGCATTTCG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AAACTGGTAT	300
35	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350
	TATTCGGTGG	TGCCGGTGTA	GGTAAAACAG	TATTAATTCA	GGAATTAATT	400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTTCG	CTGGTGTAGG	450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500
	GCGTAATCAA	GAAAAC TGCG	ATGGTATTCG	GACAAATGAA	CGAGCCACCT	550
40	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT	600
	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750
	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT		790

2) INFORMATION FOR SEQ ID NO: 1264

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

```

10 AGTTGCACTT CATTTAGGTG ATGATACAGT TCGTACAGTT GCGATGTCTT      50
   CCACAGATGG ACTTGTTTCG GGCACAGAAG TAGAAGATAC TGGTAAACCA      100
   ATCTCTGTAC CAGTTGGTGA TGTAACACTT GGTCGCGTAT TTAACGTATT      150
   AGGTGATGCA ATTGACTTAG ATGGTGAGGT TCCTGCAGAT GTACATCGTG      200
15 ATCCAATTCA CCGTCAAGCA CCTGCATTCG AAGAATTATC TACTAAAGTA      250
   GAAATTCTTG AAAGTGGTAT TAAAGTAGTA GACTTACTTG CTCCTTACAT      300
   TAAGGGTGGT AAGATCGGCC TATTCGGTGG TGCCGGCGTA GGTAAAACAG      350
   TATTAATTCA GGAATTAATT AACAACATCG CACAAGAGCA CGGTGGTATC      400
   TCTGTATTCG CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ATGACTTATA      450
20 CCACGAAATG AGCGATTCTG GCGTAATCAA GAAAACGCG ATGGTATTCG      500
   GACAAATGAA CGAGCCACCT GGAGCACGTC AACGTGTTGC ATTAACAGGT      550
   TTAACAATGG CTGAGCATTT CCGTGATGAG CAAGGACAAG ACGTACTTCT      600
   GTTCATCGAT AACATCTTCC GTTTCACGCA AGCGGGTTCT GAAG          644

```

25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 823 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

```

   GGCGGAAAGC TACCAGAAAT CTACAACGCC CTTACGGTAA AACAGAGCAA      50
   CGAAAACGGA ACAAGCATTG ACTTAACATT TGAAGTTGCA CTTCAATTTAG      100
45 GTGATGACAC AGTTCGTACA GTTGCAATGT CTTCCACAGA TGGACTTGTT      150
   CGTGGCACAG AAGTAGAAGA TACTGGTAAA GCAATCTCTG TACCAGTTGG      200
   TGATGCAACA CTTGGTCGTG TATTTAACGT ATTAGGTGAT GCAATTGACT      250
   TAGATGGTGA GGTTCCCTGCG GATGTACGTC GTGATCCAAT TCACCGTCAA      300
   GCACCTGCAT TCGAAGAATT ATCTACTAAA GTAGAAATTC TTGAAACTGG      350
50 TATTAAAGTA GTAGACTTAC TTGCTCCTTA CATTAGGGT GGTAAGATCG      400
   GTCTATTCGG TGGTGCCGGT GTAGGTAAAA CGGTATTAAT TCAGGAATTA      450
   ATCAATAACA TCGACAAGA ACACGGTGGT ATCTCTGTAT TCGCTGGTGT      500
   AGGTGAGCGT ACTCGTGAGG GTAATGACTT ATACCACGAA ATGAGCGATT      550

```

	CTGGCGTAAT	TAAGAAACT	GCGATGGTAT	TCGGACAAAT	GAACGAGCCA	600
	CCTGGAGCAC	GTCAACGTGT	TGCGTTAACA	GGTTTAACAA	TGGCTGAGCA	650
	TTTCCGTGAT	GAGCAAGGAC	AAGATGTACT	TCTGTTTCATC	GATAATATCT	700
	TCCGTTTCAC	GCAAGCAGGT	TCTGAAGTAT	CTGCCCTTCT	TGGCCGTATG	750
5	CCATCTGCGG	TAGGTTACCA	ACCAACACTT	GCAACAGAAA	TGGGTCAATT	800
	ACAAGAGCGT	ATTACATCTA	CAA			823

10 2) INFORMATION FOR SEQ ID NO: 1266

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 715 bases
	(B) TYPE: Nucleic acid
15	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Paracoccidioides brasiliensis</i>
	(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

25	TGGTCCGAGR	CCCGATTCTMA	TGAAATTATC	AAGGAAACCT	CCAAYTTCAT	50
	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	CCCATTCTCTG	100
	GTTTCCAGGG	TGACAACATG	ATCGATSCCT	CTGCCAACTG	CCCATGGTAC	150
	AAGGGCTGGT	ACMAKGAGAC	TGCCGACAGG	CAAGYACTCT	GGCAAGACCC	200
30	TTCTTGAGGC	CATTGACGSC	ATTGAGCCCC	CCAMSCGTCC	TWCCGATAAA	250
	CCTCTCCGTC	TTCTCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGMAC	300
	TGTTCTGTGTC	GGACGTRTTG	AGACTGGAGT	CATCAAGCCC	GGTATGGTCG	350
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAAATG	400
	CACCACCAGC	AGCTTTCCGA	CGGTAWCCCC	GGTGACAACG	TCGGCTTCAA	450
35	CGTCAAGAAT	GTTTCCGTCA	AAGAAGTCCG	CCGTGGTAAC	GTTGCCTGGT	500
	GACTCTAAGA	ATGATCCCGC	MAWGGGCTGC	GATTCCTTCA	ATGCYCAGGT	550
	CATCGTCCTC	AACCACCCTG	GTCAGGTTGG	CGCTGGTTAT	GCCCCAGTCC	600
	TCGAYTGCCA	TACTGCCCAC	ATTGCYTGCA	ARTTCGCTGA	GMTCMAGKAG	650
	AAGATTGAYC	GCCGAACCGG	MAAGTCTGTT	GAGAACGCCC	CCAAGTTCAT	700
40	CAAGTCCGGT	GATGC				715

45 2) INFORMATION FOR SEQ ID NO: 1267

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 875 bases
	(B) TYPE: Nucleic acid
50	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 56220

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

	GAGTCCTCTT	ATTTACTTTT	GTCATGACTA	CCTTACTAAT	CTGTCATAGA	50
	TCGTTACAAC	GAAATCGTCA	AGGAGACTTC	CAACTTCATC	AAGAAGGTCG	100
	GATACAACCC	CAAGAACGTT	CCTTTCGTTC	CTATCTCCGG	TTTCAACGGC	150
10	GACAACATGC	TTGAGCCCTC	CCCCAACTGC	CCCTGGTACA	AGGGTTGGGA	200
	GAAGGAGACC	AAGGCCGGTA	AGGTCAC TGG	TAAGACCCTC	CTCGAGGCCA	250
	TCGACGCCAT	TGAGCCCCCT	ACCCGTCCCG	CCAACAAGGT	CAGTACTACC	300
	TCAATTACTT	GAAC TCTCTT	CATACGTTCC	GATTACTGAC	TGCTTCACAG	350
	CCCCTCCGTC	TTCCCCTCCA	GGACGTTTAC	AAGATCGGTG	GTATTGGAAC	400
15	GGTGCCCGTC	GGTCGTGTTG	AGACCGGTAC	CATCTCCCCT	GGTATGGTCG	450
	TTACCTTGTA	TGTATCCTGA	CCATCCCCCT	TGGCAATCAT	TACGTACTAA	500
	CTCACTCTTC	AGCGCTCCCG	CCAACGTCAC	CACTGAAGTC	AAGAGTGTTG	550
	AAATGCACCA	CCAGCAGCTC	GCTGCCGGTC	AGCCCGGTGA	CAACGTTGGT	600
	TTCAACGTGA	AGAACGTCTC	CGTCAAGGAA	ATCCGTCGTG	GTAACGTTGC	650
20	TGGTGATAGC	AAGAACGACC	CCCCTGCCGG	TGCTGCTTCC	TTCAACGCCC	700
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGTGCTGG	TTACGCCCCA	750
	GTCCTTGACT	GCCACACTGC	CCACATTGCT	TGCAAGTTCT	CTGAACTCCT	800
	TGAGAAGATT	GACCGTCGTA	CCGGAAAGTC	TGTTGAGGAC	CACCCCAAGT	850
	TCATCAAGTC	CGGTGACGCT	GCCAT			875

2) INFORMATION FOR SEQ ID NO: 1268

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

40

(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

	GTGAGCGTGG	TATCACCATC	GATATTGCCC	TCTGGAAATT	CGAGACCCCG	50
45	AAGTACAGTG	TCAGTGTCAT	TGGTGAGTGC	TTTTTACCCC	TCTTAAGCAG	100
	ATTTCAACTT	CCAGAGTATC	TACTCTAACA	TATCCGCTTA	GATGCTCCCG	150
	GCCATCGTGA	CTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	200
	TGCGCTATCC	TCATCATTCG	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	TCTGCTTGCT	TTCACCCTTG	300
50	GTGTGAGGCA	ACTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCCGAGTCCC	GTTTCAACGA	AATCATCAAG	GAGGTTTCCA	ACTTCATCAA	400
	GAAGGTCGGA	TATAACCCCA	AGGCTGTTCC	CTTCGTGCCA	ATCTCTGGTT	450
	TCGAGGGTGA	CAACATGATT	GAACCCTCCC	CCAAC TGCAC	CTGGTACAAG	500

	GGCTGGAACA	AGGAGACTGC	CTCTGGCAAG	TCTTCTGGTA	AAACCCCTTCT	550
	CGATGCCATT	GACGCCATTG	AACCCCCAAC	CCGTCCTACC	GATAAGCCTC	600
	TCCGTCTTCC	CCTCCAGGAT	GTTTACAAAA	TCTCTGGTAT	TGGCACTGTT	650
	CCCGTCGGAC	GTGTTGAGAC	TGGTGTCATC	AAGCCCGGTA	TGGTCGTGAC	700
5	TTTCGCTCCC	TCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACCAACAAC	CCAGGCTGGT	TACCTGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTTT	CAGTCAAGGA	AGTCCGCCGT	GGCAACGTTG	CTGGCGACTC	850
	CAAAAATGAT	CCCCCAAGG	GCTGCGAATC	CTTCAATGCC	CAGGTCATCG	900
	TCCTTAACCA	CCCCGGCCAG	GTTGGCGCTG	GTTATGCCCC	AGTCCTCGAC	950
10	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCTGAACTCA	TTGAGAAGAT	1000
	CGACCGCCGT	ACTGGAAAGT	CTGTTGAGAA	CAACCCCAAG	TTCATCAAGT	1050
	CTGGTGATGC	TGCTATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTG	1100
	GAGCCCTTCA	CTGACTATCC	CCCT			1124

15

2) INFORMATION FOR SEQ ID NO: 1269

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1043 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton rubrum*
 (B) STRAIN: WSA-224

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

	GTGAGCGTGG	TATCACCATC	GATATCGCCC	TCTGGAAGTT	CGAGACCCCC	50
	AAGTACAATG	TCACCGTCAT	TGGTATGTTT	CTTTGCCTTG	TTCCCTCATG	100
35	TGGTTGTACC	ATATCTAACG	AGAGTAGACG	CCCCCGGTCA	CCGTGACTTC	150
	ATCAAGAACA	TGATCACTGG	TACCTCCCAG	GCTGACTGCG	CTATTCTCAT	200
	CATTGCTGCC	GGTACTGGTG	AGTTCGAGGC	TGGTATCTCC	AAGGATGGCC	250
	AGACCCGTGA	GCACGCTCTG	CTCGCCTTCA	CCCTCGGTGT	CAAGCAGCTC	300
	ATCGTTGCCA	TCAACAAGAT	GGACACCACC	GGCTGGTCCG	AGGATCGTTT	350
40	CAAGGAAATT	ATCAAGGAAG	TCACCAACTT	CATCAAGAAG	GTTGGCTACG	400
	ACCCCAAGGG	TGTTCCATTC	GTTCCAATCT	CTGGTTTCAA	CGGTGACAAC	450
	ATGATTGAGG	CCTCCACCAA	CTGCCCATGG	TACAAGGGAT	GGAACAAGGA	500
	GACCAAGGCC	GGTGGTGCCA	AGTCCGGCAA	GACCCTCCTC	GAGGCCATCG	550
	ATGCCATCGA	CATGCCAACC	CGTCCTACCG	ACAAGCCCCT	CCGTCTCCCA	600
45	CTCCAGGATG	TCTACAAGAT	CTCTGGTATC	GGAAGTGTGC	CAGTCGGTCG	650
	TGTTGAGACC	GGTATCATCA	AGCCCGGTAT	GGTCGTCACC	TTNGCCCCCG	700
	CCAACGTCAC	CACTGAAGTC	AAGTCCGTYK	AAATGCACCA	CCAGCAGCTT	750
	CAGCAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAATGTCA	AGAACGTTTC	800
	CGTCAAGGAA	GTCCGCCGTG	GTAACGTTGC	CGGTGACTCC	AAGAACGACC	850
50	CACCATCCGG	CTGTGCCTCC	TTCAACGCC	AGGTCATYGT	CCTCAACCAC	900
	CCCGGCCAGA	TCGGTGCTGG	TTACGSTCCA	GTCCTCGACT	GCCACACTGS	950
	TCACATTGCT	TGCAAGTTCG	CTGAGCTCCT	CGAGAAGATT	GACCGCCGTA	1000
	CCGGTAAATC	CGTCGAAGCC	AACCCCAAGT	TCGTCAAGTC	TGG	1043

2) INFORMATION FOR SEQ ID NO: 1270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium canis*
 (B) STRAIN: WSA-217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

```

GCTGAGCGTG AGCGTGGTAT CACCATTGAT ATCGCCCTCT GGAAGTTCGA      50
GACCCCAAG TACATGGTCA CCGTCATCGG TATGCTTTAT CTGTTTCCCA      100
TTTATAGTTG CGACCAGTAA CTAACAAAAA GTAGATGCCC CCGGGCACCG      150
TGACTTCATC AAGAACATGA TTACTGGTAC CTCCAGGCC GACTGCGCTA      200
TTCTCATCAT TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG      250
GATGGCCAGA CTCGTGAGCA CGCCCTGCTC GCTTTCACCC TCGGTGTCAA      300
GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAC TGGTCTGAGT      350
CCCGTTTCGG TGAAATCATC AAGGAAGTCA CCAACTTCAT CAAGAAGGTC      400
GGCTACGACC CCAAGGGTGT CCCATTTCGT CCAATCTCTG GCTTCAACGG      450
TGACAACATG ATTGAGCCCT CCACCAACTG CCCATGGTAC AAGGGATGGA      500
ACAAGGAGAC CAAGGCCGGT GGCAAATCCT CTGGTAAGAC CCTCCTTGAG      550
GCCATCGATG CCATTGACAT GCCCACTCGT CCCACCGACA AGCCTCTCCG      600
TCTCCCCTC CAGGATGTCT ACAAGATCTC TGGTATCGGA ACAGTACCAG      650
TCGGTCGTGT TGAGACTGGT ATCATCAAGC CTGGTATGGT TGTCACCTTY      700
GCCCCCGCCA ACGTCACCAC TGAAGTCAAG TCCGTCGAAA TGCACCACCA      750
GCAGCTYGTC CAGGGTGTTT CCGGTGACAA CGTTGGCTTC AACGTCAAGA      800
ACGTYTCTGT CAAGGAAGTC CGCCGTGGTA ACGTTGCCGG TGATTCCAAG      850
AACGACCCAC CAGCTGGCTG CGCCTCTTTC AAGGCCCAGG TCATCGTCCT      900
CAACCACCCC GGCCAGATCG GTGCTGGTTA CGCCCAGTC CTTGACTGCC      950
ACACTGCCCA CATTGCTTGC AAGTTCTCTG AGCTTCTTGA GAAGATTGAC     1000
CGCCGTACTG GTAAATCCGT CGAAACCAGC CCTAAGTTCG TCAAGTCTGG     1050
TGATGCCGCT ATTGCCACCA TGGTTCCATC CAAGCCCATG TGC GTTGAGG     1100
CTTTC

```

2) INFORMATION FOR SEQ ID NO: 1271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

```

5  GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA AGTTCCAGAC      50
    CCTAAGTAT GAGGTCACCG TCATTGGTAT GTTGTCCTTC TTGTGTTACC      100
    ATCGAAACAT ATCTAACCTA CAACTGCAGA CGCCCCCGGT CACCGTGA CT      150
    TCATCAAGAA CATGATCACT GGTACCTCCC AGGCCGACTG CGCTATTCTC      200
10  ATCATTGCTT CCGGTACTGG TGAATTCGAG GCTGGTATCT CCAAGGATGG      250
    CCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTCGGT GTCCGTCAGC      300
    TCATCGTTGC CCTCAACAAG ATGGACACTG CTGGCTGGGC TGAGGCTCGT      350
    TACAACGAAA TCGTCAAGGA AACTTCCGGT TTCATCAAGA AGGTCGGCTA      400
    CAACCCCAAG TCGGTTCCCT TCGTCCCCAT CTCCGGTTTC AACGGTGACA      450
15  ACATGCTTGA GCCCTCCTCC AACTGCCCTT GGTACAAGGG TTGGGAGAAG      500
    GAGACCAAGG CTGGTAAGGC CACTGGTAAG ACCCTCCTCG AGGCCATCGA      550
    CGCCATTGAG CCTCCCGTCC GTCCCTCCAA CAAGCCTCTC CGTCTTCCCC      600
    TCCAGGATGT CTACAAGATC TCTGGTATTG GAACTGTCCC CGTCGGCCGT      650
    GTCGAGACCG GTACCATCGT CCCCGGTATG GTCGTCACCT TCGCTCCCGC      700
20  CAACGTCACC ACTGAAGTCA AGTCCGTTGA GATGCACCAC CAGCAGCTCA      750
    AGGAGGGTGT TCCCGGTKAC AACGTTGGTT TCAACGTGAA GAACGTTTCC      800
    GTCAAGGAAG TCCGCCGTGG TAACGTCGCT GGTGACTCCA AGAACGACCC      850
    CCCTGCCGGT GCTGCCTCTT TCACCGCCCA GGTCATCGTC CTCAACCACC      900
    CCGGTCAGGT CGGCGCTGGT TACGCTCCCG TCCTCGACTG CCACACCGCT      950
25  CACATTGCCT GCAAGTTCGC TGAGCTCCAG GAGAAGATCG ACCGCCGTAC      1000
    CGGAAAGTCT GTCGAATYTG CCCCCAAGTT CATCAAGTCT GGTGACGCCG      1050
    CTATCGTCAA GATGATTCCC TCCAAGCCCA TGTGTGTCGA GTCTTTCACT      1100
    GACTACCCTC CTYTCGGCCG TTTCGCCGTC CGTGACGTAA GTTCTTTCCC      1150
    CAGCTTTTCG ATGCTACCCT TCTMTGAATC ACGTGTGTCG TCTTGGCACC      1200
30  CGCCCATCAC ATGACCACGC AACCTATAC CCCGCCACAC CCTT          1244
  
```

2) INFORMATION FOR SEQ ID NO: 1272

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1032 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
40  (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

45  (A) ORGANISM: Exophiala moniliae
      (B) STRAIN: WSA-219
  
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

```

50  GCTGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT GGAAGTTCGA      50
    GACCCCAAG TACTATGTCA CCGTCATCGA CGCCCCCGGT CATCGTGA CT      100
    TCATCAAGAA CATGATCACT GGTACTTCCC AAGCTGACTG CGCCATTCTC      150
    ATCATTGCTG CCGGTACTGG TGAATTCGAA GCCGGTATCT CCAAGGATGG      200
  
```

	TCAGACCCGT	GAGCACGCTC	TGCTTGCCCTA	CACCCTGGGT	GTCAAGCAGC	250
	TCATTGTCGC	CATCAACAAG	ATGGACACTA	CCAAGTGGTC	TGAGGACCGT	300
	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	AGGTCGGCTA	350
	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	AACGGTGACA	400
5	ACATGATCGA	CGTCTCCACC	AACTGCCCCCT	GGTACAAGGG	CTGGGAGAAG	450
	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTTG	AGGCCATCGA	500
	CGCCATTGAC	CCCCCTCTC	GTCCCACCGA	CAAGCCTYTC	CGTCTCCCTC	550
	TCCAGGATGT	GTACAAGATC	TCTGGTATCG	GAACGGTGCC	CGTCGGTCGT	600
	GTCGAGACTG	GTATCATCAA	GGCCGGTATG	GTCGTTACCT	TCGCTCCTGC	650
10	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	GAACAGCTCG	700
	CCGAGGGTGT	TCCAGGTGAC	AACGTCGGTT	TCAACGTCAA	GAACGYTCC	750
	GTCAAGGAGG	TTCGTCGTGG	AAACGTTTGC	GGTGACTCCA	AGAACGACCC	800
	ACCCAAGGGC	GCTGATTCCCT	TCAACGCCCA	GGTCATCGTC	TTGAACCACC	850
	CTGGTCAAGT	TGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	CCACACTGCC	900
15	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATCG	ATCGTCGKAC	950
	CGGAAAGTCG	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	GGTGACGCTG	1000
	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TG		1032

20

2) INFORMATION FOR SEQ ID NO: 1273

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1106 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*
(B) STRAIN: ATCC 34944

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

	TAACAGCCCCG	TGCGACCGTC	TCGTCCAATA	ACTAATGATT	CGCAGGTACT	50
	ATGTCGTGAG	TATCCGGTCC	TTTTTTGTTA	ATTTACCAGA	AATGACGAAA	100
	TTTTTGACTA	ATTAACACAC	TCAGACCGTC	ATTGACGCC	CGGGTCACCG	150
40	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCC	GACTGCGCTG	200
	TCCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTCGCCATCA	ATAAGATGGA	CACCACCAAG	TGGTCCGAGG	350
	AGCGTTACGG	CGAGATCATC	AAGGAGACCT	CTGCCTTCAT	CAAGAAGGTC	400
45	GGTTTCAACC	CGAAGCACGT	CCCGTTTCGT	CCGATCTCCG	GTTTCAACGG	450
	TGACAACATG	ATCGAGGCCT	YACCAACTG	CCCGTGGTAC	AAGGGCTGGG	500
	AGAAGGAGAC	CAAGGCCAAG	GTCACCGGCA	AGACCCTYCT	TGAGGCCATT	550
	GACAACATCG	ACCCGCCGAG	CCGTCCTTCC	GACAAGCCGC	TCCGTCTTCC	600
	CCTCCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGGACAGTC	CCAGTCGGCC	650
50	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTTAC	CTTCGCTCCG	700
	GCTGGTGTCA	CCACTGAAGT	GAAGTCCGTT	GARATGCACC	ACGAGCAGCT	750
	CGCTGAGGGT	YTGCCGGGTG	ACAACGTCGG	CTTCAACGTC	AAGAACGTTT	800
	CCGTCAAGGA	GATCCGTCGT	GGCAACGTTG	CTGGTGACAG	CAAGGCTGAC	850

	CCGCCGAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	TCCTGAACCA	900
	CCCTGGCCAG	GTCGGTGCTG	GTTACGCTCC	AGTCCTGGAC	TGCCACACTG	950
	CCCACATTGC	CTGCAAGTTC	GGCGAGCTCC	TCGAGAAGAT	CGACCGTCGC	1000
	TYTGGCAAGT	CCATTGAAGC	CTYGCCTAAG	TACATCAAGT	CTGGTGACGC	1050
5	TGCCATYGTC	AAGATGATTC	CGTCCAAGCC	GATGTGCGTT	GAGCCATTCA	1100
	CTGAGT					1106

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1119 bases
	(B) TYPE: Nucleic acid
15	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Fusarium solani</i>
	(B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

25	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTTCGAGACT	CCCCGCTACT	ATGTCACCGT	CATTGGTATG	TTGCTGTCAC	100
	CTCTCTCACA	CATGTCTCAC	CACTAACAAT	CAACAGACGC	CCCCGGCCAC	150
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGACTGCGC	200
30	CATTCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTTTCGAGGCT	GGTATCTCCA	250
	AGGATGGCCA	GACCCGTGAG	CACGCCCTGC	TCGCCTACAC	CCTCGGTGTC	300
	AAGAACCTCA	TTGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	350
	GTCCCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAAC TTC	ATCAAGAAGG	400
	TCGGCTACAA	CCCCAAGGCT	GTCGCTTTTCG	TCCCCATCTC	CGGTTTCAAC	450
35	GGCGACAACA	TGCTTACTCC	CTCCACCAAC	TGCCCCTGGT	ACAAGGGCTG	500
	GGAGCGTGAG	ATCAAGTCCG	GCAAGCTCAC	TGGCAAGACC	CTCCTCGAGG	550
	CCATTGACTC	CATCGAGCCC	CCCCAAGCGTC	CCGTCGACAA	GCCCCTYCGA	600
	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATTGGCA	CGGTTCCCCT	650
	CGGCCGTATC	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTMG	700
40	CCCCCTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	750
	CAGCTCTYTG	AGGGTCTTCC	CGGTGACAAC	GTCGGCTTCA	ACGTGAAGAA	800
	CGTYTCCGTC	AAGGAGATCC	GACGTGGCAA	CGTCGCTGGT	GA CTCCAAGA	850
	ACGACCCCCC	TYTGGGTGCC	GCCTCTTTCA	CCGCCCAGGT	CATTGTCTCTC	900
	AACCACCCTG	GCCAGGTCGG	TGCCCGTTAC	GCCCCCGTTY	TGGACTGCCA	950
45	CACTGCCCCAC	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	1000
	GCCGA ACTGG	TAAGGCTGTT	GAGTCCGCCC	CCAAGTTCAT	CAAGTCTGGT	1050
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1100
	TTTCACTGAC	TACCCCCCT				1119

50

2) INFORMATION FOR SEQ ID NO: 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

```

15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGA CTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC T GCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTTGAGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA      800
   CCCCCCAAG GGTTGTGACT CCTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTCGGTGCT GGTTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG      1000
35 CCGCCATCGT CAAGATGGTT CCCTCCAAGC CCATGTGTGT TGAGGCTTTC      1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113

```

2) INFORMATION FOR SEQ ID NO: 1276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

	GGTCTGAGAC	CCGTTTCAAC	GAAATTATCA	AGGAAGTCAG	CAACTTCATC	50
5	AAGAAGGTCG	GATACAACCC	CAAGTCTGTT	CCCTTCGTGC	CAATCTCCGG	100
	TTTCGAGGGT	GACAACATGA	TTGAGCCTTC	CCCCAACTGC	CCTTGGTACA	150
	AGGGCTGGAA	CAAGGAGACT	GCTGCTGGCA	AGGCCGCCGG	TAAGACTCTT	200
	CTCGATGCCA	TTGACGCCAT	CGACCCCCCC	GTCCGTCCTA	CCGAGAAGCC	250
	TCTCCGTCTT	CCCCTCCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	300
10	TTCCCGTTGG	ACGTGTCGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTG	350
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TTGAAATGCA	400
	CCACCAGCAG	CTCCAGGCTG	GTTACCTCTG	TGACAACGTC	GGCTTCAACG	450
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCGGTGAC	500
	TCCAAGAACG	ACCCCCCCAA	GGGCTGCGAG	TCCTTCAACG	CCCAGGTCAT	550
15	CGTCCTCAAC	CACCCCGGCC	AGGTTGGCGC	TGGTTATGCC	CCAGTCCTCG	600
	ACTGCCACAC	TGCCACATT	GCTTGCAAGT	TCTCTGAGCT	CATCGAGAAG	650
	ATTGACCGCC	GTACCGGAAA	GTCTGTTGAG	GACAACCCCA	AGTTCATCAA	700
	GTCCGGTGAT	GCTGCTATCG	TCAAGATGAT	T		731

20

2) INFORMATION FOR SEQ ID NO: 1277

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1046 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exophiala dermatitidis*
 (B) STRAIN: ATCC 76088

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCCCTCTG	GAAGTTCGAG	50
	ACCCCCAAGT	ACTATGTCAC	CGTCATCGAC	GCCCCGGGTC	ATCGTGACTT	100
40	TATCAAGAAC	ATGATCACTG	GTACCTCGCA	GGCCGACTGC	GCCATCTTGA	150
	TCATTGCCGC	CGGTACCGGT	GAATTCGAAG	CCGGTATCTC	CAAGGATGGT	200
	CAGACCCGTG	AGCACGCTCT	GCTCGCCTAC	ACCTTGGGTG	TCAAGCAGCT	250
	CATCGTCGCC	ATCAACAAGA	TGGACACCAC	CAAGTGGTCC	GAGGAGCGTT	300
	TCAACGAAAT	CATCAAGGAG	ACTTCCAAC	TCATCAAGAA	GGTCGGCTAC	350
45	AACCCCAAGG	CCGTTCCTTT	CGTCCCCATC	TCCGGCTTCA	ACGGTGACAA	400
	CATGATTGAG	GTCTCCACCA	ACTGCCCCGTG	GTACAAGGGA	TGGGAGAAGG	450
	AGTCCAAGGC	TGGCAAGGCC	ACCGGCAAGA	CCCTCCTCGA	GGCCATTGAC	500
	GCCATCGACC	CACCCACCCG	TCCCACCGAC	AAGCCTCTCC	GTCTCCCTCT	550
	CCAGGATGTC	TACAAGATCT	CTGGTATCGG	AACGGTTCCT	GTCGGTCGTG	600
50	TCGAGACCGG	TACCATCAAG	GCCGGTATGG	TCGTCACCTT	CGCTCCGGCC	650
	AACGTCACCA	CTGAAGTCAA	GTCCGTCGAA	ATGCACCACG	AGCAGCTCGC	700
	CGAGGGTYTG	CCAGGTGACA	ACGTTGGCTT	CAACGTCAAG	AACGTYTCCG	750
	TCAAGGAGGT	TCGTCGTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCG	800

	CCCAAGGGTG	CCGAGTCCTT	CAACGCCCAG	GTCATTGTCC	TCAACCACCC	850
	TGGTCAGATC	GGTGCCGGCT	ACGCTCCAGT	CTTGGATTGC	CACACTGCCC	900
	ACATTGCTTG	CAAGTTCGCC	GAGTTGCTCG	AGAAGATCGA	CCGTCGTACC	950
	GGAAAGTCCA	TCGAGAACAA	CCCCAAGTTC	ATCAAGTCTG	GTGATGCTGC	1000
5	CATCGTCAAG	ATGATTCCCA	GCAAGCCCAT	GTGTGTCGAG	GCTTTC	1046

2) INFORMATION FOR SEQ ID NO: 1278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
 (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

25	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	TCGAGACTCC	50
	TCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GTCGCTCATA	CCTCATCCTA	100
	CTTCCTCATA	CTAACACATC	ATTCAGACGC	TCCCGGTCAC	CGTGATTTCA	150
	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGATTGCGC	CATTCTCATC	200
	ATTGCCGCCG	GTACTGGTGA	GTTCGAGGCT	GGTATCTCCA	AGGATGGCCA	250
30	GACCCGTGAG	CACGCTCTTC	TTGCCTACAC	CCTTGGTGTC	AAGAACCTCA	300
	TCGTGCGCAT	CAACAAGATG	GACACCACCA	AGTGGTCTGA	GGCCCGTTAC	350
	CAGGAGATCA	TCAAGGAGAC	CTCCTCTTTC	ATCAAGAAGG	TCGGCTACAA	400
	CCCCAAGGCT	GTCGCTTTCG	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	450
	TGCTTACCCC	CTCCACCAAC	TGCCCCTGGT	ACAAGGGTTG	GGAGCGTGAG	500
35	ATCAAGTCCG	GCAAGCTCTC	CGGCAAGACC	CTCCTCGAGG	CCATTGACTC	550
	CATCGAGCCT	CCCAAGCGTC	CCGTTGACAA	GCCCCTCCGT	CTTCCCCTCC	600
	AGGATGTCTA	CAAGATCGGT	GGTATTGGAA	CGGTTCCCGT	CGGCCGTATT	650
	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTCG	CTCCCTCCAA	700
	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	CAGYTCAGTK	750
40	AGGGCCAGCC	CGGTGACAAC	GTTGGTTTCA	ACGTGAAGAA	CGTTTCCGTC	800
	AAGGACATCC	GACGTGGTAA	CGTCGCTGGT	GACTCCAAGA	ACGACCCCCC	850
	CCAGGGTGCC	GCTTCTTTCA	CCGCCCAGGT	CATCGTCCTC	AACCACCCCG	900
	GCCAGGTCGG	TGCTGGTTAC	GCTCCTGTCC	TCGATTGCCA	CACTGCCCCAC	950
	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	GCCGAACCGG	1000
45	TAAGGCTACT	GAGGCCGCTC	CCAAGTTCAT	CAAGTCTGGT	GACTCCGCCA	1050
	TCGTCAAGAT	GGTTCCTCCT	AAGCCCATGT	GTGTCGAGGC	TTTCACTGAC	1100
	TACCTCTCT					1109

2) INFORMATION FOR SEQ ID NO: 1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*
 (B) STRAIN: WSA-174

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

	CCTGCAAGTG	GTCTGAGGAC	CGTTACAACG	AAATCGTGAA	GGAGACCTCC	50
15	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	100
	CATCTCCGGT	TTCAACGGTG	ACAACATGCT	TGAGCCTTCC	CCCAACTGCC	150
	CCTGGTACAA	GGGTGGGAG	AAGGAGGGCA	AGTCCGGCAA	GGTCACCGGT	200
	AAGACTCTCC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCG	TCCGTCCTGC	250
	CAACAAGCCT	CTCCGTCTTC	CCCTCCAGGA	TGTGTACAAG	ATCTCTGGTA	300
20	TCGGAAGTGT	CCCCGTCGGC	CGTGTCGAGA	CTGGTGTCAT	CACCCCCGGC	350
	ATGGTTGTTA	CCTTCGCTCC	TTCCAACGTC	ACCACTGAAG	TGAAGTCCGT	400
	TGAGATGCAC	CACCAGCAGC	TCAAGGAGGG	TCTCCCCGGT	GACAACGTTG	450
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AGGTCCGTCG	TGGTAACGTC	500
	GCTGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCGCTGCCT	CCTTCACCGC	550
25	CCAGGTCATC	GTTCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGCTACGCCC	600
	CCGTCCTCGA	CTGCCACACT	GCCCCATTG	CCTGCAAGTT	CGCTGAGCTC	650
	CAGGAGAAGA	TTGACCGCCG	TACCGGAAAG	TCTGTTGAGT	CTTCTCCCAA	700
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATC	CCTYCAAAGC	750
30	CCATGTGCGT	CGAAG				765

2) INFORMATION FOR SEQ ID NO: 1280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	GAAGTTCCAG	ACTCCCAAGT	50
50	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	CGCCCCGATA	TGTTTTGGTG	100
	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	150
	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	CTGCGCTATC	CTCATCATTTG	200
	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	TCTCCAAGGA	TGGCCAGACC	250

	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	GGTGTC AAGC	AGCTCATCGT	300
	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	GTCCGAGGAT	CGTTACAACG	350
	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	400
	AAGGCCGTTT	CCTTCGTMCC	CATCKCTGGC	TTCAACGGTG	ACAACATGCT	450
5	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	GGGATGGGAG	AAGGAGACCA	500
	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	TCGAGGCCAT	YGACGCCATT	550
	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	CTYCGTCTTC	CCCTCCAGGA	600
	TGTYTACAAG	ATCTCTGGTA	TCGGAACGGT	CCCTGTCGGC	CGTGTCGAGA	650
	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	CCTTTGCCCC	CGCCAACGTC	700
10	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	CACCAGCAGC	TCCAGGAGGG	750
	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	CAAGAACGTT	TCCGTCAAGG	800
	AAGTCCSCCG	TGGTAACGTT	TGCGGTGACT	CCAAGAACGA	TCCCCCTCAG	850
	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	GTCTCAACC	ACCCCGGTCA	900
	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	CTGCCACACT	GCCCACATTG	950
15	CTTGCAAGTT	CTYT GAGCTG	CTTGAGAAGA	TTGACCGCCG	TACCGGCAAG	1000
	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	TCCGGTGAWG	CCGCCATCGT	1050
	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	CGAGTCCTTC	ACTGACTACC	1100
	CCCCT					1105

20

2) INFORMATION FOR SEQ ID NO: 1281

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 1343 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus laurentii*
(B) STRAIN: ATCC 44096
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

	GCCGAGCGAG	AGCGAGGTAT	CACCATCGAC	ATTGCTCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACAACGTCA	CCGTCA TTGA	CGCCCCCGGA	CACCGAGACT	100
40	TCATCAAGAA	CATGATCACC	GGTACCTCCC	AGGCCGACTG	CGCCATCCTT	150
	ATCATTGCCA	CCGGTATCGG	AGAGTTCGAG	GCCGGTATCT	CTAAGGACGG	200
	TCAGACCCGA	GAGCACGCTT	TGCTCGCCTT	CACCCTCGGT	GTCAGGCAGC	250
	TCATCGTTGC	TTGCAACAAG	ATGGACACCT	GCAAGTGGTC	CGAGGACCGA	300
	TTCAACGAGA	TCGTCAAGGA	GACCAACGGT	TTCATCAAGA	AGGTCGGATA	350
45	CAACCCCAAG	GCTGTTCCCT	TCGTCCCCAT	CTCTGGATGG	CACGGAGACA	400
	AGTGAGTGCC	GTTCTTTGCG	TTGAGCCCTC	TTTGTCGCTC	CCCCTCCCTC	450
	TCAAGTGGCG	GCGGCGGTCT	CCACCCACAA	ATCGGGTGGC	GAATCCGCCA	500
	CACCCACCAC	TTCTCGCCAC	CGAGTGTGGC	ACTTCTTCCA	ACTCCTCTTT	550
	CCACTCCTCC	TCGTCTCGTC	TCTTTTTTTC	TCCGTTGTCT	TTGACAAGGG	600
50	GAGTGTGCTG	ATAGTAAAGC	ATGCTTGAGG	AGACCACCAA	CATGCCGTGG	650
	TACAAGGGAT	GGACCAAGGA	GACCAAGTCC	GGTGTCGTTA	AGGGTAAGAC	700
	CCTCCTCGAC	GCCATCGACG	CCATCGAGCC	TCCTCAACGA	CCCACCGACA	750
	AGCCCCTCCG	ACTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATCGGT	800

	ACGGTGTCCCG	TCGGCCGAGT	CGAGACCGGT	GTCATCAAGG	CCGGGTAAGT	850
	CACGGGAGCC	TGACGGCTGT	TGTTGCCACA	CCCAACTTAT	ATCCAGTATG	900
	GTCGTCACCT	TCGCTCCTAC	CAACGTCACC	ACTGAGGTTA	AGTCCGTTGA	950
	GATGCACCAC	GAGCAGATCC	CTGAGGGTCT	TCCCGGAGAC	AACGTTGGTT	1000
5	TCAACGTGAA	GAACGTTTCC	ATCAAGGACA	TCCGACGAGG	AAACGTYTGC	1050
	TCCGACTCCA	AGAACGACCC	CGCTAAGGAG	GCCGCTTCTT	TCAACGCCCA	1100
	GGTCATTGTC	CTCAACCACC	CTGGACAGAT	TGGTGCCGGT	TACACCCCCG	1150
	TCCTCGACTG	CCACACCGCC	CACATTGCCT	GCAAGTTCGC	CGAGCTCATC	1200
	GAGAAGATCG	ACCGACGAAC	TGGTAAGACC	ATGGAGGCCG	CCCCCAAGTT	1250
10	CGTCAAGTCC	GGAGACGCCG	CCATTGTCAA	GCTCGTTGCC	CAGAAGCCCA	1300
	TCTGTGTCGA	GTCTTACTCT	GACTACCCTC	CCCTTGACG	ATT	1343

15 2) INFORMATION FOR SEQ ID NO: 1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

30	TGGTCCGAGG	CTCGTTTCAA	CGAAATCATC	AAGGAAGTCA	CCAACTTCAT	50
	CAAGAAGGTC	GGATACAACC	CCAAGTCTGT	TCCCTTCGTG	CCAATCTCTG	100
	GTTTCGAGGG	TGATAACATG	ATTGAGCCCT	CCACCAACTG	CCCCTGGTAC	150
	AAGGGCTGGA	CCAAGGAGAC	CGCTGCCGGC	AAGTCAACCG	GTAAGACTCT	200
35	TCTTGACGCC	ATTGATGCCA	TCGATCAACC	CTCCCGTCCT	ACCGACAAGC	250
	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AGATCTCCGG	TATTGGCACT	300
	GTTCCCGTTG	GACGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTCGT	350
	GACCTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	400
	ACCACCAACA	GCTCTTGGCT	GGTAACCCCG	GTGACAACGT	CGGTTTCAAC	450
40	GTCAAGAACG	TTTCCGTCAA	GGAAAGTCCG	CGTGGCAACG	TTGCTGGTGA	500
	CTCAAAGAAC	GACCCCCCCA	AGGGCTGCGA	CTCCTTCAAC	GCCCAGGTCA	550
	TCGTCTCAA	TCACCCCGGT	CAAGTTGGCG	CTGGTTATGC	CCCAGTCCTC	600
	GACTGCCACA	CTGCCACAT	TGCTTGCAAG	TTCTCTGAGC	TCCTCGAGAA	650
	GATTGACCGC	CGTACCGGAA	AGTCCACTGA	GAACAACCCC	AAGTTCATCA	700
45	AGTCTGGTGA	CGCCGCTATC	GTCAAGATGG	TTCC		734

2) INFORMATION FOR SEQ ID NO: 1283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*

(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

	CGTGAGCGTG	GTATCACCAT	CGACATTGCC	CTCTGGAAGT	TCGAGACTCC	50
	CCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GCTGTCACCT	CTCTCACACA	100
	TGTCTCACCA	CTAACAATCA	ACAGACGCCC	CCGGCCACCG	TGACTTCATC	150
15	AAGAACATGA	TCACTGGTAC	TTCCCAGGCC	GACTGCGCCA	TTCTCATCAT	200
	TGCCGCTGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	250
	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GAACCTCATT	300
	GTCGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTACCA	350
	GGAGATCATC	AAGGAGACCT	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	400
20	CCAAGGCTGT	CGCTTTCGTC	CCCATCTCCG	GTTTCAACGG	CGACAACATG	450
	CTTACTCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGCTGGG	AGCGTGAGAT	500
	CAAGTCCGGC	AAGCTCACTG	GCAAGACCCT	CCTCGAGGCC	ATTGACTCCA	550
	TCGAGCCCCC	CAAGCGTCCC	GTCGACAAGC	CCCTCCGACT	TCCCCTCCAG	600
	GATGTCTACA	AGATCGGTGG	TATTGGCACG	GTTCCCGTCG	GCCGTATCGA	650
25	GACTGGTGTC	ATCAAGCCCG	GTATGGTCGT	TACCTTCGCC	CCCTCCAACG	700
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTCTYTGAG	750
	GGTCTTCCCG	GTGACAACGT	CGGCTTCAAC	GTKAAGAACG	TYTCCGTCAA	800
	GGAGATCCGA	CGTGGAACG	TCGCTGGTGA	CTCCAAGAAC	GACCCCCCTY	850
	TGGGTGCCGC	CTCTTTCACC	GCCCAGGTCA	TTGTCCTCAA	CCACCCTGGC	900
30	CAGGTCGGTG	CCGGTTACGC	CCCCGTTYTG	GACTGCCACA	CTGCCCACAT	950
	TGCCTGCAAG	TTCGCCGAGA	TCCAGGAGAA	GATCGACCGC	CGAACTGGTA	1000
	AGGCTGTTGA	GTCCGCCCCC	AAGTTCATCA	AGTCTGGTGA	CTCCGCCATC	1050
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACTGACTA	1100
	CCCCCCT					1107

35

2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*

50

(B) STRAIN: ATCC 14285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

	GCTCAAGGCC	GAGCGTGAGC	GCGGTATCAC	CATCGATATT	GCTCTGTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TACGTCACCG	TCATTGACGC	CCCCGGTCAT	100
	CGCGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATTCTCATC	ATTGCCGCTG	GTA CTGGTGA	GTTTCGAGGCT	GGTATCTCCA	200
5	AGGATGGCCA	GACTCGTGAG	CACGCTCTGC	TCGCCTACAC	CCTGGGTGTG	250
	CGGCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACACGGCCA	AGTGGGCTGA	300
	GGCTCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCA ACTTC	ATCAAGAAGG	350
	TCGGCTACAA	CCCCAAGACT	GTTGCCTTCG	TCCCCATCTC	GGGCTTCCAC	400
	GGCGACAACA	TGCTTACTCC	CTCGACCAAC	TGCCCCTGGT	ACAAGGGCTG	450
10	GGAGAAGGAG	GGCAAGAGCG	GCAAGGTTAC	CGGTAAGACT	CTGCTGGACG	500
	CCATTGACGC	CGTCGAGCCC	CCCAAGCGCC	CCACGGACAA	GCCCCTGCGT	550
	CTGCCCCTCC	AGGATGTCTA	CAAGATCGGC	GGTATCGGCA	CTGTCCCTGT	600
	CGGCCGTATC	GAGACTGGTG	TCCTGAAGCC	CGGCATGGTC	GTCACCTTTG	650
	CCCCGTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
15	CAGCTTGTTG	AGGGTGTTCC	CGGCGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
	CGTYTCCGTC	AAGGAGATCC	GTGTTGGCAA	CGTTGCCGGT	GA CTCCAAGA	800
	ACGACCCCCC	CTCGGGCGCC	GCCACCTTCA	ACGCCCAGGT	CATTGTCTTG	850
	AACCACCCCG	GCCAGGTCGG	CAACGGCTAC	GCCCCGGTTY	TGGACTGCCA	900
	CACCGCCCAC	ATTGCCTGCA	AGTTCACCGA	GATCCTTGAG	AAGATCGACC	950
20	GCCGTACCGG	CAAGTCGGTT	GAGAACAACC	CCAAGTTCAT	CAAGTCGGGT	1000
	GACGCCGCCA	TTGTCAAGCT	GACGCCCTYG	AAGCCCATGT	GCGTT	1045

25 2) INFORMATION FOR SEQ ID NO: 1285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

40	TTGCCAGTGG	TCCGAGGCCC	GTTACAACGA	AATCGTCAAG	GAGACTTCCG	50
	GTTTCATCAA	GAAGGTCGGA	TACAACCCCA	AGTCCGTTGC	CTTCGTCCCC	100
	ATCTCCGTTT	TCAACGGTGA	CAACATGCTC	GAGGCCCTCTA	CCA ACTGCCC	150
	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	GGCCGGTAAG	GCCACTGGTA	200
45	AGACCCTCCT	TGAGGCCATC	GACGCCATTG	AGCCCCCCAC	CCGTCCCTCC	250
	AACAAGCCCC	TCCGTCTTCC	CCTCCAGGAT	GTCTACAAGA	TCTCCGGTAT	300
	TGGA ACTGTC	CCCGTCGGCC	GTGTCGAGAC	TGGTGT TATC	ACCCCCG GCA	350
	TGGTCGTCAC	CTTCGCTCCT	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTT	400
	GAGATGCACC	ACCAGCAGCT	CAAGGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
50	TTTCAACGTC	AAGAACGTTT	CCGTCAAGGA	AATCCGTCGT	GGTAACGTTG	500
	CCTCCGACTC	CAAGAACGAC	CCCGCCTCCG	GCGCTGCCTC	TTTCAACGCC	550
	CAGGTCATCG	TTCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	600
	CGTCCTCGAC	TGCCACACCG	CCCACATTGC	TTGCAAGTTC	TCTGAGCTTC	650

TTGAGAAGAT	TGACCGCCGT	ACCGGAAAGG	CTGTTGAAAC	CAGCCCCAAG	700
TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	CTTCCAAGCC	750
CATGTGCGKT	CCGA				764

5

2) INFORMATION FOR SEQ ID NO: 1286

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 971 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 16264

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

ACCATCGATA	TCGCGCTCTG	GAAGTTCGAG	ACTCCCAAGT	ACTTCGTCAC	50
CGTCATCGAT	GCCCCTGGTC	ATCGTGACTT	CATCAAGAAC	ATGATCACTG	100
25 GTACCTCCCA	GGCTGATTGT	GCTATTCTCA	TCATTGCCGC	TGGTACTGGT	150
GAGTTCGAGG	CCGGTATCTC	CAAGGATGGC	CAGACCCGTG	AGCATGCTCT	200
GCTCGCCTAC	ACCCTGGGCG	TGAAGCAGCT	TATCGTCGCC	ATCAACAAGA	250
TGGACACCAC	CAAATGGTCT	GAGGATCGTT	TCAACGAAAT	CATCAAGGAG	300
ACTTCCAACT	TCATCAAGAA	GGTCGGATAC	AACCCCAAGT	CCGTTCATT	350
30 CGTGCCCATC	TCCGGCTTCA	ACGGTGACAA	CATGATCGAC	GTCTCCACCA	400
ATGCCCCCTG	GTACAAGGGC	TGGGAAAAGG	AGTCCAAGGC	TGGCAAGGCC	450
ACCGGCAAGA	CCCTCCTTGA	GGCTATCGAC	TCCATCGACC	CTCCTGCTCG	500
TCCCACCGAC	AAGCCTCTCC	GTCTCCCACT	CCAGGATGTC	TACAAGATTT	550
CTGGTATCGG	CACGGTGCCC	GTCGGTCGTG	TTGAGACTGG	TACCATCAAG	600
35 GCCGGTATGG	TCGTCACCTT	TGCCCCCGCC	AACGTCACCA	CTGAAGTCAA	650
GTCCGTCGAA	ATGCACCACG	AACAGCTYGC	CGAGGGCGTT	CCGGGTGACA	700
ACGTCGGCTT	CAACGTCAAG	AACGTYTCCG	TGAAGGAGGT	TCGTCTGGA	750
AACGTTGCTG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTG	CCGACTCCTT	800
CAACGCCCAG	GTCATCGTCC	TCAACCACCC	TGGTCAGGTC	GGTGCTGGCT	850
40 ACGCCCCGGT	CTTGATTGTC	CACACTGCCC	ACATTGCCTG	CAAGTTCTYT	900
GAGCTCCTCG	AGAAGATCGA	TCGTGKACC	GGCAAGTCCA	TGGAAAACAA	950
CCCCAAGTTC	ATCAAGTCTG	G			971

45

2) INFORMATION FOR SEQ ID NO: 1287

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exserohilum rostratum*

(B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

10	GGTCTGAGGA	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	50
	AAGAAGGTCG	GCTACAACCC	CAAGCACGTT	CCCTTCGTCC	CCATCTCCGG	100
	TTTCAACGGA	GACAACATGA	TCGAGGCCTC	CAGCAACTGC	CCCTGGTACA	150
	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACTGGTAA	GACCCTCCTT	200
	GAGGCCATTG	ACGCCATCGA	CCCTCCCAGC	CGTCCTACCG	ACAAGCCCCT	250
	CCGTCTTCCC	CTCCAGGATG	TCTACAAGAT	TGGTGGTATT	GGCACGGTTC	300
15	CCGTCGGTCG	TGTCGAGACC	GGTATCATCA	AGGCCGGTAT	GGTCGTCACC	350
	TTCGCCCCCG	CTGGTGTGAC	CACTGAAAGT	AAGTCCGTCG	AGATGCACCA	400
	CGAGCAGCTT	ACCGAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAACGTCA	450
	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GTAACGTTGC	CGGTGACTCC	500
	AAGAACGACC	CCCCCAAGGG	CTGCGAGTCT	TTCAACGCTC	AGGTCATTGT	550
20	CCTCAACCAC	CCTGGTCAGG	TCGGTGCCGG	TTACGCGCCA	GTCCTCGACT	600
	GCCACACCGC	CCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	CGAGAAGATT	650
	GACCGCCGTA	CCGGAAGTC	TGTCGAAGCC	TCTCCCAAGT	TCATCAAGTC	700
	TGGTGACGCG	GCCATCGTCA	AGATGGTTCC	CT		732

25

2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1236

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

45	AATGGATCCT	GTATACGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTTC	50
	TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTGGAAAT	CGCGGAAGCA	100
	CTTGTACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
	TCTTGTACCG	AAAGCAGAGA	TTGAAGGCGA	TATGGGTGAC	TCACACGTAG	200
	GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTMGTAAGCT	TTCAGGAGCA	250
	ATCAACAAAT	CARRARCAAT	WGCAATCTTT	ATTAACCAAA	TTCGWGAAAA	300
50	AGTTGGGGTT	ATGTTCCGGA	ACCCAGAAAC	AACTCCA		337

2) INFORMATION FOR SEQ ID NO: 1289

700

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

AATGGATCCT	GTATATGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTTC	50
TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTGGAAAT	CGCGGAAGCA	100
CTTGACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
TCTTGACCG	AAAGCAGAGA	TTGAAGGCGA	TATGGGTGAC	TCACACGTAG	200
GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTMGTAAGCT	TTCAGGAGCA	250
ATCAACAAAT	CARAARCAAT	TGCAATCTTT	ATTAACCAAA	TTCGTGAAAA	300
AGTTGGGGTT	ATGTTTCGAA	ACCCAGAAAC	AACTCC		336

2) INFORMATION FOR SEQ ID NO: 1290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT

23

2) INFORMATION FOR SEQ ID NO: 1291

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

GCIYTICIG AYGTMGIGA YGG

23

5 2) INFORMATION FOR SEQ ID NO: 1292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

ARISCYTCIA RIATRTGIGC

20

20

2) INFORMATION FOR SEQ ID NO: 1293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

ATGGCTGAAT TACCTCAATC

20

35

2) INFORMATION FOR SEQ ID NO: 1294

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

ATGATTGTTG TATATCTTCT TCAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295

CAGAAAGTTT GAAGCGTTGT

20

2) INFORMATION FOR SEQ ID NO: 1296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296

AACGATTCGT GAGTCAGATA

20

2) INFORMATION FOR SEQ ID NO: 1297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297

CGGTCAACAT TGAGGAAGAG CT

22

2) INFORMATION FOR SEQ ID NO: 1298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

ACGAAATCGA CCGTCTCTTT TTC

23

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 2711 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: 601055
(C) ACCESSION NUMBER: X71437

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

	ATGGCTGAAT	TACCTCAATC	AAGAATAAAT	GAACGAAATA	TTACCAGTGA	50
	AATGCGTGAA	TCATTTTTAG	ATTATGCGAT	GAGTGTTATC	GTTGCTCGTG	100
30	CATTGCCAGA	TGTTTCGTGAC	GGTTTAAAAC	CAGTACATCG	TCGTATACTA	150
	TATGGATTAA	ATGAACAAGG	TATGACACCG	GATAAATCAT	ATAAAAAATC	200
	AGCACGTATC	GTTGGTGACG	TAATGGGTAA	ATATCACCCT	CATGGTGACT	250
	CATCTATTTA	TGAAGCAATG	GTACGTATGG	CTCAAGATTT	CAGTTATCGT	300
	TATCCGCTTG	TTGATGGCCA	AGGTAACTTT	GGTTCAATGG	ATGGAGATGG	350
35	CGCAGCAGCA	ATGCGTTATA	CTGAAGCGCG	TATGACTAAA	ATCACACTTG	400
	AACTGTTACG	TGATATTAAT	AAAGATACAA	TAGATTTTAT	CGATAACTAT	450
	GATGGTAATG	AAAGAGAGCC	GTCAGTCTTA	CCTGCTCGAT	TCCCTAATTT	500
	ATTAGCCAAT	GGTGCATCAG	GTATCGCGGT	AGGTATGGCA	ACGAATATTC	550
	CACCACATAA	CTTAACAGAA	TTAATCAATG	GTGTACTTAG	CTTAAGTAAG	600
40	AACCCTGATA	TTTCAATTGC	TGAGTTAATG	GAAGATATTG	AAGGTCCTGA	650
	TTTCCCAACT	GCTGGACTTA	TTTTAGGTAA	GAGTGGTATT	AGACGTGCAT	700
	ATGAAACAGG	TCGTGGTTCA	ATTCAAATGC	GTTCTCGTGC	AGTTATTGAA	750
	GAACGTGGAG	GCGGACGTCA	ACGTATTGTT	GTCACTGAAA	TTCCTTTCCA	800
	AGTGAATAAG	GCTCGTATGA	TTGAAAAAAT	TGCAGAGCTC	GTTTCGTGACA	850
45	AGAAAATTGA	CGGTATCACT	GATTTACGTG	ATGAAACAAG	TTTACGTACT	900
	GGTGTGCGTG	TCGTTATTGA	TGTGCGTAAG	GATGCAAATG	CTAGTGTCAT	950
	TTTAAATAAC	TTATACAAAC	AAACACCTCT	TCAAACATCA	TTTGGTGTGA	1000
	ATATGATTGC	ACTTGTAAT	GGTAGACCGA	AGCTTATTAA	TTTAAAAGAA	1050
	GCGTTGGTAC	ATTATTTAGA	GCATCAAAAG	ACAGTTGTTA	GAAGACGTAC	1100
50	GCAATATAAC	TTACGTAAAG	CTAAAGATCG	TGCCCATATT	TTAGAAGGGT	1150
	TACGTATCGC	ACTTGACCAT	ATCGATGAAA	TTATTTCAAC	GATTCGTGAG	1200
	TCAGATACAG	ATAAAGTTGC	AATGGAAAGC	TTGCAACAAC	GCTTCAAAC	1250
	TTCTGAAAAA	CAAGCTCAAG	CTATTTTAGA	CATGCGTTTA	AGACGTCTAA	1300

	CAGGTTTAGA	GAGAAACAAA	ATTGAAGCTG	AATATAATGA	GTTATTAAAT	1350
	TATATTAGTG	AATTAGAAGC	CATCTTAGCT	GATGAAGAAG	TGTTATTACA	1400
	GTTAGTTAGA	GATGAATTGA	CTGAAATTAG	AGATCGTTTC	GGTGATGAGC	1450
	GTCGTACAGA	AATTCAATTA	GGTGGATTTG	AAGACTTAGA	GGACGAAGAC	1500
5	TTAATTCCAG	AAGAACAAAT	AGTAATTACT	TTGAGCCATA	ATAACTACAT	1550
	TAAACGTTTG	CCGGTATCTA	CATATCGTGC	TCAAAACCGT	GGTGGTCGTG	1600
	GTGTTCAAGG	TATGAATACA	TTGGAAGAAG	ATTTTGTCTG	TCAATTGGTA	1650
	ACTTTAAGTA	CACATGACCA	TGTATTGTTC	TTTACTAACA	AAGGTCGTGT	1700
	ATACAAACTA	AAAGGTTATG	AAGTGCCTGA	GTTATCAAGA	CAGTCTAAAG	1750
10	GTATTCCTGT	AGTGAATGCT	ATTGAACTTG	GAAATGATGA	AGTCATTAGT	1800
	ACAATGATTG	CTGTTAAAGA	CCTTGAAAGT	GAAGACAACT	TCTTAGTGTT	1850
	TGCAACTAAA	CGTGGTGTTG	TTAAACGTTT	AGCATTAAGT	AACTTCTCAA	1900
	GAATAAATAG	AAATGGTAAG	ATTGCGATTT	CGTTCAGAGA	AGATGATGAG	1950
	TTAATTGCAG	TTCGTTTAAC	AAGTGGTCAA	GAAGATATCT	TGATTGGTAC	2000
15	ATCACATGCA	TCATTAATTC	GATTCCCTGA	ATCAACATTA	CGTCCTTTAG	2050
	GCCGTACAGC	AACGGGTGTG	AAAGGTATTA	CACTTCGTGA	AGGTGACGAA	2100
	GTTGTAGGGC	TTGATGTAGC	TCATGCAAAC	AGTGTTGATG	AAGTATTAGT	2150
	AGTTACTGAA	AATGGTTATG	GTAAACGTAC	GCCAGTTAAT	GACTATCGTT	2200
	TATCAAATCG	TGGTGGTAAA	GGTATTAAAA	CAGCTACGAT	TACTGAGCGT	2250
20	AATGGTAATG	TTGTATGTAT	CACTACAGTA	ACTGGTGAAG	AAGATTTAAT	2300
	GATTGTTACT	AATGCCGGTG	TCATTATTCG	ACTAGATGTT	GCAGATATTT	2350
	CTCAAATGG	TCGTGCAGCA	CAAGGTGTTC	GCTTAATTCG	CTTAGGCGAT	2400
	GATCAATTTG	TTTCAACGGT	TGCTAAAGTA	AAAGAGGATG	CAGATGAAGT	2450
	AAATGAAGAT	GAACAATCTA	CTGTATCTGA	AGATGGTACT	GAACAACAAC	2500
25	GTGAAGCGGT	TGTAAATGAT	GAAACACCAG	GAAATGCAAT	TCATACTGAA	2550
	GTGATTGATT	CAGAAGAAAA	TGATGAAGAT	GGACGTATTG	AAGTAAGACA	2600
	AGATTTTCATG	GATCGTGTTG	AAGAAGATAT	ACAACAATCA	TCAGATGAAG	2650
	ATGAAGAATA	A				2711

30

2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 2628 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: K12

45 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

	ATGAGCGACC	TTGCGAGAGA	AATTACACCG	GTCAACATTG	AGGAAGAGCT	50
50	GAAGAGCTCC	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	100
	TGCCAGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	150
	GCCATGAACG	TACTAGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCTGC	200
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCATCCCCAT	GGTGACTCGG	250

	CGGTCTATGA	CACGATCGTC	CGCATGGCGC	AGCCATTCTC	GCTGCGTTAT	300
	ATGCTGGTAG	ACGGTCAGGG	TAAC TTCGGT	TCTATCGACG	GCGACTCTGC	350
	GGCGGCAATG	CGTTATACGG	AAATCCGTCT	GGCGAAAATT	GCCCATGAAC	400
	TGATGGCCGA	TCTCGAAAAA	GAGACGGTCG	ATTTTCGTTGA	TAAC TATGAC	450
5	GGCACGGAAA	AAATTCCGGA	CGTCATGCCA	ACCAAAATTC	CTAACCTGCT	500
	GGTGAACGGT	TCTTCCGGTA	TCGCCG TAGG	TATGGCAACC	AACATCCCGC	550
	CGCACAACT	GACGGAAGTC	ATCAACGGTT	GTCTGGCGTA	TATTGATGAT	600
	GAAGACATCA	GCATTGAAGG	GCTGATGGAA	CACATCCCGG	AGCCGGACTT	650
	CCCGACGGCG	GCAATCATT	ACGGTCGTCG	CGGTATTGAA	GAAGCTTACC	700
10	GTACCGGTCG	CGGCAAGGTG	TATATCCGCG	CTCGCGCAGA	AGTGGAAGTT	750
	GACGCCAAAA	CCGGTCGTGA	AACCATTATC	GTCCACGAAA	TTCCGTATCA	800
	GGTAAACAAA	GCGCGCCTGA	TCGAGAAGAT	TGCGGAACTG	GTAAAAGAAA	850
	AACGCGTGGA	AGGCATCAGC	GCGCTGCGTG	ACGAGTCTGA	CAAAGACGGT	900
	ATGCGCATCG	TGATTGAAGT	GAAACGCGAT	GCGGTCGGTG	AAGTTGTGCT	950
15	CAACAACCTC	TACTCCCAGA	CCCAGTTGCA	GGTTTCTTTC	GGTATCAACA	1000
	TGGTGGCATT	GCACCATGGT	CAGCCGAAGA	TCATGAACCT	GAAAGACATC	1050
	ATCGCGGCGT	TTGTTCGTCA	CCGCCGTGAA	GTGGTGACCC	GTCGTACTAT	1100
	TTTCGAACTG	CGTAAAGCTC	GCGATCGTGC	TCATATCCTT	GAAGCATTAG	1150
	CCGTGGCGCT	GGCGAACATC	GACCCGATCA	TCGAACTGAT	CCGTCATGCG	1200
20	CCGACGCCTG	CAGAAGCGAA	AACTGCGCTG	GTTGCTAATC	CGTGGCAGCT	1250
	GGGCAACGTT	GCCGCGATGC	TCGAACGTGC	TGGCGACGAT	GCTGCGCGTC	1300
	CGGAATGGCT	GGAGCCAGAG	TTGGCGGTGC	GTGATGGTCT	GTACTACCTG	1350
	ACCGAACAGC	AAGCTCAGGC	GATTCTGGAT	CTGCGTTTGC	AGAAACTGAC	1400
	CGGTCTTGAG	CACGAAAAAC	TGCTCGACGA	ATACAAAGAG	CTGCTGGATC	1450
25	AGATCGCGGA	ACTGTTGCGT	ATTCTTG GTA	GCGCCGATCG	TCTGATGGAA	1500
	GTGATCCGTG	AAGAGCTGGA	GCTGGTTCGT	GAACAGTTCG	GTGACAAACG	1550
	TCGTACTGAA	ATCACCGCCA	ACAGCGCAGA	CATCAACCTG	GAAGATCTGA	1600
	TCACCCAGGA	AGATGTGGTC	GTGACGCTCT	CTCACCAGGG	CTACGTTAAG	1650
	TATCAGCCGC	TTTCTGAATA	CGAAGCGCAG	CGTCGTGGCG	GGAAAGGTAA	1700
30	ATCTGCCGCA	CGTATTAAAG	AAGAAGACTT	TATCGACCGA	CTGCTGGTGG	1750
	CGAACACTCA	CGACCATATT	CTGTGCTTCT	CCAGCCGTGG	TCGCGTCTAT	1800
	TCGATGAAAG	TTTATCAGTT	GCCGGAAGCC	ACTCGTGGCG	CGCGCGGTCTG	1850
	TCCGATCGTC	AACCTGCTGC	CGCTGGAGCA	GGACGAACGT	ATCACTGCGA	1900
	TCCTGCCAGT	GACCGAGTTT	GAAGAAGGCG	TGAAAGTCTT	CATGGCGACC	1950
35	GCTAACGGTA	CCGTGAAGAA	AACTGTCCTC	ACCGAGTTCA	ACCGTCTGCG	2000
	TACCGCCGGT	AAAGTG GCGA	TCAAAC TGGT	TGACGGCGAT	GAGCTGATCG	2050
	GCGTTGACCT	GACCAGCGGC	GAAGACGAAG	TAATGCTGTT	CTCCGCTGAA	2100
	GGTAAAGTGG	TGCGCTTTAA	AGAGTCTTCT	GTCCGTGCGA	TGGGCTGCAA	2150
	CACCACCGGT	GTTTCGCGGTA	TTCGCTTAGG	TGAAGGCGAT	AAAGTCGTCT	2200
40	CTCTGATCGT	GCCTCGTGGC	GATGGCGCAA	TCCTCACC GC	AACGCAAAAC	2250
	GGTTACGGTA	AACGTACCGC	AGTGGCGGAA	TACCCAACCA	AGTCGCGTGC	2300
	GACGAAAGGG	GTTATCTCCA	TCAAGGTTAC	CGAACGTAAC	GGTTTAGTTG	2350
	TTGGCGCGGT	ACAGGTAGAT	GACTGCGACC	AGATCATGAT	GATCACCGAT	2400
	GCCGGTACGC	TGGTACGTAC	TCGCGTTTCG	GAAATCAGCA	TCGTGGGCCG	2450
45	TAACACCCAG	GGCGTGATCC	TCATCCGTAC	TGCGGAAGAT	GAAAACGTAG	2500
	TGGGTCTGCA	ACGTGTTGCT	GAACCGGTTG	ACGAGGAAGA	TCTGGATACC	2550
	ATCGACGGCA	GTGCCGCGGA	AGGGGACGAT	GAAATCGCTC	CGGAAGTGGA	2600
	CGTTGACGAC	GAGCCAGAAG	AAGAATAA			2628

50

2) INFORMATION FOR SEQ ID NO: 1301

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301

GTIMGIAWIM GICCIGSIAT GTA

2) INFORMATION FOR SEQ ID NO: 1302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302

TAIADIGGIG GIKKIGCIAT RTA

2) INFORMATION FOR SEQ ID NO: 1303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303

GGIGAIGAID YIMGIGARGG

2) INFORMATION FOR SEQ ID NO: 1304

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

5

CIARYTTIKY ITTIGTYTG

19

10 2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

ATGGTGACTG CATTGTCAGA TG

22

25

2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

GTCTACGGTT TTCTACAACG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1923 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

5	ATGGTGACTG	CATTGTCAGA	TGTAAACAAC	ACGGATAATT	ATGGTGCTGG	50
	GCAAATACAA	GTATTAGAAG	GTTTAGAAGC	AGTACGTAAA	AGACCAGGTA	100
	TGTATATAGG	ATCGACTCAG	AGAGAGTTGC	ACATTAGTGT	GGAAATTGTC	150
	GATAATAGTA	TCGATGAAGC	ATTAGCTGGT	TATGCAAATA	AAATTGAAGT	200
	TGTTATTGAA	AAAGATAACT	GGATTAAAGT	AACGGATAAC	GGACGTGGTA	250
10	TCCCAGTTGA	TATTCAAGAA	AAAATGGGAC	GTCCAGCTGT	CGAAGTTATT	300
	TTAACTGTTT	TACATGCTGG	TGGTAAATTC	GGCGGTGGCG	GATACAAAGT	350
	ATCTGGTGGT	TTACATGGTG	TTGGTTCATC	AGTTGTAAAC	GCATTGTCAC	400
	AAGACTTAGA	AGTATATGTA	CACAGAAATG	AGACTATATA	TCATCAAGCA	450
	TATAAAAAAG	GTGTACCTCA	ATTTGACTTA	AAAGAAGTTG	GCACAACTGA	500
15	TAAGACAGGT	ACTGTCATTC	GTTTTAAAGC	AGATGGAGAA	ATCTTCACAG	550
	AGACAACGTG	ATACAACCTAT	GAAACATTAC	AGCAGCGTAT	TAGAGAGCTT	600
	GCTTTCTTAA	ACAAAGGAAT	TCAAATCACA	TTAAGAGATG	AACGTGATGA	650
	AGAAAACGTT	AGAGAAGACT	CCTATCACTA	TGAGGGCGGT	ATTAAATCGT	700
	ACGTTGAGTT	ATTGAACGAA	AATAAAGAAC	CTATTCATGA	TGAGCCAATT	750
20	TATATTCATC	AATCTAAAGA	TGATATTGAA	GTAGAAATTG	CGATTCAATA	800
	TAACCTCAGGA	TATGCCACAA	ATCTTTTAAAC	TTACGCAAAT	AACATTCATA	850
	CGTACGAAGG	TGGTACGCAT	GAAGACGGAT	TCAAACGTGC	ATTAACGCGT	900
	GTCTTAAATA	GTTATGGTTT	AAGTAGCAGA	TATGAAGAAG	AAAAGATAGC	950
	TTCTGGTGAA	GATACACGAG	AAGGTATGAC	AGCAATTATA	TCTATCAAAC	1000
25	ATGGTGATCC	TCAATTCGAA	GGTCAAACGA	AGACAAAATT	AGGTAATTCT	1050
	GAAGTGCGTC	AAGTTGTAGA	TAAATTATTC	TCAGAGCACT	TTGAACGATT	1100
	TTTATATGAA	AATCCACAAG	TCGCACGTAC	AGTGGTTGAA	AAAGGTATTA	1150
	TGGCGGCACG	TGCACGTGTT	GCTGCGAAAA	AAGCGCGTGA	AGTAACACGT	1200
	CGTAAATCAG	CGTTAGATGT	AGCAAGTCTT	CCAGGTAAAT	TAGCCGATTG	1250
30	CTCTAGTCAA	AGTCCTGAAG	AATGTGAGAT	TTTCTTAGTC	GAAGGGGACT	1300
	CTGCCGGAGG	GTCTACAAAA	TCTGGTCGTG	ACTCTAGAAC	GCAGGCGATT	1350
	TTACCATTAC	GAGGTAAGAT	ATTAAATGTT	GAAAAAGCAC	GATTAGATAG	1400
	AATTTTGAAT	AACAATGAAA	TTCGTCAAAT	GATCACAGCA	TTTGGTACAG	1450
	GAATCGGTGG	CGACTTTGAT	CTAGCGAAAG	CAAGATATCA	CAAAATCGTC	1500
35	ATTATGACTG	ATGCCGATGT	GGATGGAGCG	CATATTAGAA	CATTGTTATT	1550
	AATATTCTTC	TATCGATTTA	TGAGACCGTT	AATTGAAGCA	GGCTATGTGT	1600
	ATATTGCACA	GCCACCGTTG	TATAAACTGA	CACAAGGTAA	ACAAAAGTAT	1650
	TATGTATACA	ATGATAGGGA	ACTTGATAAA	CTTAAATCTG	AATTGAATCC	1700
	AACACCAAAA	TGGTCTATTG	CGCTATACAA	AGGTCTTGGA	GAAATGAATG	1750
40	CAGATCAATT	ATGGGAAACA	ACAATGAACC	CTGAGCACCG	CGCTCTTTTA	1800
	CAAGTAAAAC	TTGAAGATGC	GATTGAAGCG	GACCAAACAT	TTGAAATGTT	1850
	AATGGGTGAC	GTTGTAGAAA	ACCGTAGACA	ATTTATAGAA	GATAATGCAG	1900
	TTTATGCAAA	CTTAGACTTC	TAA			1923

45

2) INFORMATION FOR SEQ ID NO: 1308

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

5

ATGTAYGTIA TIATGGAYMG IGC

23

10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATIATYTTRT TICCYTTICC YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATIATITSIA TIACYTCRTC

20

40

2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

GARATGAARA TIMGIGGIGA RCA

23

5 2) INFORMATION FOR SEQ ID NO: 1312

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

AARTAYATIA TICARGARMG IGC

23

20

2) INFORMATION FOR SEQ ID NO: 1313

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

AMIAYICKRT GIGGITTITT YTT

23

35

2) INFORMATION FOR SEQ ID NO: 1314

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

TAIGAITYA CIGAISMICA RGC

23

50

2) INFORMATION FOR SEQ ID NO: 1315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315

ACIATIGCIT CIGCYTGIKS YTC

23

2) INFORMATION FOR SEQ ID NO: 1316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316

GTGAGTGAAA TAATTCAAGA TT

22

2) INFORMATION FOR SEQ ID NO: 1317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317

CACCAAAATC ATCTGTATCT AC

22

2) INFORMATION FOR SEQ ID NO: 1318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

10

2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCCTCIA CCATCGGYAG YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 2259 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 MG1655

(C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

45	ATGAGCGATA	TGGCAGAGCG	CCTTGCGCTA	CATGAATTTA	CGGAAAACGC	50
	CTACTTAAAC	TACTCCATGT	ACGTGATCAT	GGACCGTGCG	TTGCCGTTTA	100
	TTGGTGATGG	TCTGAAACCT	GTTTCAGCGCC	GCATTGTGTA	TGCGATGTCT	150
	GAAGTGGGCC	TGAATGCCAG	CGCCAAATTT	AAAAAATCGG	CCCGTACCGT	200
	CGGTGACGTA	CTGGGTAAAT	ACCATCCGCA	CGGCGATAGC	GCCTGTTATG	250
	AAGCGATGGT	CCTGATGGCG	CAACCGTTCT	CTTACCGTTA	TCCGCTGGTT	300
50	GATGGTCAGG	GGAAGTGGGG	CGCGCCGGAC	GATCCGAAAT	CGTTCGCGGC	350
	AATGCGTTAC	ACCGAATCCC	GGTTGTCGAA	ATATTCCGAG	CTGCTATTGA	400
	GCGAGCTGGG	GCAGGGGACG	GCTGACTGGG	TGCCAAACTT	CGACGGCACT	450
	TTGCAGGAGC	CGAAAATGCT	ACCTGCCCGT	CTGCCAAACA	TTTTGCTTAA	500

	CGGCACCACC	GGTATTGCCG	TCGGCATGGC	GACCGATATT	CCACCGCATA	550
	ACCTGCGTGA	AGTGGCTCAG	GCGGCAATCG	CATTAATCGA	CCAGCCGAAA	600
	ACCACGCTCG	ATCAGCTGCT	GGATATCGTG	CAGGGGCCGG	ATTATCCGAC	650
	TGAAGCGGAA	ATTATCACTT	CGCGCGCCGA	GATCCGTAAA	ATCTACGAGA	700
5	ACGGACGTGG	TTCAGTGCCT	ATGCGCGCGG	TGTGGAAGAA	AGAAGATGGC	750
	GCGGTGGTTA	TCAGCGCATT	GCCGCATCAG	GTTTCAGGTG	CGCGCGTACT	800
	GGAGCAAATT	GCTGCGCAAA	TGCGCAACAA	AAAGCTGCCG	ATGGTTGACG	850
	ATCTGCGCGA	TGAATCTGAC	CACGAGAACC	CGACCCGCCT	GGTGATTGTG	900
	CCGCGTTCCA	ACCGCGTGGA	TATGGATCAG	GTGATGAACC	ACCTCTTCGC	950
10	TACCACCGAT	CTGGAAAAGA	GCTATCGTAT	TAACCTTAAT	ATGATCGGTC	1000
	TGGATGGTCG	TCCGGCGGTG	AAAAACCTGC	TGGAAATCCT	CTCCGAATGG	1050
	CTGGTGTTCC	GCCGCGATAC	CGTGCGCCGC	CGACTGAACT	ATCGTCTGGA	1100
	GAAAGTCCTC	AAGCGCCTGC	ATATCCTCGA	AGGTTTGCTG	GTGGCGTTTC	1150
	TCAATATCGA	CGAAGTGATT	GAGATCATTC	GTAATGAAGA	TGAACCGAAA	1200
15	CCGGCGCTGA	TGTCGCGGTT	TGGCCTTACG	GAAACCCAGG	CGGAAGCGAT	1250
	CCTCGAACTG	AAACTGCGTC	ATCTTGCCAA	ACTGGAAGAG	ATGAAGATTC	1300
	GCGGTGAGCA	GAGTGAAGTG	GAAAAAGAGC	GCGACCAGTT	GCAGGGCATT	1350
	TTGGCTTCCG	AGCGTAAAAT	GAATAACCTG	CTGAAGAAAG	AACTGCAGGC	1400
	AGACGCGCAA	GCCTACGGTG	ACGATCGTCG	TTCGCCGTTG	CAGGAACGCG	1450
20	AAGAAGCGAA	AGCGATGAGC	GAGCACGACA	TGCTGCCGTC	TGAACCTGTC	1500
	ACCATTGTGC	TGTCGCAGAT	GGGCTGGGTA	CGCAGCGCTA	AAGGCCATGA	1550
	TATCGACGCG	CCGGGCCTGA	ATTATAAAGC	GGGTGATAGC	TTCAAAGCGG	1600
	CGGTGAAAGG	TAAGAGCAAC	CAACCGGTAG	TGTTTGTTGA	TTCCACCGGT	1650
	CGTAGCTATG	CCATTGACCC	GATTACGCTG	CCGTCGGCGC	GTGGTCAGGG	1700
25	CGAGCCGCTC	ACCGGCAAAT	TAACGTTGCC	GCCTGGGGCG	ACCGTTGACC	1750
	ATATGCTGAT	GGAAAGCGAC	GATCAGAAAC	TGCTGATGGC	TTCCGATGCG	1800
	GGTTACGGTT	TCGTCTGCAC	CTTTAACGAT	CTGGTGGCGC	GTAACCGTGC	1850
	AGGTAAGGCT	TTGATCACCT	TACCGGAAAA	TGCCCATGTT	ATGCCGCCGG	1900
	TGGTGATTGA	AGATGCTTCC	GATATGCTGC	TGGCAATCAC	TCAGGCAGGC	1950
30	CGTATGTTGA	TGTTCCCGGT	AAGTGATCTG	CCGCAGCTGT	CGAAGGGCAA	2000
	AGGCAACAAG	ATTATCAACA	TTCCATCGGC	AGAAGCCGCG	CGTGGAGAAG	2050
	ATGGTCTGGC	GCAATTGTAC	GTTCTGCCGC	CGCAAAGCAC	GCTGACCATT	2100
	CATGTTGGGA	AACGCAAAAT	TAAACTGCGC	CCGGAAGAGT	TACAGAAAGT	2150
	CACTGGCGAA	CGTGGACGCC	GCGGTACGTT	GATGCGCGGT	TTGCAGCGTA	2200
35	TCGATCGTGT	TGAGATCGAC	TCTCCTCGCC	GTGCCAGCAG	CGGTGATAGC	2250
	GAAGAGTAA					2259

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 2403 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: KMP9
 (C) ACCESSION NUMBER: D67074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

	GTGAGTGAAA	TAATTCAAGA	TTTATCACTT	GAAGATGTTT	TAGGTGATCG	50
5	CTTTGGAAGA	TATAGTAAAT	ATATTATTCA	AGAGCGTGCA	TTGCCAGATG	100
	TTCGTGATGG	TTTAAAACCA	GTACAACGTC	GTATTTTATA	TGCAATGTAT	150
	TCAAGTGGTA	ATACACACGA	TAAAAATTTT	CGTAAAAGTG	CGAAAACAGT	200
	CGGTGATGTT	ATTGGTCAAT	ATCATCCACA	TGGAGACTTC	TCAGTGTACA	250
	AAGCAATGGT	CCGTTTAAGT	CAAGACTGGA	AGTTACGACA	TGTCTTAATA	300
10	GAAATGCATG	GTAATAATGG	TAGTATCGAT	AATGATCCGC	CAGCGGCAAT	350
	GCGTTACACT	GAAGCTAAGT	TAAGCTTACT	AGCTGAAGAG	TTATTACGTG	400
	ATATTAATAA	AGAGACAGTT	TCTTTCATTC	CAAACATGA	TGATACGACA	450
	CTCGAACCAA	TGGTATTGCC	ATCAAGATTT	CCTAACTTAC	TAGTGAATGG	500
	TTCTACAGGT	ATATCTGCAG	GTTACGCGAC	AGATATACCA	CCACATAATT	550
15	TAGCTGAAGT	GATTCAAGCA	ACACTTAAAT	ATATTGATAA	TCCGGATATT	600
	ACAGTCAATC	AATTAATGAA	ATATATTAAA	GGTCCTGATT	TTCCAACCTGG	650
	TGGTATTATT	CAAGGTATTG	ATGGTATTAA	AAAAGCTTAT	GAATCAGGTA	700
	AAGGTAGAAT	TATAGTTCGT	TCTAAAGTTG	AAGAAGAAAC	TTTACGCAAT	750
	GGACGTAAAC	AGTTAATTAT	TACTGAAATT	CCATATGAAG	TGAACAAAAG	800
20	TAGCTTAGTA	AAACGTATCG	ATGAATTACG	TGCTGACAAA	AAAGTCGATG	850
	GTATCGTTGA	AGTACGTGAT	GAAACTGATA	GAAGTGGTTT	ACGAATAGCA	900
	ATTGAATTGA	AAAAAGATGT	GAACAGTGAA	TCAATCAAAA	ATTATCTTTA	950
	TAAAACTCT	GATTTACAGA	TTTCATATAA	TTTCAACATG	GTCGCTATTA	1000
	GTGATGGTCG	TCCAAAATTG	ATGGGTATTC	GTCAAATTAT	AGATAGTTAT	1050
25	TTGAATCATC	AAATTGAGGT	TGTTGCAAAT	AGAACGAAGT	TTGAATTAGA	1100
	TAATGCTGAA	AAACGTATGC	ATATCGTTGA	AGGTTTGATT	AAAGCGTTGT	1150
	CAATTTTAGA	TAAAGTAATT	GAATTGATTC	GTAGCTCTAA	AAACAAGCGT	1200
	GACGCTAAAG	AAAACCTTAT	CGAAGTATTC	GAGTTCACAG	AAGAACAGGC	1250
	TGAAGCAATT	GTAATGTTAC	AGTTATATCG	TTTAACAAAC	ACTGACATAG	1300
30	TTGCGCTTGA	AGGTGAACAT	AAAGAACTTG	AAGCATTAAT	CAAACAATTA	1350
	CGTCATATTC	TTGATAACCA	TGATGCATTA	TTGAATGTCA	TAAAAGAAGA	1400
	ATTGAATGAA	ATTAATAAGA	AATTCAAATC	TGAACGACTG	TCTTTAATTG	1450
	AAGCAGAAAT	TGAAGAAATT	AAAATTGACA	AAGAAGTTAT	GGTGCCTAGT	1500
	GAAGAAGTTA	TTTTAAGTAT	GACACGTCAT	GGATATATTA	AACGTACTTC	1550
35	TATTCGTAGC	TTTAATGCTA	GCGGTGTTGA	GGATATTGGT	TTAAAAGATG	1600
	GTGACAGTTT	ACTTAAACAT	CAAGAAGTAA	ATACGCAAGA	TACCGTACTA	1650
	GTATTTACAA	ATAAAGGTCG	TTATCTATTT	ATACCGGTTT	ATAAATTAGC	1700
	AGATATTTCG	TGGAAAGAAT	TGGGGCAACA	TGTATCACAA	ATAGTTCCTA	1750
	TCGAAGAAGA	TGAAGTGGTT	ATTAATGTCT	TTAATGAAAA	GGACTTTAAT	1800
40	ACAGATGCAT	TTTATGTTTT	TGCGACTCAA	AATGGCATGA	TTAAGAAAAG	1850
	TACAGTGCCT	CTATTTAAAA	CAACGCGTTT	TAATAAACCT	TTAATTGCTA	1900
	CTAAAGTTAA	AGAAAATGAT	GATTTGATTA	GTGTTATGCG	CTTTGAAAAA	1950
	GATCAATTAA	TTACCGTCAT	TACTAATAAA	GGTATGTCAT	TAACGTATAA	2000
	TACAAGTGAA	CTATCAGATA	CCGGATTAAAG	GGCAGCTGGT	GTTAAATCAA	2050
45	TAAATCTTAA	AGCTGAAGAT	TTCGTTGTTA	TGACAGAAGG	TGTTTCTGAA	2100
	AATGATACTA	TATTGATGGC	CACACAACGC	GGCTCGTTAA	AACGTATTAG	2150
	TTTTAAAAATC	TTACAAGTTG	CTAAAAGAGC	ACAACGTGGA	ATAACTTTAT	2200
	TAAAAGAATT	AAAGAAAAAT	CCACATCGTA	TTGTAGCTGC	ACATGTAGTG	2250
	ACAGGTGAAC	ATAGTCAATA	TACATTATAT	TCAAAATCAA	ATGAAGAACA	2300
50	TGGTTTAATT	AATGATATTC	ATAAATCTGA	ACAATATACA	AATGGCTCAT	2350
	TCATTGTAGA	TACAGATGAT	TTTGGTGAAG	TAATAGACAT	GTATATTAGC	2400
	TAA					2403

2) INFORMATION FOR SEQ ID NO: 1322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIAAYI SIGTIGAYGA RG

22

2) INFORMATION FOR SEQ ID NO: 1323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

2) INFORMATION FOR SEQ ID NO: 1324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

CCICCGICIS WRTCICCYTC

20

2) INFORMATION FOR SEQ ID NO: 1325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

RTTCATYTCI CCIARICCYT T

21

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

TGATTCAATA CAGGTTTTAG AG

22

25

2) INFORMATION FOR SEQ ID NO: 1327

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

40

CTAGATTTC TCCTCATCAA AT

22

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1992 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: RN4220

(C) ACCESSION NUMBER: D67075

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

	ATGAATAAAC	AAAATAATTA	TTCAGATGAT	TCAATACAGG	TTTTAGAGGG	50
	GTTAGAAGCA	GTTTCGTAAAA	GACCTGGTAT	GTATATTGGA	TCAACTGATA	100
10	AACGGGGATT	ACATCATCTA	GTATATGAAA	TTGTCGATAA	CTCCGTCGAT	150
	GAAGTATTGA	ATGGTTACGG	TAACGAAATA	GATGTAACAA	TTAATAAAGA	200
	TGGTAGTATT	TCTATAGAAG	ATAATGGACG	TGGTATGCCA	ACAGGTATAC	250
	ATAAATCAGG	TAAACCGACA	GTCGAAGTTA	TCTTTACTGT	TTTACATGCA	300
	GGAGGTAAAT	TTGGACAAGG	CGGCTATAAA	ACTTCAGGTG	GTCTTCACGG	350
15	TGTTGGTGCT	TCAGTTGTAA	ATGCATTGAG	TGAATGGCTT	GAAGTTGAAA	400
	TCCATCGAGA	TGGTAATATA	TATCATCAAA	GTTTTAAAAA	CGGTGGTTTCG	450
	CCATCTTCTG	GTTTAGTGAA	AAAAGGTAAG	ACTAAGAAAA	CAGGTACCAA	500
	AGTAACATTT	AAACCTGATG	ACACAATTTT	TAAAGCATCT	ACATCATTTA	550
	ATTTTGATGT	TTTAAGTGAA	CGACTACAAG	AGTCTGCGTT	CTTATTGAAA	600
20	AATTTAAAAA	TAACGCTTAA	TGATTTACGC	AGTGGTAAAG	AGCGTCAAGA	650
	GCATTACCAT	TATGAAGAAG	GAATCAAAGA	GTTTGTTAGT	TATGTCAATG	700
	AAGGAAAAGA	AGTTTTGTCAT	GACGTGGCTA	CATTTTCAGG	TGAAGCAAAT	750
	GGTATAGAGG	TAGACGTAGC	TTTCCAATAT	AATGATCAAT	ATTCAGAAAG	800
	TATTTTAAGT	TTTGTAATA	ATGTACGTAC	TAAAGATGGT	GGTACACATG	850
25	AAGTTGGTTT	TAAAACAGCA	ATGACACGTG	TATTTAATGA	TTATGCACGT	900
	CGTATTAATG	AACTTAAAAC	AAAAGATAAA	AACTTAGATG	GTAATGATAT	950
	TCGTGAAGGT	TAAACAGCTG	TTGTGTCTGT	TCGTATTCCA	GAAGAATTAT	1000
	TGCAATTTGA	AGGACAAACG	AAATCTAAAT	TGGGTACTTC	TGAAGCTAGA	1050
	AGTGCTGTTG	ATTCAGTTGT	TGCAGACAAA	TTGCCATTCT	ATTTAGAAGA	1100
30	AAAAGGACAA	TTGTCTAAAT	CACTTGTTGAA	AAAAGCGATT	AAAGCACAAAC	1150
	AAGCAAGGGA	AGCTGCACGT	AAAGCTCGTG	AAGATGCTCG	TTCAGGTAAG	1200
	AAAAACAAGC	GTAAAGACAC	TTTGCTATCT	GGTAAATTAA	CACCTGCACA	1250
	AAGTAAAAAC	ACTGAAAAAA	ATGAATTGTA	TTTAGTCGAA	GGTGATTCTG	1300
	CGGGAGGTTT	AGCAAAACTT	GGACGAGACC	GCAAATTCCA	AGCGATATTA	1350
35	CCATTACGTG	GTAAGGTAAT	TAATACAGAG	AAAGCACGTC	TAGAAGATAT	1400
	TTTTAAAAAT	GAAGAAATTA	ATACAATTAT	CCACACAATC	GGGGCAGGCG	1450
	TTGGTACTGA	CTTTAAAATT	GAAGATAGTA	ATTATAATCG	TGTAATTATT	1500
	ATGACTGATG	CTGATACTGA	TGGTGCGCAT	ATTCAAGTGC	TATTGTTAAC	1550
	ATTCTTCTTC	AAATATATGA	AACCGCTTGT	TCAAGCAGGT	CGTGTATTTA	1600
40	TTGCTTTACC	TCCACTTTAT	AAATTGGAAG	AAGGTAAAGG	CAAAACAAAG	1650
	CGAGTTGAAT	ACGCTTGGAC	AGACGAAGAG	CTTAATAAAT	TGCAAAAAGA	1700
	ACTTGGTAAA	GGCTTCACGT	TACAACGTTA	CAAAGGTTTG	GGTGAAATGA	1750
	ACCCTGAGCA	ATTATGGGAA	ACGACGATGA	ACCCAGAAAC	ACGAACTTTA	1800
	ATTCGTGTAC	AAGTTGAAGA	TGAAGTGCGT	TCATCTAAAC	GTGTAACAAC	1850
45	ATTAATGGGT	GACAAAGTAC	AACCTAGACG	TGAATGGATT	GAAAAGCATG	1900
	TTGAGTTTGG	TATGCAAGAG	GACCAAAGTA	TTTTAGATAA	TTCTGAAGTA	1950
	CAAGTGCTTG	AAAATGATCA	ATTTGATGAG	GAGGAAATCT	AG	1992

50

2) INFORMATION FOR SEQ ID NO: 1329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

10 TGTAGAGCGC GGTATCATCA AAGTA

25

2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

25

AGATTCGAAC TTGGTGTGCG GG

22

2) INFORMATION FOR SEQ ID NO: 1331

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

40

GCCCTTGAGG TACAGAATGG TAATGAAGTT

30

2) INFORMATION FOR SEQ ID NO: 1332

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA

20

2) INFORMATION FOR SEQ ID NO: 1333

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG

23

2) INFORMATION FOR SEQ ID NO: 1334

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

35

CATCTATTTA TAAAGCAATG GTA

23

2) INFORMATION FOR SEQ ID NO: 1335

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

50

CTATTTATGG AGCAATGGT

19

2) INFORMATION FOR SEQ ID NO: 1336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

2) INFORMATION FOR SEQ ID NO: 1337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

2) INFORMATION FOR SEQ ID NO: 1338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

GTGTACGGAG CAATG

15

2) INFORMATION FOR SEQ ID NO: 1339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TGCCT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

40 GATAACTGAA ATCCTGAGCC ATACG

25

2) INFORMATION FOR SEQ ID NO: 1342

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

29

20

2) INFORMATION FOR SEQ ID NO: 1344

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

2) INFORMATION FOR SEQ ID NO: 1346

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

2) INFORMATION FOR SEQ ID NO: 1347

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

2) INFORMATION FOR SEQ ID NO: 1348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Unidentified bacterium
(C) ACCESSION NUMBER: X04555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

ATGCGCTCAC	GCAACTGGTC	CAGAACCTTG	ACCGAACGCA	GCGGTGGTAA	50
CGGCGCAGTG	GCGGTTTTCA	TGGCTTGTTA	TGACTGTTTT	TTTGTACAGT	100
CTATGCCTCG	GGCATCCAAG	CAGCAAGCGC	GTTACGCCGT	GGGTCGATGT	150
TTGATGTTAT	GGAGCAGCAA	CGATGTTACG	CAGCAGGGCA	GTCGCCCTAA	200
AACAAAGTTA	GGCCGCATGG	ACACAACGCA	GGTCACATTG	ATACACAAAA	250

	TTCTAGCTGC	GGCAGATGAG	CGAAATCTGC	CGCTCTGGAT	CGGTGGGGGC	300
	TGGGCGATCG	ATGCACGGCT	AGGGCGTGTA	ACACGCAAGC	ACGATGATAT	350
	TGATCTGACG	TTTCCCGGCG	AGAGGCGCGG	CGAGCTCGAG	GCAATAGTTG	400
	AAATGCTCGG	CGGGCGCGTC	ATGGAGGAGT	TGGACTATGG	ATTCTTAGCG	450
5	GAGATCGGGG	ATGAGTTACT	TGACTGCGAA	CCTGCTTGGT	GGGCAGACGA	500
	AGCGTATGAA	ATCGCGGAGG	CTCCGCAGGG	CTCGTGCCCA	GAGGCGGCTG	550
	AGGGCGTCAT	CGCCGGGCGG	CCAGTCCGTT	GTAACAGCTG	GGAGGCGATC	600
	ATCTGGGATT	ACTTTTACTA	TGCCGATGAA	GTACCACCAG	TGGACTGGCC	650
	TACAAAGCAC	ATAGAGTCCT	ACAGGCTCGC	ATGCACCTCA	CTCGGGGCGG	700
10	AAAAGGTTGA	GGTCTTGCGT	GCCGCTTTCA	GGTCGCGATA	TGCGGCCTAA	750

2) INFORMATION FOR SEQ ID NO: 1349

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

30 2) INFORMATION FOR SEQ ID NO: 1350

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

TAATCAGGGC AGTTGCGACT CCTA

24

45

2) INFORMATION FOR SEQ ID NO: 1351

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: Stone 130
(C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

```
10 ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAC      50
   AAAGTTAGGT GGCTCAATGA GCATCATTGC AACCGTCAAG ATCGGCCCTG      100
   ACGAAATTC AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT      150
   GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC      200
   CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG      250
15 GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCCAA GTTCGAGCAA      300
   GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG      350
   AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG      400
   TTGAACTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CGGTGACGAT      450
   CCGGCAGTCG CTCTCTACAC AAAGCTTGGA GTTCGGAAG ACGTCATGCA      500
20 CTTCGACATT GATCCAAGAA CCGCCACCTA A              531
```

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG

22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG

22

2) INFORMATION FOR SEQ ID NO: 1354

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

15

2) INFORMATION FOR SEQ ID NO: 1355

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

30

2) INFORMATION FOR SEQ ID NO: 1356

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 45 (C) ACCESSION NUMBER: M97172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

50 ATGAACACGA TCGAATCGAT CACGGCGGAC CTGCACGGAC TGGGCGTCCG 50
 GCCCGGCGAC CTGATCATGG TCCATGCATC GCTGAAAGCC GTCGGCCCCG 100
 TCGAGGGAGG TGCGGCCTCG GTGGTGTGCG CCCTTCGCGC CGCGGTCTGG 150
 TCCGCAGGGA CCCTGATGGG TTATGCCTCA TGGGACCGCT CGCCCTATGA 200
 GGAGACGCTG AACGGCGCGC GGATGGACGA AGAACTGCGC CGCCGGTGGC 250

	CACCCTTCGA	TCTGGCCACA	TCCGGTACCT	ATCCCGGCTT	CGGCCTGCTC	300
	AACCGGTTTC	TGCTTGAGGC	GCCCGACGCA	CGGCGCAGCG	CGCATCCCGA	350
	CGCCTCCATG	GTCGCGGTCG	GCCCCCTTGC	CGCCACGCTG	ACAGAGCCGC	400
	ACCGGCTTGG	GCAGGCGCTG	GGCGAAGGCT	CGCCGCTGGA	GCGCTTCGTC	450
5	GGGCATGGCG	GAAAGGTCCT	GCTTCTGGGA	GCGCCGCTCG	ACTCCGTCAC	500
	CGTGCTGCAT	TACGCCGAGG	CCATCGCCCC	CATCCCGAAC	AAACGCCGCG	550
	TGACCTATGA	AATGCCGATG	CTCGGCCCGG	ATGGCAGGGT	CCGATGGGAG	600
	CTGGCCGAGG	ATTTGACAG	CAACGGCATT	CTCGATTGCT	TCGCGGTCGA	650
	TGGGAAGCCG	GATGCCGTCG	AGACGATCGC	CAAGGCTTAT	GTCGAACTGG	700
10	GCCGGCATCG	GGAAGGCATC	GTCGGTTCGC	CACCCTCCTA	TCTGTTTGAA	750
	GCGCAGGATA	TCGTCTCGTT	CGGCGTCACC	TATCTCGAAC	AGCATTTCGG	800
	CGCGCCCTGA					810

15

2) INFORMATION FOR SEQ ID NO: 1357

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

2) INFORMATION FOR SEQ ID NO: 1358

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

2) INFORMATION FOR SEQ ID NO: 1359

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCTGCC ACCTCACTC

19

10 2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25 2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 786 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X01385

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

GTGCAATACG	AATGGCGAAA	AGCCGAGCTC	ATCGGTCAGC	TTCTCAACCT	50
TGGGGTTACC	CCCGGCGGTG	TGCTGCTGGT	CCACAGCTCC	TTCCGTAGCG	100
45 TCCGGCCCCCT	CGAAGATGGG	CCACTTGGAC	TGATCGAGGC	CCTGCGTGCT	150
GCGCTGGGTC	CGGGAGGGAC	GCTCGTCATG	CCCTCGTGGT	CAGGTCTGGA	200
CGACGAGCCG	TTGATCCTG	CCACGTCGCC	CGTTACACCG	GACCTTGGAG	250
TTGTCTCTGA	CACATTCTGG	CGCCTGCCAA	ATGTAAAGCG	CAGCGCCCAT	300
CCATTTGCCT	TTGCGGCAGC	GGGGCCACAG	GCAGAGCAGA	TCATCTCTGA	350
50 TCCATTGCCC	CTGCCACCTC	ACTCGCCTGC	AAGCCCGGTC	GCCCGTGTCC	400
ATGAACTCGA	TGGGCAGGTA	CTTCTCCTCG	GCGTGCGACA	CGATGCCAAC	450
ACGACGCTGC	ATCTTGCCGA	GTTGATGGCA	AAGGTTCCCT	ATGGGGTGCC	500
GAGACACTGC	ACCATTCTTC	AGGATGGCAA	GTTGGTACGC	GTCGATTATC	550

TCGAGAATGA CCACTGCTGT GAGCGCTTTG CTTGGCGGA CAGGTGGCTC 600
AAGGAGAAGA GCCTTCAGAA GGAAGGTCCA GTCGGTCATG CCTTTGCTCG 650
GTTGATCCGC TCCCGCGACA TTGTGGCGAC AGCCCTGGGT CAACTGGGCC 700
GAGATCCGTT GATCTTCCTG CATCCGCCAG AGGGCGGGAT GCGAAGAATG 750
5 CGATGCCGCT CGCCAGTCGA TTGGCTGAGC TCATGA 786

2) INFORMATION FOR SEQ ID NO: 1362

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

CGCCGCCATC GCCCAAAGCT GG

22

2) INFORMATION FOR SEQ ID NO: 1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

CGGCATAATG GAGCGCGGTG ACTG

24

2) INFORMATION FOR SEQ ID NO: 1364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

TTTCTCGCCC ACGCAGGAAA AATC

24

2) INFORMATION FOR SEQ ID NO: 1365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

2) INFORMATION FOR SEQ ID NO: 1366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
(C) ACCESSION NUMBER: M88012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

	ATGACTGATC	CCCGCAAAAA	CGGCGATTTG	CACGAACCCG	CGACGGCACC	50
	CGCGACGCCC	TGGTCCAAAA	GCGAGCTGGT	CCGGCAATTG	CGCGACCTCG	100
35	GCGTGCGCTC	AGGCGATATG	GTGATGCCGC	ATGTGTCGTT	GCGCGCCGTC	150
	GGGCCGCTGG	CGGACGGACC	GCAGACACTT	GTCGATGCGC	TGATCGAGGC	200
	CGTCGGCCCC	ACCGGGAATA	TTCTCGCCTT	CGTCTCGTGG	CGCGATTTCG	250
	CCTATGAACA	GACGCTGGGT	CATGATGCGC	CGCCCGCCGC	CATCGCCCAA	300
	AGCTGGCCTG	CGTTCGACCC	CGACCATGCG	CCCGCCTACC	CCGGCTTTGG	350
40	CGCGATCAAC	GAATTTATCC	GAACCTATCC	GGGGTGTCGG	CGCACGGCCC	400
	ATCCCGACGC	ATCGATGGCG	GCGATCGGGC	CCGATGCGGC	GTGGCTGGTG	450
	GCGCCGCACG	AGATGGGCGC	CGCTTATGGC	CCCCGCTCGC	CGATCGCGCG	500
	TTTTCTCGCC	CACGCAGGAA	AAATCCTGTC	GATCGGCGCC	GGGCCCAGATG	550
	CAGTCACCGC	GCTCCATTAT	GCCGAAGCGG	TGGCGCGGAT	CGAGGGCAAG	600
45	CGCCGCGTCA	CTTATTCGAT	GCCCTTACTG	CGCGAAGGCA	AGCGCGTCTG	650
	GGTCACCACG	TCCGACTGGG	ATTCGAACGG	CATCCTCGAC	GAATATGCCG	700
	CGCCCGACGG	CCCCGACGCG	GTCGAACGGA	TCGCCCCGCA	CTATCTCGCC	750
	CGCACCAGGG	TTGCGCAAGG	CCCGGTCGGC	GGCGCGCAAT	CCCGGCTGAT	800
	CGACGCGGCC	GATATCGTTT	CCTTCGGCAT	CGAATGGCTC	GAGGCGCGCC	850
50	ACGCCGCGCC	AGCGGCGGCA	GCGCTGAAGC	CGAAACAACG	CCGCGACTGA	900

2) INFORMATION FOR SEQ ID NO: 1367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

2) INFORMATION FOR SEQ ID NO: 1368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

2) INFORMATION FOR SEQ ID NO: 1369

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

AAACCTTTGT TTCGGTCTGC TAAT

24

2) INFORMATION FOR SEQ ID NO: 1370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 558 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter diversus*
(C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

30

ATGAATTATC	AAATTGTGAA	TATTGCGGAA	TGCAGCAATT	ATCAGTTAGA	50
AGCAGCAAAT	ATACTAACAG	AAGCGTTCAA	TGATCTTGGT	AACAATTCAT	100
GGCCAGATAT	GACGAGTGCA	ACAAAAGAAG	TAAAAGAATG	TATTGAGAGT	150
CCAAACCTTT	GTTTCGGTCT	GCTAATAAAT	AACCTCTTAG	TTGGCTGGAT	200
AGGCTTAAGG	CCAATGTACA	AGGAAACCTG	GGAATTGCAT	CCATTGGTTG	250
TCAGACCAGA	TTATCAAAAT	AAAGGTATTG	GCAAGATCCT	GCTTAAGGAA	300
TTAGAAAACA	GAGCTAGAGA	GCAAGGTATT	ATTGGAATCG	CTTTAGGAAC	350
AGATGATGAA	TACTATAGAA	CAAGTCTCTC	TTTAATAACT	ATAACAGAAG	400
ATAATATATT	TGATTCAATA	AAAAATATTA	AAAATATTAA	TAAACATCCA	450
TATGAGTTTT	ATCAGAAGAA	TGGTTATTAT	ATTGTTGGAA	TAATTCCAAA	500
TGCCAATGGT	AAAAACAAAC	CAGATATTTG	GATGTGGAAA	AGTTTAATCA	550
AAGAGTAA					558

40

2) INFORMATION FOR SEQ ID NO: 1372

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TTCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1376

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
(C) ACCESSION NUMBER: M94066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

ATGATCGTCA	TCTGCGACCA	CGACAACCTC	GACGCCTGGC	TGGCGCTGCG	50
CACCGCGCTG	TGGCCCTCCG	GCTCGCCTGA	AGATCACCGC	GCGGAAATGC	100
GCGAGATATT	GGCTTCGCCG	CACCACACCG	CGTTTATGGC	GCGGGGGCTG	150
GACGGCGCTT	TCGTTGCCTT	TGCCGAGGTC	GCGCTGCGCT	ACGATTACGT	200
CAACGGCTGC	GAATCGTCGC	CGGTGGCGTT	TTTGAAGGA	ATTTATACCG	250
CCGAACGCGC	CCGCCGCCAG	GGCTGGGCCG	CGCGCCTGAT	CGCGCAGGTG	300
CAGGAGTGGG	CGAAGCAACA	GGGGTGCAGC	GAGCTGGCGT	CGGATAACCGA	350
TATCGCCAAT	CTGGACTCCC	AGCGCCTGCA	TGCGGCGCTG	GGCTTTGCCG	400
AAACGGAGCG	AGTAGTGTTT	TACCGCAAAA	CGCTGGGCTG	A	441

2) INFORMATION FOR SEQ ID NO: 1377

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

GCCGTGGGTC GATGTTTGAT GTTA

24

2) INFORMATION FOR SEQ ID NO: 1378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

2) INFORMATION FOR SEQ ID NO: 1379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

CGCTCGATGA CGCCAACTAC CTCT

24

2) INFORMATION FOR SEQ ID NO: 1381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

	GTGGTAACGG	CGCAGTGGCG	GTTTTTCATGG	CTTCTTGTTA	TGACATGTTT	50
	TTTTGGGGTA	CAGTCTATGC	CTCGGGCATC	CAAGCAGCAA	GCGCGTTACG	100
5	CCGTGGGTCG	ATGTTTGATG	TTATGGAGCA	GCAACGATGT	TACGCAGCAG	150
	GGCAGTCGCC	CTAAAACAAA	GTTAAACATC	ATGAGGGAAG	CGGTGATCGC	200
	CGAAGTATCG	ACTCAACTAT	CAGAGGTAGT	TGGCGTCATC	GAGCGCCATC	250
	TCGAACCGAC	GTTGCTGGCC	GTACATTTGT	ACGGCTCCGC	AGTGGATGGC	300
	GGCCTGAAGC	CACACAGTGA	TATTGATTTG	CTGGTTACGG	TGACCGTAAG	350
10	GCTTGATGAA	ACAACGCGGC	GAGCTTTGAT	CAACGACCTT	TTGGAAACTT	400
	CGGCTTCCCC	TGGAGAGAGC	GAGATTCTCC	GCGCTGTAGA	AGTCACCATT	450
	GTTGTGCACG	ACGACATCAT	TCCGTGGCGT	TATCCAGCTA	AGCGCGAACT	500
	GCAATTTGGA	GAATGGCAGC	GCAATGACAT	TCTTGCAAGT	ATCTTCGAGC	550
	CAGCCACGAT	CGACATTGAT	CTGGCTATCT	TGCTGACAAA	AGCAAGAGAA	600
15	CATAGCGTTG	CCTTGGTAGG	TCCAGCGGCG	GAGGAACTCT	TTGATCCGGT	650
	TCCTGAACAG	GATCTATTTG	AGGCGCTAAA	TGAAACCTTA	ACGCTATGGA	700
	ACTCGCCGCC	CGACTGGGCT	GGCGATGAGC	GAAATGTAGT	GCTTACGTTG	750
	TCCCGCATTT	GGTACAGCGC	AGTAACCGGC	AAAATCGCGC	CGAAGGATGT	800
	CGCTGCCGAC	TGGGCAATGG	AGCGCCTGCC	GGCCCAGTAT	CAGCCCGTCA	850
20	TACTTGAAGC	TAGACAGGCT	TATCTTGGAC	AAGAAGAAGA	TCGCTTGGCC	900
	TCGCGCGCAG	ATCAGTTGGA	AGAATTTGTC	CACTACGTGA	AAGGCGAGAT	950
	CACCAAGGTA	GTCGGCAAAT	AA			972

25

2) INFORMATION FOR SEQ ID NO: 1382

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

5 2) INFORMATION FOR SEQ ID NO: 1384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

2) INFORMATION FOR SEQ ID NO: 1385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

2) INFORMATION FOR SEQ ID NO: 1386

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- 50 (C) ACCESSION NUMBER: V01282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50

	CGAGGAAAGT	GGAGAAGTAA	TAGAGGTAGA	TAAGCTATAC	CGTAAACAAA	100
	CGTCTGGTAA	CTTTGTAAAA	GCGTATATCG	TCCAATTAAT	AAGTATGTTA	150
	GATATGATAG	GCGGTAAAAA	GCTCAAGATT	GTTAATTATA	TATTAGATAA	200
	TGTACATCTA	AGTAATAACA	CAATGATAGC	AACTGTTAGA	GAAATAGCAG	250
5	AAGGAACAAA	TACAAGCACG	AAAACCGTAA	ATACAACGCT	TAAAATCTTA	300
	GAAGAAGGAA	ATATCATTAA	AAGAAGAACT	GGAGCATTAA	TGCTAAACCC	350
	AGAGCTACTC	ATGAGAGGCG	ATGACCAAAA	ACAAAAATAC	CTCTTACTCG	400
	AATTTGGGAA	CTTTGAGCAA	GAGGACGACC	AAAAGCAAGA	AAATGCTTTA	450
	TCAGAATATT	ATTCTTTCAA	GGAGTAG			477

10

2) INFORMATION FOR SEQ ID NO: 1387

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387

25 TTATGCCTCT TCCGACCATC AAGC

24

2) INFORMATION FOR SEQ ID NO: 1388

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388

40

TACGCTCGTC ATCAAAATCA CTCG

24

45 2) INFORMATION FOR SEQ ID NO: 1389

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

2) INFORMATION FOR SEQ ID NO: 1390

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

40	ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC	50
	CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG	100
	GGCAATCAGG TGCGACAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA	150
	GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA	200
	TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCCGACCA	250
45	TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTTACT CACCACTGCG	300
	ATCCCCGGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG	350
	TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCGA	400
	TTCTGTGTTG TAATTGTCCT TTTAACAGCG ATCGCGTATT TCGTCTCGCT	450
	CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA	500
50	TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA	550
	AGCTTTTGCC ATTCTCACCG GATTTCAGTCG TCACTCATGG TGATTTCTCA	600
	CTTGATAACC TTATTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT	650
	TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA	700

ACTGCCTCGG	TGAGTTTTCT	CCTTCATTAC	AGAAACGGCT	TTTTCAAAAA	750
TATGGTATTG	ATAATCCTGA	TATGAATAAA	TTGCAGTTTC	ATTTGATGCT	800
CGATGAGTTT	TTCTAA				816

5

2) INFORMATION FOR SEQ ID NO: 1392

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

TGGGTGGAGA GGCTATTCGG CTAT

24

20

2) INFORMATION FOR SEQ ID NO: 1393

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC

23

2) INFORMATION FOR SEQ ID NO: 1394

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

50

GACGTTGTCA CTGAAGCGGG AAGG

24

2) INFORMATION FOR SEQ ID NO: 1395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

2) INFORMATION FOR SEQ ID NO: 1396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: V00618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

ATGATTGAAC	AAGATGGATT	GCACGCAGGT	TCTCCGGCCG	CTTGGGTGGA	50
GAGGCTATTC	GGCTATGACT	GGGCACAACA	GACAATCGGC	TGCTCTGATG	100
CCGCCGTGTT	CCGGCTGTCA	GCGCAGGGGC	GCCCGGTTCT	TTTTGTCAAG	150
ACCGACCTGT	CCGGTGCCCT	GAATGAACTG	CAGGACGAGG	CAGCGCGGCT	200
ATCGTGGCTG	GCCACGACGG	GCGTTCCTTG	CGCAGCTGTG	CTCGACGTTG	250
TCACTGAAGC	GGGAAGGGAC	TGGCTGCTAT	TGGGCGAAGT	GCCGGGGCAG	300
GATCTCCTGT	CATCTCACCT	TGCTCCTGCC	GAGAAAGTAT	CCATCATGGC	350
TGATGCAATG	CGGCGGCTGC	ATACGCTTGA	TCCGGCTACC	TGCCCCATTCG	400
ACCACCAAGC	GAAACATCGC	ATCGAGCGAG	CACGTACTCG	GATGGAAGCC	450
GGTCTTGTCG	ATCAGGATGA	TCTGGACGAA	GAGCATCAGG	GGCTCGCGCC	500
AGCCGAACTG	TTCGCCAGGC	TCAAGGCGCG	CATGCCCGAC	GGCGAGGATC	550
TCGTCTGTGAC	CCATGGCGAT	GCCTGCTTGC	CGAATATCAT	GGTGGAAAAT	600
GGCCGCTTTT	CTGGATTTCAT	CGACTGTGGC	CGGCTGGGTG	TGGCGGACCG	650
CTATCAGGAC	ATAGCGTTGG	CTACCCGTGA	TATTGCTGAA	GAGCTTGCGG	700
GCGAATGGGC	TGACCGCTTC	CTCGTGCTTT	ACGGTATCGC	CGCTCCCGAT	750
TCGCAGCGCA	TCGCCTTCTA	TCGCCTTCTT	GACGAGTTCT	TCTGA	795

2) INFORMATION FOR SEQ ID NO: 1397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397

GTGGGAGAAA ATGAAACCT AT

22

2) INFORMATION FOR SEQ ID NO: 1398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398

ATGGAGTGAA AGAGCCTGAT

20

2) INFORMATION FOR SEQ ID NO: 1399

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399

ACCTATGATG TGGAACGGGA AAAG

24

2) INFORMATION FOR SEQ ID NO: 1400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

5

CGATGGAGTG AAAGAGCCTG ATG

23

10 2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

25

ATGGCTAAAA	TGAGAATATC	ACCGGAATTG	AAAAAACTGA	TCGAAAAATA	50
CCGCTGCGTA	AAAGATACGG	AAGGAATGTC	TCCTGCTAAG	GTATATAAGC	100
TGGTGGGAGA	AAATGAAAAC	CTATATTTAA	AAATGACGGA	CAGCCGGTAT	150
AAAGGGACCA	CCTATGATGT	GGAACGGGAA	AAGGACATGA	TGCTATGGCT	200
30 GGAAGGAAAG	CTGCCTGTTC	CAAAGGTCCT	GCACTTTGAA	CGGCATGATG	250
GCTGGAGCAA	TCTGCTCATG	AGTGAGGCCG	ATGGCGTCCT	TTGCTCGGAA	300
GAGTATGAAG	ATGAACAAAG	CCCTGAAAAG	ATTATCGAGC	TGTATGCGGA	350
GTGCATCAGG	CTCTTTCACT	CCATCGACAT	ATCGGATTGT	CCCTATACGA	400
ATAGCTTAGA	CAGCCGCTTA	GCCGAATTGG	ATTACTTACT	GAATAACGAT	450
35 CTGGCCGATG	TGGATTGCGA	AAACTGGGAA	GAAGACACTC	CATTTAAAGA	500
TCCGCGCGAG	CTGTATGATT	TTTTTAAAGAC	GGAAAAGCCC	GAAGAGGAAC	550
TTGTCTTTTC	CCACGGCGAC	CTGGGAGACA	GCAACATCTT	TGTGAAAGAT	600
GGCAAAGTAA	GTGGCTTTAT	TGATCTTGGG	AGAAGCGGCA	GGGCGGACAA	650
GTGGTATGAC	ATTGCCTTCT	GCGTCCGGTC	GATCAGGGAG	GATATCGGGG	700
40 AAGAACAGTA	TGTCGAGCTA	TTTTTTGACT	TACTGGGGAT	CAAGCCTGAT	750
TGGGAGAAAA	TAAATATTA	TATTTTACTG	GATGAATTGT	TTTAG	795

45 2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

TATTCAACAA TTTATCGGAA ACAG

24

5

2) INFORMATION FOR SEQ ID NO: 1403

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

TCAGAGAGCC AACTCAACAT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1404

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

AAACAGCGTT TTAGAGCCAA ATAA

24

35

2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT

24

50

2) INFORMATION FOR SEQ ID NO: 1406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: BM2580
 (C) ACCESSION NUMBER: X07753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

	ATGGAATTGC	CCAATATTAT	TCAACAATTT	ATCGGAAACA	GCGTTTTAGA	50
	GCCAAATAAA	ATTGGTCAGT	CGCCATCGGA	TGTTTATTCT	TTTAATCGAA	100
20	ATAATGAAAC	TTTTTTTCTT	AAGCGATCTA	GCACTTTATA	TACAGAGACC	150
	ACATACAGTG	TCTCTCGTGA	AGCGAAAATG	TTGAGTTGGC	TCTCTGAGAA	200
	ATTAAAGGTG	CCTGAACTCA	TCATGACTTT	TCAGGATGAG	CAGTTTGAAT	250
	TCATGATCAC	TAAAGCGATC	AATGCAAAAC	CAATTTTCAGC	GCTTTTTTTTA	300
	ACAGACCAAG	AATTGCTTGC	TATCTATAAG	GAGGCACTCA	ATCTGTATAA	350
25	TTCAATTGCT	ATTATTGATT	GTCCATTTAT	TTCAAACATT	GATCATCGGT	400
	TAAAAGAGTC	AAAATTTTTT	ATTGATAACC	AACTCCTTGA	CGATATAGAT	450
	CAAGATGATT	TTGACACTGA	ATTATGGGGA	GACCATAAAA	CTTACCTAAG	500
	TCTATGGAAT	GAGTTAACCG	AGACTCGTGT	TGAAGAAAGA	TTGGTTTTTTT	550
	CTCATGGCGA	TATCACGGAT	AGTAATATTT	TTATAGATAA	ATTCAATGAA	600
30	ATTTATTTTT	TAGATCTTGG	TCGTGCTGGG	TTAGCAGATG	AATTTGTAGA	650
	TATATCCTTT	GTTGAACGTT	GCCTAAGAGA	GGATGCATCG	GAGGAAACTG	700
	CGAAAATATT	TTTAAAGCAT	TTAAAAAATG	ATAGACCTGA	CAAAGGAAT	750
	TATTTTTTAA	AACTTGATGA	ATTGAATTGA			780

2) INFORMATION FOR SEQ ID NO: 1407

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

24

2) INFORMATION FOR SEQ ID NO: 1408

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408

TTGTCGTATC CCTCAAATCA CC

22

2) INFORMATION FOR SEQ ID NO: 1409

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409

TGGGATTACA ATGGCAATCA GCG

23

2) INFORMATION FOR SEQ ID NO: 1410

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410

GGGGAATAGG TCACAAGATC TGCTT

25

2) INFORMATION FOR SEQ ID NO: 1411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

```

10  ATGCTTTTAT ATAAAATGTG TGACAATCAA AATTATGGGG TTACTTACAT      50
    GAAGTTTTTA TTGGCATTTC CGCTTTTAAT ACCATCCGTG GTTTTTGCAA      100
    GTAGTTCAAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT      150
    TCTCTTCTG CTCGTATAGG TGTTTCCGTT CTTGATACTC AAAATGGAGA      200
15  ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA      250
    AAACAATAGC TTGCGCTAAA TTACTATATG ATGCTGAGCA AGGAAAAGTT      300
    AATCCCAATA GTACAGTCGA GATTAAAGAA GCAGATCTTG TGACCTATTC      350
    CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT      400
    GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAAA TATCATCCTA      450
20  AGTGCTGTAG GTGGCCCCAA AGGCGTACT GATTTTTTAA GACAAATTGG      500
    GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA      550
    AGCTCGGTGA TTTGAGGGAT ACGACAAC TCAGGCAAT AGCCAGTACT      600
    TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA      650
    ATTAGAGTCT TGGATGGTGA ACAATCAAGT CACTGGTAAT TTACTACGTT      700
25  CAGTATTGCC GCGGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA      750
    TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC      800
    AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC      850
    GAAATGATGC GATTGTAAA ATTGGTCATT CAATTTTGA CGTTTATACA      900
    TCACAGTCGC GC                                          912
30

```

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

10

2) INFORMATION FOR SEQ ID NO: 1414

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

25

2) INFORMATION FOR SEQ ID NO: 1415

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

40

ATGCAGTAAT GCGGCTTTAT C

21

2) INFORMATION FOR SEQ ID NO: 1416

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: HEL-1

(C) ACCESSION NUMBER: X91840

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

	ATGATGAAAA	AATCGTTATG	CTGCGCTCTG	CTGCTGACAG	CCTCTTTCTC	50
	CACATTTGCT	GCCGCAAAAA	CAGAACAACA	GATTGCCGAT	ATCGTTAATC	100
10	GCACCATCAC	CCCGTTGATG	CAGGAGCAGG	CTATTCCGGG	TATGGCCGTT	150
	GCCGTTATCT	ACCAGGGAAA	ACCCTATTAT	TTCACCTGGG	GTAAAGCCGA	200
	TATCGCCAAT	AACCACCCAG	TCACGCAGCA	AACGCTGTTT	GAGCTAGGAT	250
	CGGTTAGTAA	GACGTTTAAC	GGCGTGTTGG	GCGGCGATGC	TATCGCCCCG	300
	GGCGAAATTA	AGCTCAGCGA	TCCGGTCACG	AAATACTGGC	CAGAACTGAC	350
15	AGGCAAACAG	TGGCAGGGTA	TCCGCCTGCT	GCACTTAGCC	ACCTATACGG	400
	CAGGCGGCCT	ACCGCTGCAG	ATCCCCGATG	ACGTTAGGGA	TAAAGCCGCA	450
	TTACTGCATT	TTTATCAAAA	CTGGCAGCCG	CAATGGACTC	CGGGCGCTAA	500
	GCGACTTTAC	GCTAACTCCA	GCATTGGTCT	GTTTGGCGCG	CTGGCGGTGA	550
	AACCCTCAGG	AATGAGTTAC	GAAGAGGCAA	TGACCAGACG	CGTCCTGCAA	600
20	CCATTAAAAC	TGGCGCATA	CTGGATTACG	GTTCCGCAGA	ACGAACAAAA	650
	AGATTATGCC	TGGGGCTATC	GCGAAGGGAA	GCCCGTACAC	GTTTCTCCGG	700
	GACAACTTGA	CGCCGAAGCC	TATGGCGTGA	AATCCAGCGT	TATTGATATG	750
	GCCCGCTGGG	TTCAGGCCAA	CATGGATGCC	AGCCACGTTC	AGGAGAAAAC	800
	GCTCCAGCAG	GGCATTGCGC	TTGCGCAGTC	TCGCTACTGG	CGTATTGGCG	850
25	ATATGTACCA	GGGATTAGGC	TGGGAGATGC	TGAACTGGCC	GCTGAAAGCT	900
	GATTCGATCA	TCAACGGCAG	CGACAGCAAA	GTGGCATTGG	CAGCGCTTCC	950
	CGCCGTTGAG	GTAAACCCGC	CCGCCCCCGC	AGTGAAAGCC	TCATGGGTGC	1000
	ATAAAACGGG	CTCCACTGGT	GGATTTGGCA	GCTACGTAGC	CTTCGTTCCA	1050
	GAAAAAAACC	TTGGCATCGT	GATGCTGGCA	AACAAAAGCT	ATCCTAACCC	1100
30	TGTCCGTGTC	GAGGCGGCCT	GGCGCATTCT	TGAAAAGCTG	CAATAA	1146

2) INFORMATION FOR SEQ ID NO: 1417

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

50 2) INFORMATION FOR SEQ ID NO: 1418

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

10 ATGCTTTACC CAGCGTCAGA TT

22

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTCT CACG

24

2) INFORMATION FOR SEQ ID NO: 1420

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40

TGCTTTACCC AGCGTCAGAT TACG

24

45 2) INFORMATION FOR SEQ ID NO: 1421

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

2) INFORMATION FOR SEQ ID NO: 1422

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: GRI-1
- (C) ACCESSION NUMBER: X92506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

40	ATGGTTAAAA	AATCACTGCG	TCAGTTCACG	CTGATGGCGA	CGGCAACCGT	50
	CACGCTGTTG	TTAGGAAGTG	TGCCGCTGTA	TGCGCAAACG	GCGGACGTAC	100
	AGCAAAAAC	TGCCGAATTA	GAGCGGCAGT	CGGGAGGAAG	ACTGGGTGTG	150
	GCATTGATTA	ACACAGCAGA	TAATTCGCAA	ATACTTTATC	GTGCTGATGA	200
45	GCGCTTTGCG	ATGTGCAGCA	CCAGTAAAGT	GATGGCCGTG	GCCGCGGTGC	250
	TGAAGAAAAG	TGAAAGCGAA	CCGAATCTGT	TAAATCAGCG	AGTTGAGATC	300
	AAAAAATCTG	ACTTGGTAA	CTATAATCCG	ATTGCGGAAA	AGCACGTCGA	350
	TGGGACGATG	TCACTGGCTG	AGCTTAGCGC	GGCCGCGCTA	CAGTACAGCG	400
	ATAACGTGGC	GATGAATAAG	CTGATTTCTC	ACGTTGGCGG	CCCGGCTAGC	450
50	GTCACCGCGT	TCGCCCGACA	GCTGGGAGAC	GAAACGTTCC	GTCTCGACCG	500
	TACCGAGCCG	ACGTAAACA	CCGCCATTCC	GGGCGATCCG	CGTGATACCA	550
	CTTCACCTCG	GGCAATGGCG	CAAACCTCTG	GTAATCTGAC	GCTGGGTAAA	600
	GCATTGGGTG	ACAGCCAACG	GGCGCAGCTG	GTGACATGGA	TGAAAGGCAA	650

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700
TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750
GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800
CCAGCCTCAA CCTAAGGCAG AAAGCCGCTG CGATGTATTA GCGTCGGCGG 850
5 CTAAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

25 2) INFORMATION FOR SEQ ID NO: 1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

35

GAATTATCGG CGGTGTTAAT CAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

50

CACGCTCAAT ACCGCCATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1427

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

15

2) INFORMATION FOR SEQ ID NO: 1428

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 876 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: CAS-5
 30 (C) ACCESSION NUMBER: X92507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

	ATGATGACTC	AGAGCATTCG	CCGCTCAATG	TTAACGGTGA	TGGCGACGCT	50
35	ACCCCTGCTA	TTTAGCAGCG	CAACGCTGCA	TGCGCAGGCG	AACAGCGTGC	100
	AACAGCAGCT	GGAAGCCCTG	GAGAAAAGTT	CGGGAGGTCG	GCTTGCGGTT	150
	GCGCTGATTA	ACACCGCCGA	TAATTCGCAG	ATTCTCTACC	GTGCCGATGA	200
	ACGTTTTGCG	ATGTGCAGTA	CCAGTAAGGT	GATGGCGGCC	GCGGCGGTGC	250
	TTAAACAGAG	CGAGAGCGAT	AAGCACCTGC	TAAATCAGCG	CGTTGAAATC	300
40	AAGAAGAGCG	ACCTGGTTAA	CTACAATCCC	ATTGCGGAGA	AACACGTTAA	350
	CGGCACGATG	ACGCTGGCTG	AGCTTGCGCG	AGCGGCGCTG	CAGTATAGCG	400
	ACAATACTGC	CATGAATAAG	CTGATTGCCC	ATCTGGGTGG	TCCCGATAAA	450
	GTGACGGCGT	TTGCTCGCTC	GTTGGGTGAT	GAGACCTTCC	GTCTGGACAG	500
	AACCGAGCCC	ACGCTCAATA	CCGCCATTCC	AGGCGACCCG	CGTGATACCA	550
45	CCACGCCGCT	CGCGATGGCG	CAGACCCTGA	AAAATCTGAC	GCTGGGTAAA	600
	GCGCTGGCGG	AAACTCAGCG	GGCACAGTTG	GTGACGTGGC	TTAAGGGCAA	650
	TACTACCGGT	AGCGCGAGCA	TTCGGGCGGG	TCTGCCGAAA	TCATGGGTAG	700
	TGGGCGATAA	AACCGGCAGC	GGAGATTATG	GCACCACCAA	CGATATCGCG	750
	GTTATCTGGC	CGGAAAACCA	CGCACCCTG	GTTCTGGTGA	CCTACTTTAC	800
50	CCAACCGGAG	CAGAAGGCGG	AAAGCCGTCG	GGATATTCTG	GCTGCGGCGG	850
	CGAAAATCGT	AACCCACGGT	TTCTGA			876

2) INFORMATION FOR SEQ ID NO: 1429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

2) INFORMATION FOR SEQ ID NO: 1430

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAAA ACAACCACCG AATAAT

26

2) INFORMATION FOR SEQ ID NO: 1431

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

TAATTGACAC TCCATTTACG GCTAA

25

2) INFORMATION FOR SEQ ID NO: 1432

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: AJ223604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

ATGAGCAAGT	TATCTGTATT	CTTTATATTT	TTGTTTTGCA	GCATTGCTAC	50
CGCAGCAGAG	TCTTTGCCAG	ATTTAAAAAT	TGAAAAGCTT	GATGAAGGCG	100
TTTATGTTCA	TACTTCGTTT	GAAGAAGTTA	ACGGGTGGGG	CGTTGTTCTT	150
AAACATGGTT	TGGTGGTTCT	TGTAAATGCT	GAGGCTTACC	TAATTGACAC	200
TCCATTTACG	GCTAAAGATA	CTGAAAAGTT	AGTCACTTGG	TTTGTGGAGC	250
GTGGCTATAA	AATAAAAGGC	AGCATTTTCT	CTCATTTTCA	TAGCGACAGC	300
ACGGGCGGAA	TAGAGTGGCT	TAATTCTCGA	TCTATCCCCA	CGTATGCATC	350
TGAATTAACA	AATGAACTGC	TTAAAAAAGA	CGGTAAGGTT	CAAGCCACAA	400
ATTCATTTAG	CGGAGTTAAC	TATTGGCTAG	TTAAAAATAA	AATTGAAGTT	450
TTTTATCCAG	GCCCGGGACA	CACTCCAGAT	AACGTAGTGG	TTTGGTTGCC	500
TGAAAGGAAA	ATATTATTCG	GTGGTTGTTT	TATTAAACCG	TACGGTTTAG	550
GCAATTTGGG	TGACGCAAAT	ATAGAAGCTT	GGCCAAAGTC	CGCCAAATTA	600
TTAAAGTCCA	AATATGGTAA	GGCAAACCTG	GTTGTTCCAA	GTCACAGTGA	650
AGTTGGAGAC	GCATCACTCT	TGAAACTTAC	ATTAGAGCAG	GCGGTTAAAG	700
GGTTAAACGA	AAGTAAAAAA	CCATCAAAAC	CAAGCAACTA	A	741

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT

25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG

25

2) INFORMATION FOR SEQ ID NO: 1436

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

35

CAGCATCAAC ATTTAAGATC CCCA

24

2) INFORMATION FOR SEQ ID NO: 1437

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGC GG AAATTC

26

2) INFORMATION FOR SEQ ID NO: 1438

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X06046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

ATGGCAATCC	GAATCTTCGC	GATACTTTTC	TCCATTTTTT	CTCTTGCCAC	50
TTTCGCGCAT	GCGCAAGAAG	GCACGCTAGA	ACGTTCTGAC	TGGAGGAAGT	100
TTTTTCAGCGA	ATTTCAAGCC	AAAGGCACGA	TAGTTGTGGC	AGACGAACGC	150
CAAGCGGATC	GTGCCATGTT	GGTTTTTGAT	CCTGTGCGAT	CGAAGAAACG	200
CTACTCGCCT	GCATCGACAT	TCAAGATACC	TCATACACTT	TTTGCACTTG	250
ATGCAGGCGC	TGTTCTGTGAT	GAGTTCCAGA	TTTTTCGATG	GGACGGCGTT	300
AACAGGGGCT	TTGCAGGCCA	CAATCAAGAC	CAAGATTTGC	GATCAGCAAT	350
GCGGAATTCT	ACTGTTTGGG	TGTATGAGCT	ATTTGCAAAG	GAAATTGGTG	400
ATGACAAAGC	TCGGCGCTAT	TTGAAGAAAA	TCGACTATGG	CAACGCCGAT	450
CCTTCGACAA	GTAATGGCGA	TTACTGGATA	GAAGGCAGCC	TTGCAATCTC	500
GGCGCAGGAG	CAAATTGCAT	TTCTCAGGAA	GCTCTATCGT	AACGAGCTGC	550
CCTTTCGGGT	AGAACATCAG	CGCTTGGTCA	AGGATCTCAT	GATTGTGGAA	600
GCCGGTTCGA	ACTGGATACT	GCGTGCAAAG	ACGGGCTGGG	AAGGCCGTAT	650
GGGTTGGTGG	GTAGGATGGG	TTGAGTGGCC	GACTGGCTCC	GTATTCTTCG	700
CACTGAATAT	TGATACGCCA	AACAGAATGG	ATGATCTTTT	CAAGAGGGAG	750
GCAATCGTGC	GGGCAATCCT	TCGCTCTATT	GAAGCGTTAC	CGCCCAACCC	800
GGCAGTCAAC	TCGGACGCTG	CGCGATAA			828

2) INFORMATION FOR SEQ ID NO: 1439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: J03427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

ATGAAAACAT	TTGCCGCATA	TGTAATTATC	GCGTGTCTTT	CGAGTACGGC	50
------------	------------	------------	------------	------------	----

	ATTAGCTGGT	TCAATTACAG	AAAATACGTC	TTGGAACAAA	GAGTTCTCTG	100
	CCGAAGCCGT	CAATGGTGTC	TTCGTGCTTT	GTAAAAGTAG	CAGTAAATCC	150
	TGCGCTACCA	ATGACTTAGC	TCGTGCATCA	AAGGAATATC	TTCCAGCATC	200
	AACATTTAAG	ATCCCCAACG	CAATTATCGG	CCTAGAAACT	GGTGTCATAA	250
5	AGAATGAGCA	TCAGGTTTTTC	AAATGGGACG	GAAAGCCAAG	AGCCATGAAG	300
	CAATGGGAAA	GAGACTTGAC	CTTAAGAGGG	GCAATACAAG	TTTCAGCTGT	350
	TCCCGTATTT	CAACAAATCG	CCAGAGAAGT	TGGCGAAGTA	AGAATGCAGA	400
	AATACCTTAA	AAAATTTTCC	TATGGCAACC	AGAATATCAG	TGGTGGCATT	450
	GACAAATTCT	GGTTGGAAGG	CCAGCTTAGA	ATTTCCGCAG	TTAATCAAGT	500
10	GGAGTTTCTA	GAGTCTCTAT	ATTTAAATAA	ATTGTCAGCA	TCTAAAGAAA	550
	ACCAGCTAAT	AGTAAAAGAG	GCTTTGGTAA	CGGAGGCGGC	ACCTGAATAT	600
	CTAGTGCATT	CAAAAACCTG	TTTTTCTGGT	GTGGGAACTG	AGTCAAATCC	650
	TGGTGTGCGA	TGGTGGGTTG	GGTGGGTGA	GAAGGAGACA	GAGGTTTACT	700
	TTTTCGCCTT	TAACATGGAT	ATAGACAACG	AAAGTAAGTT	GCCGCTAAGA	750
15	AAATCCATTC	CCACCAAAT	CATGGAAAGT	GAGGGCATCA	TTGGTGGCTA	800
	A					801

20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35 2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AAACTTTTTC AGGATC

26

50 2) INFORMATION FOR SEQ ID NO: 1442

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: RNL-1
 (C) ACCESSION NUMBER: Z21957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

```

15  ATGAATGTCA TTATAAAAGC TGTAGTTACT GCCTCGACGC TACTGATGGT      50
    ATCTTTTAGT TCATTTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC      100
    AAATTGAATC CATAGTCATT GGAAAAAAAG CCACTGTAGG CGTTGCAGTG      150
    TGGGGGGCCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT      200
20  CCAATGCAA AGTGTATTTA AATTGCATTT AGCTATGTTG GTACTGCATC      250
    AGGTTGATCA GGGAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG      300
    GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG      350
    AGACGAGTTT AGTGTTCCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC      400
    ACAGCGATAA CGTGGCCTGT GATTTGTTAT TTGAACTGGT TGGTGGACCA      450
25  GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT      500
    GGTGCGAAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA      550
    ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA      600
    AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT      650
    CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTTA CCAGCTGGTA      700
30  CTGTGGTCGC ACATAAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT      750
    GCGGCCACTA ATGATTTAGG TATCATTCTG TTGCCTGATG GACGGCCCTT      800
    GCTGGTTGCT GTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG      850
    AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA      900
    AAGCTTTCTG CCCTAAGCCC AAATTAA      927

```

2) INFORMATION FOR SEQ ID NO: 1443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

CTTCTGCTCT GCTGATGCTT GGC

23

2) INFORMATION FOR SEQ ID NO: 1444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTTGTAA TACTGC

26

2) INFORMATION FOR SEQ ID NO: 1445

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: JMC
 (C) ACCESSION NUMBER: X93314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

	ATGAATGTCA	TCACAAAATG	TGTTTTTCACC	GCTTCTGCTC	TGCTGATGCT	50
35	TGGCTTAAGT	TCATTTGTAG	TATCAGCCCA	ATCCCCTTTG	TTAAAAGAGC	100
	AGATTGAAAC	CATAGTGACG	GGTAAAAAGG	CCACTGTAGG	TGTAGCAGTG	150
	TGGGGGCCCTG	ACGATCTGGA	ACCTTTGTTG	CTGAATCCAT	TTGAAAAGTT	200
	TCCGATGCAA	AGTGTGTTTA	AACTGCATTT	AGCTATGTTA	GTTCTGCATC	250
	AGGTCGATCA	GGGGAAACTG	GATTTAAATC	AGTCTGTTAC	TGTTAATCGT	300
40	GCTGCAGTAT	TACAAAATAC	CTGGTCGCCA	ATGATGAAAG	ATCATCAGGG	350
	CGATGAATTT	ACTGTTGCAG	TACAGCAGTT	ACTGCAGTAT	TCGGTGTCAC	400
	ACAGCGACAA	TGTGGCCTGC	GATTTGTTAT	TTGAACTGGT	GGGCGGGCCG	450
	CAAGCTTTGC	ATGCTTATAT	CCAGTCTTTA	GGCGTTAAAG	AAGCTGCCGT	500
	GGTAGCAAAT	GAAGCGCAAA	TGCATGCGGA	TGATCAGGTG	CAATATCAAA	550
45	ACTGGACGTC	GATGAAAGCC	GCAGCACAAG	TTCTGCAAAA	GTTTGAACAG	600
	AAAAAGCAGT	TGTCTGAAAC	CTCTCAGGCC	TTGTTATGGA	AATGGATGGT	650
	TGAAACCACC	ACAGGACCAC	AGCGGTAAA	AGGCTTGTTA	CCTGCTGGTA	700
	CTATAGTGGC	GCATAAAACC	GGTACTTCGG	GCGTCAGAGC	AGGAAAAACT	750
	GCGGCGACTA	ATGATGCGGG	CGTCATTATG	TTGCCTGATG	GACGGCCTTT	800
50	ATTGGTGCG	GTATTTGTCA	AGGATTCGGC	TGAATCAGAA	CGAACCAATG	850
	AAGCTATTAT	TGCGCAGGTT	GCGCAAGCGG	CTTATCAGTT	TGAGCTGAAA	900
	AAACTCTCTG	CAGTGAGTCC	GGATTGA			927

2) INFORMATION FOR SEQ ID NO: 1446

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT

27

2) INFORMATION FOR SEQ ID NO: 1447

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC

23

2) INFORMATION FOR SEQ ID NO: 1448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

GATCAGGTGC ARTATCAAAA CTGGAC

26

2) INFORMATION FOR SEQ ID NO: 1449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

ATCTACCTGG TCAATCATTG CTTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: BM10393
 (C) ACCESSION NUMBER: AF045472

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

```

10  ATGACATTAT CAATAATTGT CGCTCACGAT AAACAAAGAG TCATTGGGTA      50
    CCAAAATCAA TTACCTTGGC ACTTACCAA TGATTAAAG CATATTAAAC      100
    AACTGACCAC TGGGAATACA CTTGTAATGG CACGGAAAAC TTTTAATTCT      150
    ATAGGGAAGC CATTGCCAAA TAGACGTAAC GTCGTACTCA CTAACCAAGC      200
    TTCATTTTAC CATGAAGGGG TAGATGTTAT AAACCTCTCTT GATGAAATTA      250
    AAGAGTTATC TGGTCATGTT TTTATATTTG GAGGACAAAC GTTATACGAA      300
    GCAATGATTG ACCAGGTTAG TGATATGTAT ATCACAGTAA TAGATGGAAA      350
15  GTTTC AAGGA GACACATTCT TTCCACCATA CACATTTCGAA AACTGGGAAG      400
    TCGAATCTTC AGTAGAAGGT CAACTAGATG AAAAAAATAC TATACCGCAT      450
    ACATTCTTAC ATTTAGTGCG TAGAAAAGGG AAATAG                      486
  
```

20

2) INFORMATION FOR SEQ ID NO: 1453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

ATCGAAGAAT GGAGTTATCG GRAATG 26

35

2) INFORMATION FOR SEQ ID NO: 1454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

CCTAAAYTR CTGGGGATTT CWGGA 25

50

2) INFORMATION FOR SEQ ID NO: 1455

764

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455

CAGGTGGTGG GGAGATATAC AAAA

24

2) INFORMATION FOR SEQ ID NO: 1456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456

TATGTTAGAS RCGAAGTCTT GGKTAA

26

2) INFORMATION FOR SEQ ID NO: 1457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457

CAAAGGTGAA CAGCTCCTGT TT

22

2) INFORMATION FOR SEQ ID NO: 1458

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTAAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

```
5      GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA      50
      TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG      100
      CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA      150
      ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT      200
10     TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT      250
      TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG      300
      GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC      350
      AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA      400
      ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT      450
15     TACCAAATCT GGCAAAGGG TTAA                                     474
```

2) INFORMATION FOR SEQ ID NO: 1462

```
20     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Single
25     (D) TOPOLOGY: Linear
```

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

```
30     GCACTCCCYA ATAGGAAATA CGC                                     23
```

35 2) INFORMATION FOR SEQ ID NO: 1463

```
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 bases
          (B) TYPE: Nucleic acid
40     (C) STRANDEDNESS: Single
          (D) TOPOLOGY: Linear
```

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

```
      AGTGTGCTC AAAAACAAC TCG                                     23
```

```
50 2) INFORMATION FOR SEQ ID NO: 1464
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

30 2) INFORMATION FOR SEQ ID NO: 1466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

AAGCATTGAC CTACAATCAG TGT

23

45

2) INFORMATION FOR SEQ ID NO: 1467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467

5 AATACAAC TA CATTGTCATC ATTTGAT

27

2) INFORMATION FOR SEQ ID NO: 1468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468

CGTTACCCGC TCAGGTTGGA CATCAA

26

2) INFORMATION FOR SEQ ID NO: 1469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1469

CATCCCCCTC TGGCTCGATG TCG

23

2) INFORMATION FOR SEQ ID NO: 1470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: Z50804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470

```

5  TTGAAAGTAT CATTGATAGC TGCGAAACGA AAAAACGGCG TGATTGGTTG      50
   CGGTCCAGAC ATACCGTGGT CCGCGAAAGG GGAGCAGCTA CTTTTTAAAG      100
   CATTGACCTA CAATCAGTGT CTTCTGGTGG GTCGCAAGAC GTTTGAATCT      150
   ATGGGCGCAC TCCCAATAG GAAATACGCG GTCGTTACCC GCTCAGGTTG      200
   GACATCAAAT GATGACAATG TAGTTGTATT TCAGTCAATC GAAGAGGCCA      250
   TGGACAGGCT AGCTGAATTC ACCGGTCACG TTATAGTGTC TGGTGGCGGA      300
10 GAAATTTACC GAGAAACATT ACCCATGGCC TCTACGCTCC ACTTATCGAC      350
   GATCGACATC GAGCCAGAGG GGGATGTTTT CTTCCCGAGT ATTCCAAATA      400
   CCTTCGAAGT TGTTTTTGAG CAACACTTTA CTTCAAACAT TAACTATTGC      450
   TATCAAATTT GGAAAAGGG TTAA                                     474

```

15

2) INFORMATION FOR SEQ ID NO: 1471

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471

GATAATGACA ACGTAATAGT ATTCCC

26

30

2) INFORMATION FOR SEQ ID NO: 1472

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472

45 GCTCAATATC AATCGTCGAT ATA

23

2) INFORMATION FOR SEQ ID NO: 1473

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473

TTAAAGCCTT GACGTACAAC CAGTGG

26

10

2) INFORMATION FOR SEQ ID NO: 1474

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474

TGGGCAATGT TTCTCTGTAA ATCTCC

26

25

2) INFORMATION FOR SEQ ID NO: 1475

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X12868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475

45	GTGAAAGTAT	CATTAATGGC	TGCAAAAGCG	AAAAACGGAG	TGATTGGTTG	50
	CGGTCCACAC	ATACCCTGGT	CCGCGAAAGG	AGAGCAGCTA	CTCTTTAAAG	100
	CCTTGACGTA	CAACCAGTGG	CTTTTGGTGG	GCCGCAAGAC	GTTCGAATCT	150
	ATGGGAGCAC	TCCCTAATAG	GAAATACGCG	GTCGTTACTC	GCTCAGCCTG	200
	GACGGCCGAT	AATGACAACG	TAATAGTATT	CCCGTCGATC	GAAGAGGCCA	250
	TGTACGGGCT	GGCTGAACTC	ACCGATCACG	TTATAGTGTC	TGGTGGCGGG	300
50	GAGATTTACA	GAGAAACATT	GCCCATGGCC	TCTACGCTCC	ATATATCGAC	350
	GATTGATATT	GAGCCGGAAG	GAGATGTTTT	CTTTCCGAAT	ATTCCCAATA	400
	CCTTCGAAGT	TGTTTTTGAG	CAACACTTTA	GCTCAAACAT	TAATAATTGC	450
	TATCAAATTT	GGCAAAAGGG	TTAA			474

2) INFORMATION FOR SEQ ID NO: 1476

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476

GGCGAGCAGC TCCTATTCAA AG

22

2) INFORMATION FOR SEQ ID NO: 1477

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477

TAGGTAAGCT AATGCCGATT CAACA

25

2) INFORMATION FOR SEQ ID NO: 1478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478

GAGAATGGAG TAATTGGCTC TGGATT

26

2) INFORMATION FOR SEQ ID NO: 1479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479

GCGAAATACA CAACATCAGG GTCAT

25

2) INFORMATION FOR SEQ ID NO: 1480

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
(B) STRAIN: J120
(C) ACCESSION NUMBER: Z86002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480

ATGAAAATAT	CTCTTATGGC	AGCTGTTTCC	GAGAATGGAG	TAATTGGCTC	50
TGGATTGGAT	ATACCTTGGC	ATGTACAAGG	CGAGCAGCTC	CTATTCAAAG	100
CCATGACTTA	CAATCAATGG	CTTCTAGTTG	GTCGTAAAAC	CTTCGACTCA	150
ATGGGTAAAC	TTCCGAATAG	AAAATATGCA	GTGGTTACTC	GTTCTAAAAT	200
TATCTCGAAT	GACCCTGATG	TTGTGTATTT	CGCAAGTGTT	GAATCGGCAT	250
TAGCTTACCT	AAACAATGCG	ACAGCACATA	TCTTTGTTTC	TGGTGGTGGT	300
GAAATATATA	AAGCTTTAAT	CGATCAAGCA	GATGTTATCC	ATCTTTCAGT	350
GATTCAACAAG	CATATCTCTG	GCGATGTGTT	TTTTCCTCCA	GTTCCACAGG	400
GCTTCAAGCA	AACATTTGAG	CAAAGTTTCA	GTTCAAATAT	TGATTACACG	450
TACCAAATTT	GGGCAAAGGG	CTAA			474

2) INFORMATION FOR SEQ ID NO: 1481

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481

RTTACAGATC ATKTATATGT CTCT

24

5 2) INFORMATION FOR SEQ ID NO: 1482

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482

TAATTTATAT TAGACAWAAA AAAC TG

26

20

2) INFORMATION FOR SEQ ID NO: 1483

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483

CARYGTCAGA AAATGGCGTA ATC

23

35

2) INFORMATION FOR SEQ ID NO: 1484

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1484

TKCAAAGCRW TTTCTATTGA AGGAAA

26

50

2) INFORMATION FOR SEQ ID NO: 1485

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485

AAAATGGCGT AATCGGTAAT GGC

23

2) INFORMATION FOR SEQ ID NO: 1486

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486

CATTTGAGCT TGAAATTCCT TTCCTC

26

2) INFORMATION FOR SEQ ID NO: 1487

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487

AATCGAAAAT ATGCAGTAGT GTCGAG

26

2) INFORMATION FOR SEQ ID NO: 1488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488

AGACTATTGT AGATTTGACC GCCA

24

10

2) INFORMATION FOR SEQ ID NO: 1489

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: VA292

(C) ACCESSION NUMBER: U31119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489

30

TTGAAAATTT	CATTGATTTC	TGCAACGTCA	GAAAATGGCG	TAATCGGTAA	50
TGGCCCTGAT	ATCCCATGGT	CAGCAAAAGG	TGAGCAGTTA	CTCTTTAAAG	100
CGCTCACATA	TAATCAGTGG	CTCCTTGTTG	GAAGGAAAAC	ATTTGACTCT	150
ATGGGTGTTC	TTCCAAATCG	AAAATATGCA	GTAGTGTCTG	GGAAAGGAAT	200
TTCAAGCTCA	AATGAAAATG	TATTAGTCTT	TCCTTCAATA	GAAATCGCTT	250
TGCAAGAACT	ATCGAAAATT	ACAGATCATT	TATATGTCTC	TGGTGGCGGT	300
CAAATCTACA	ATAGTCTTAT	TGAAAAAGCA	GATATAATTC	ATTTGTCTAC	350
35 TGTTACGTT	GAGGTTGAAG	GTGATATCAA	TTTTCCTAAA	ATTCCAGAGA	400
ATTTCAATTT	GGTTTTTGAG	CAGTTTTTTT	TGTCTAATAT	AAATTACACA	450
TATCAGATTT	GGAAAAAAGG	CTAA			474

40

2) INFORMATION FOR SEQ ID NO: 1490

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490

GACCTATGAG AGCTTGCCCG TCAAA

25

2) INFORMATION FOR SEQ ID NO: 1491

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491

TCGCCTTCGT ACAGTCGCTT AACAAA

26

2) INFORMATION FOR SEQ ID NO: 1492

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492

CATTTTAGCT GCCACCGCCA ATGGTT

26

2) INFORMATION FOR SEQ ID NO: 1493

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493

GCGTCGCTGA CGTTGTTTAC GAAGA

25

2) INFORMATION FOR SEQ ID NO: 1494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(B) STRAIN: BL26A
(C) ACCESSION NUMBER: U10186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494

ATGATCGAGC	TTCATGCCAT	TTAGCTGCC	ACCGCCAATG	GTTGCATTGG	50
GAAGGACAAC	GCACTTCCCT	GGCCACCACT	AAAAGGCGAT	CTGGCCAGAT	100
15 TCAAAAAATT	GACCATGGGG	AAGGTGGTCA	TTATGGGGCG	CAAGACCTAT	150
GAGAGCTTGC	CCGTCAAATT	AGAAGGTCGC	ACCTGCATCG	TTATGACGCG	200
CCAAGCGCTG	GAGCTTCCGG	GTGTTCTGTA	CGCTAACGGC	GCTATCTTCG	250
TGAACAACGT	CAGCGACGCC	ATGCGGTTTCG	CTCAAGAAGA	GAGCGTGGGC	300
GATGTGGCCT	ACGTCATTGG	TGGCGCTGAG	ATATTCAAGC	GACTTGCCTT	350
20 GATGATCACG	CAGATTGAAT	TGACCTTTGT	TAAGCGACTG	TACGAAGGCG	400
ACACCTACGT	TGATCTGGCC	GAAATGGTCA	AAGACTACGA	GCAGAATGGC	450
ATGGAAGAAC	ATGACCTTCA	CACTTACTTC	ACTTACCGTA	AAAAGGAGCT	500
TACAGAATGA					510

2) INFORMATION FOR SEQ ID NO: 1495

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495

TCTCTAAACA TGATTGTCGC TGTC

24

2) INFORMATION FOR SEQ ID NO: 1496

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496

CAGTGAGGCA AAAGTTTTTC TACC

24

5

2) INFORMATION FOR SEQ ID NO: 1497

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1497

CGGACGACTT CATGTGGTAG TCAGT

25

20

2) INFORMATION FOR SEQ ID NO: 1498

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498

TTTGTTTTCA GTAATGGTCG GGACCT

26

35

2) INFORMATION FOR SEQ ID NO: 1499

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X57730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499

	ATGGCTTCTC	TAAACATGAT	TGTCGCTGTC	AATAAGACAG	GAGGTATCGG	50
	ATTTGAAAAT	CAGATTCGGT	GGCATGAACC	AGAAGATTTA	AAACACTTCA	100
	AAGCTGTTAC	AATGAACTCA	GTTTTGATTA	TGGGTAGAAA	AACTTTTGCC	150
	TCACTGCCTA	AAGTGCTGCC	CGGACGACTT	CATGTGGTAG	TCAGTAAAC	200
5	AGTACCACCC	ACCCAGAACA	CTGATCAAGT	TGTGTATGTA	AGTACATACC	250
	AGATCGCAGT	AAGAACTGCA	AGCTTGTTGG	TTGACAAACC	AGAGTATTCT	300
	CAAATTTTGT	TAATTGGTGG	GAAGAGTGCG	TACGAGAACT	TAGCTGCCTA	350
	CGTGGACAAA	CTCTACTTAA	CTAGAGTACA	GCTCAACACA	CAACAAGACA	400
	CTGAACTGGA	TTTATCCCTA	TTCAAGTCAT	GGAAACTCGT	ATCTGAGGTC	450
10	CCGACCATTA	CTGAAAACAA	AACAAAACCT	ATTTTCCAAA	TTTGGATTAA	500
	CCCTAACCT	ATTAGTGAGG	AACCCACATG	TTAG		534

15 2) INFORMATION FOR SEQ ID NO: 1500

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500

ATCGGGTTAT TGGCAATGGT CCTA

24

30

2) INFORMATION FOR SEQ ID NO: 1501

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501

GCGGTAGTTA GCTTGGCGTG AGATT

25

45

2) INFORMATION FOR SEQ ID NO: 1502

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502

5 GCGGGCGGAG CTGAGATATA CA 22

10 2) INFORMATION FOR SEQ ID NO: 1503

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503

AACGGAGTGG GTGTACGGAA TTACAG 26

25 2) INFORMATION FOR SEQ ID NO: 1504

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 498 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(B) STRAIN: TKS84
(C) ACCESSION NUMBER: Z21672

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504

	ATGAACTCGG	AATCAGTACG	CATTTATCTC	GTTGCTGCGA	TGGGAGCCAA	50
	TCGGGTATT	GGCAATGGTC	CTAATATCCC	CTGGAAAATT	CCGGGTGAGC	100
45	AGAAGATTTT	TCGCAGACTC	ACTGAGGGAA	AAGTCGTTGT	CATGGGGCGA	150
	AAGACCTTTG	AGTCTATCGG	CAAGCCTCTA	CCGAACCGTC	ACACATTGGT	200
	AATCTCACGC	CAAGCTAACT	ACCGCGCCAC	TGGCTGCGTA	GTTGTTTCAA	250
	CGCTGTCGCA	CGCTATCGCT	TTGGCATCCG	AACTCGGCAA	TGAACTCTAC	300
	GTCGCGGGCG	GAGCTGAGAT	ATACACTCTG	GCACTACCTC	ACGCCCACGG	350
50	CGTGTTTCTA	TCTGAGGTAC	ATCAAACCTT	CGAGGGTGAC	GCCTTCTTCC	400
	CAATGCTCAA	CGAAACAGAA	TTCGAGCTTG	TCTCAACCGA	AACCATTCAA	450
	GCTGTAATTC	CGTACACCCA	CTCCGTTTAT	GCGCGTCGAA	ACGGCTAA	498

2) INFORMATION FOR SEQ ID NO: 1505

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505

ATTTTTCGCA GGCTCACCGA GAGC

24

2) INFORMATION FOR SEQ ID NO: 1506

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506

CGGATGAGAC AACCTCGAAT TCTGCTG

27

2) INFORMATION FOR SEQ ID NO: 1507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: RA33.2
 (C) ACCESSION NUMBER: Z50802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507

ATGAACCCGG	AATCGGTCCG	CATTTATCTG	GTCGCTGCCA	TGGGTGCCAA	50
TCGGGTATT	GGCAATGGTC	CCGATATCCC	CTGGAAAATC	CCAGGTGAGC	100
AGAAGATTTT	TCGCAGGCTC	ACCGAGAGCA	AAGTGGTCGT	TATGGGCCGC	150
AAGACATTTG	AGTCCATAGG	CAAGCCCTTA	CCAAACCGCC	ACACAGTGTT	200

	GCTCTCGCGC	CAAGCTGGTT	ATAGCGCTCC	TGGTTGTGCA	GTTGTTTCAA	250
	CGCTGTCACA	CGTATCGCCA	TCGACAGCCG	AACACGGCAA	AGAACTCTAC	300
	GTAGCGCGCG	GAGCCGAGGT	ATATGCGCTG	GCGCTACCGC	ATGCCAACGG	350
	CGTCTTTCTA	TCTGAGGTAC	ATCAAACCTT	TGAGGGTGAC	GCCTTCTTCC	400
5	CAGTGCTTAA	CGCAGCAGAA	TTCGAGGTTG	TCTCATCCGA	AACCATTCAA	450
	GGCACAATCA	CGTACACGCA	CTCCGTCTAT	GCGCGTCGTA	ACGGCTAA	498

10 2) INFORMATION FOR SEQ ID NO: 1508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508

AGAATGTATT GGTATTTCCA TCTATCG

27

25 2) INFORMATION FOR SEQ ID NO: 1509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- 30 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509

CAATGTCGAT TGTGAAATA TGTA

26

40 2) INFORMATION FOR SEQ ID NO: 1510

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510

TGGAGTGCCA AAGGGGAACA AT

5 2) INFORMATION FOR SEQ ID NO: 1511

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511

CAGACACAAT CACATGATCC GTTATCG

27

20

2) INFORMATION FOR SEQ ID NO: 1512

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 474 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: UI14
 (C) ACCESSION NUMBER: Z83331

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512

GTGAAACTAT CACTAATGGC AGCAATTTTCG AAGAATGGAG TTATCGGAAA 50
 TGGCCCAGAT ATTCCATGGA GTGCCAAAGG GGAACAATTA CTCTTCAAAG 100
 40 CGATTACCTA TAATCAGTGG CTTTGGGTAG GCCGAAAGAC TTTCGAGTCA 150
 ATGGGGGCTT TACCCAACCG AAAATATGCC GTTGTAAGTTC GTTCAAGCTT 200
 CACTTCCAGT GATGAGAATG TATTGGTATT TCCATCTATC GATGAAGCGC 250
 TAAATCATCT GAAGACGATA ACGGATCATG TGATTGTGTC TGGTGGTGGT 300
 GAAATATACA AAAGCCTGAT CGATAAAGTT GATACTTTAC ATATTTCAAC 350
 45 AATCGACATT GAGCCAGAAG GTGATGTCTA TTTTCCAGAA ATCCCCAGTA 400
 GTTTTAGGCC AGTTTTTAGC CAAGACTTCG TGTCTAACAT AAATTATAGT 450
 TACCAAATCT GGCAAAGGG TTAA 474

50

2) INFORMATION FOR SEQ ID NO: 1513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513

10 TTCAAGCTCA AATGAAAACG TCC

23

2) INFORMATION FOR SEQ ID NO: 1514

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514

25

GAAATTCTCA GGCATTATAG GGAAT

25

30 2) INFORMATION FOR SEQ ID NO: 1515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515

40

GTGGTCAGTA AAAGGTGAGC AAC

23

45

2) INFORMATION FOR SEQ ID NO: 1516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

PAGE 786

MISSING AT THE TIME OF PUBLICATION

CTATGTCTCA	AGGCCGTGCA	ACATACTCTA	TGGAATTTGC	TAAATATGCT	50
GAAACTCCAC	GTAACGTGGC	TGAAGGCATC	ATTTCTAAAT	TTCAGTCTGG	100
CGGTAAAAAA	GGTGACGACG	AGTAA			125

5

2) INFORMATION FOR SEQ ID NO: 1519

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter lwoffii*
 - (B) STRAIN: CDCF 3697
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519

TCTTTCGATT	ACTATAAGCC	CAAACATAATT	CATAGTTAAA	AACCAAGTGC	50
TCATGCAGTG	ATCCTGCATG	AGTAGTTTAA	AAAGGAAGAT	CTC	93

25

2) INFORMATION FOR SEQ ID NO: 1520

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1106 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter lwoffii*
 - (B) STRAIN: CDCF 3697
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520

ATGGCTAAGG	CTAAGTTTGA	ACGTAATAAG	CCACACGTTA	ACGTGGGCAC	50
AATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACAGCT	GCAATTGCAA	100
CTGTATGTGC	GAAGAAATTC	GGTGGCGAAG	CGAAAGACTA	CGCTGCAATT	150
GACTCTGCAC	CAGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACTTCACA	200
CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTA	GACTGCCCCG	250
GCCACGCCGA	TTATGTTAAA	AACATGATTA	CTGGTGCTGC	TCAGATGGAC	300
GGCGCGATCC	TTGTATGTGC	TGCGACTGAT	GGTCCAATGC	CACAGACTCG	350
TGAACACATC	CTTCTTTCTC	GTCAGGTTGG	TGTACCTTAC	ATTCTTGAT	400
TCCTTAACAA	GTGTGACCTT	GTTGATGATG	AAGAACTTCT	TGAGCTAGTG	450

50

	GAAATGGAAG	TTCGTGAACT	TCTTTCTACT	TATGACTTCC	CAGGTGATGA	500
	CACTCCAGTT	ATCCGTGGTT	CAGCTCTTCT	TGCACTTAAC	GGTGACGCTG	550
	GTCAGTATGG	CGAAGAAGCA	GTTGTTGCGC	TTGTTGACGC	ACTTGACACT	600
	TACATTCCAG	AGCCAGTACG	TGCAATCGAC	CAAGCATTCT	TAATGCCAAT	650
5	CGAAGACGTA	TTCTCTATTT	CTGGTCGTGG	TACAGTAGTA	ACTGGCCGTG	700
	TAGAAACTGG	TATTGTGAAA	GTAGGCGAAT	CAGTTGAAAT	CGTTGGTATC	750
	CGTGATACTC	AAGTAACTAC	AGTTACTGGC	GTAGAAATGT	TCCGTAAATT	800
	GCTTGACGAA	GGTCGTGCGG	GCGAGAACTG	TGGTGTTCTT	CTACGTGGTA	850
	CTAAGCGTGA	AGACGTACAA	CGTGGTCAAG	TACTTGCTAA	ACCAGGTGCA	900
10	ATCAAGCCAC	ACACTAAATT	CGATGCAGAA	GTATACGTAC	TTTCTAAAGA	950
	AGAAGGTGGT	CGTCACACTC	CATTCCTTAA	CGGTTACCGT	CCACAGTTCT	1000
	ACTTCCGTAC	AACTGACGTA	ACTGGCGCGA	TCAAATTACA	AGATGGCGTT	1050
	GAAATGGTTA	TGCCTGGTGA	CAACGTAGAA	ATGTCAGTAG	AATTAATCCA	1100
	CCCAAT					1106

2) INFORMATION FOR SEQ ID NO: 1521

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Haemophilus influenzae*
 30 (B) STRAIN: ATCC 9006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521

	ACAAACTCAA	GGTCGTGCAT	CTTACTCAAT	GGAACCGTTA	AAATATGCTG	50
35	AAGCTCCAAC	AAGTGTTGCG	GCTGCAGTAA	TTGAAGCGCG	TAAAAAATAA	100

2) INFORMATION FOR SEQ ID NO: 1522

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522

TTTTTGTAAG CCAGCGGTGT AAAATATGAT TGTTTTATAC CGCACTTCTT 50
 AGGAAACATT AGAA 64

5

2) INFORMATION FOR SEQ ID NO: 1523

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523

	ATGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTAA	ACGTGGGTAC	50
	AATCGGCCAC	GTTGACCACG	GTAAAACAAC	TTTAACAGCA	GCAATTACAA	100
25	CCGTATTAGC	AAAACACTAC	GGTGGTGCAG	CGCGTGCATT	TGACCAAATC	150
	GATAACGCGC	CAGAAGAAAA	AGCGCGTGGT	ATTACCATCA	ACACTTCACA	200
	TGTTGAATAC	GATACACCAA	CTCGCCACTA	TGCACACGTA	GACTGTCCAG	250
	GACACGCCGA	CTATGTTAAA	AACATGATTA	CCGGTGCGGC	GCAAATGGAT	300
	GGTGCTATTT	TAGTAGTAGC	AGCAACAGAT	GGTCCTATGC	CACAAACTCG	350
30	TGAACATATC	TTATTAGGTC	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	400
	TCTTAAACAA	ATGCGACATG	GTAGATGATG	AAGAGTTATT	AGAATTAGTA	450
	GAAATGGAAG	TGCGTGAACT	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	500
	TACACCAATC	GTACGTGGTT	CAGCATTACA	AGCATTGAAC	GGCGTAGCAG	550
	AATGGGAAGA	AAAAATCCTT	GAATTAGCTG	GTCACTTAGA	TACTTACATC	600
35	CCAGAACCAG	AACGTGCGAT	TGACCAACCG	TTCCTTCTTC	CAATTGAAGA	650
	CGTATTCTCA	ATTTTCAGGTG	GTGGTACAGT	AGTAACTGGT	CGTGTAGAAC	700
	GTGGTATCAT	CCGTACTGGT	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	750
	ACAGCGAAAA	CTACTGTAAAC	AGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	800
	CGAAGGTCGT	GCAGGTGAAA	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	850
40	GTGAAGAAAT	CGAACGTGGT	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	900
	CCACACACTG	ATTTTGAATC	AGAAGTATAC	GTATTATCAA	AAGATGAAGG	950
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	1000
	GTACAACAGA	CGTAACTGGT	ACAATTGAAT	TACCAGAAGG	CGTGGAATG	1050
45	GTAATGCCAG	GCGATAACAT	CAAGATGACA	GTAAGCTTAA	TCCACCCA	1098

2) INFORMATION FOR SEQ ID NO: 1524

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524

10 CAATGGAGTT CTTGAAGTAC AACGAAGCGC CTAGCAACGT CGCTCAGGCT 50
ATTATCGAAG CTCGTAAAGC GAAATAA 77

15

2) INFORMATION FOR SEQ ID NO: 1525

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 67 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525

GATCCTTTCG AGTTCAATTT AGTTTACGCT CCCTCTGTGA GAGGGAGCGA 50
TATTAAGGAA TATAGTC 67

35

2) INFORMATION FOR SEQ ID NO: 1526

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1112 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526

GTGTCTAAAG AAAAATTTGA ACGTTCAAAA CCGCACGTTA ACGTTGGTAC 50

	TATCGGCCAC	GTTGACCACG	GTAACAACAAC	TCTGACTGCT	GCAATCACTA	100
	CAGTTTTTAGC	TAAAACTTAC	GGTGGTGCTG	CTCGTGCAAT	CGACCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCGCGTGGT	ATCACCATCT	CTACTTCACA	200
	CGTAGAATAC	GATACTCCAA	CTCGCCACTA	CGCACACGTA	GACTGCCAG	250
5	GTCACGCCGA	CTATGTTAAA	AACATGATCA	CTGGTGCTGC	GCAAATGGAC	300
	GGCGCTATTC	TGGTAGTAGC	AGCAACTGAT	GGTCCAATGC	CACAACTCG	350
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGTGACATG	GATAGATGATG	AAGAGCTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTCC	CAGGTGATGA	500
10	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	550
	AGTGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCTTATATC	600
	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATCGAAGA	650
	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	TATCAAAGAA	750
15	ACCACCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	800
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACAAAAC	850
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CAAACCCAGG	CTCAATCAAC	900
	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAC	ACACCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
20	GTACAACCTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	1050
	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGAACTGA	TCCACCCAAT	1100
	CGCAATGGAC	GA				1112

25

2) INFORMATION FOR SEQ ID NO: 1527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527

	ATCAACGAAG	CTATCGAGGT	TTATTTTGAG	GTTGAGGGCA	AGAAAAATAG	50
	ATTGATCCTG	GAGGTCGCGG	CTCACTTGGG	TGATAACCGC	GTCAGAACGA	100
	TCGCTATGGA	TATGAGTGAG	GGGCTTACTC	GCGGGCTTGA	AGCTACCGCT	150
45	CTTGGTGCGC	CTATTAGTGT	GCCGGTTGGC	GAGAAGGTTT	TGGGAAGAAT	200
	TTTTAACGTC	GTCGGCGATC	TCATCGACGA	GGGCGAGGGC	GTAAATTTTG	250
	ATAAACATTG	GTCTATCCAC	CGCGATCCGC	CACCATTTGA	AGAACAAAGC	300
	ACGAAAAGTG	AAATTTTTGA	AACCGGTATA	AAGGTTGTGG	ATCTTCTTGC	350
	GCCTTACGCA	AAGGGCGGTA	AGGTCGGACT	ATTTGGCGGT	GCAGGTGTGC	400
50	GTAAAACGGT	CATCATCATG	GAGCTCATCC	ACAATGTCGC	CTTCAAACAC	450
	AGCGGATACT	CTGTATTTGC	AGGTGTTGGC	GAGAGGACGC	GCGAAGGAAA	500
	CGACCTTTAT	CACGAGATGA	AAGAAAGTAA	CGTTTTGGAT	AAAGTCGCCT	550
	TGTGCTACGG	ACAGATGAAC	GAGCCGCCAG	GGGCGAGAAA	TCGTATCGCA	600

CTGACTGGTC	TAACGATGGC	TGAGTATTTTC	CGCGATGAGA	TGGGACTTGA	650
TGTGCTTATG	TTTATCGACA	ACATCTTCCG	CTTCTCTCAA	TCTGGTGCAG	700
AGATGTCGGC	ACTCCTCGGA	CGTATCCCAT	CAGCCGTTGG	TTACCAGCCG	750
ACGCTGGCAA	GCGAGATGGG	TAAATTTCAA	GAAAGGATCA	CATCGACTAA	800

5

2) INFORMATION FOR SEQ ID NO: 1528

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528

20 AACTTGAGCG ATTTTCGGAT ACCCTG

26

2) INFORMATION FOR SEQ ID NO: 1529

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529

35

TTGCCGATGA AATAACCGCC GACT

24

40 2) INFORMATION FOR SEQ ID NO: 1530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: M11277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530

	ATGCGATTGG	TTTGAAATG	TGGGGCGATT	CAGGCATCCC	GGTTATCTGA	50
	ATGGCTCAAC	TCAACAGCCG	GTGCTCATGA	ACTTGAGCGA	TTTTTCGGATA	100
5	CCCTGACCTT	TTCTGTGTAT	GGCTCAGTGC	TGATCTGGCT	GAAATCATAT	150
	CTCCGCGAAT	CAGGAAGAAA	ACTGCAGTTA	GTCGGAATCG	CCTTACCCAA	200
	CACCCTGAAC	CCAAGGGACG	ACCTAGCGCA	ATTGGCCGAA	ATTATCCAGC	250
	TCATCGATCA	CCTCATGAAA	CCGCACGTTG	ATATGTTGAC	TCACTTGTTG	300
	GCGTCCATTG	ATGGCCAGTC	GGCGGTTATT	TCATCGGCAA	AATGGGGGGA	350
10	GCTAGAAACG	GCTCGGCAGG	AGAAAGCTAT	CTCAGGGGTA	ACCAGATTGA	400
	AGCTCCGCTT	GGCGTCGCTT	GCCCCGTCC	TGAAAAACA	CGTCAACAGC	450
	GATTTGTTCC	GAAAAGCCTC	TGATCGAATA	GAGTCGATAG	AGTATACGTT	500
	GGAAACCTTG	CGTATAATGA	AAACTTTCTT	CGATGGTACC	TCTCTTGAGG	550
	GAGATACTTC	CGTACGTGAC	TCGTATATGG	CGGGCGTAGT	AGATGGAATG	600
15	GTTTCGAGCGA	ATCCGGATGT	GAAGATAATT	CTGCTGGCGC	ACAACAATCA	650
	TCTACAAAAA	ACTCCAGTCT	CCTTTTCAGG	CGAGCTTACG	GCTGTTCCCA	700
	TGGGGCAGCA	CCTCGCAGAG	AGGGTGAATT	ACCGTGCGAT	TGCATTACACC	750
	CATCTTGAC	CCACCGTGCC	GGAAATGCAT	TTCCCATCGC	CAAAAAGTCC	800
	TCTTGATTTC	TCTGTTGTGA	CCACGCCTGC	CGATGCAATC	CGTGAGGATA	850
20	GTATGGAACA	GTATGTCATC	GACGCCTGTG	GTACGGAGAA	TTCATGTCTG	900
	ACATTGACAG	ATGCCCCCAT	GGAAGCAAAG	CGAATGCGGT	CTCAAAGCGC	950
	CTCTGTAGAA	ACGAAATTGA	GCGAGGCATT	TGATGCCATC	GTCTGTGTTA	1000
	CAAGCGCCGG	CAAGGACAGC	CTGGTTGCCC	TATAG		1035

25

2) INFORMATION FOR SEQ ID NO: 1531

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531

TCTTTTTGTT ACGACATACG CTTTT

40

25

2) INFORMATION FOR SEQ ID NO: 1532

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532

AGTGCTTCTT TATCCGCTGT TCTA

24

5

2) INFORMATION FOR SEQ ID NO: 1533

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533

CAGCGGATAA AGAAGCACTA CACATT

26

20

2) INFORMATION FOR SEQ ID NO: 1534

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534

CCTCCTGAAA TAAAGCCCGA CAT

23

35

2) INFORMATION FOR SEQ ID NO: 1535

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: A15097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535

	ATGAGGTTTCG	AAGAATGGGT	CAAAGATAAG	CATATTCCTT	NCAAACNGAA	50
	TCACCCTGAT	GATAATTACG	ATGATTTTAA	GCCATTAAGA	AANATAATTG	100
	GAGATACCCG	AGTTGTAGCA	TTAGGTGAAA	ATTCTCATTT	CATAAAAGAA	150
	TTCTTTTTGT	TACGACATAC	GCTTTTGCGT	TTTTTTATCG	AAGATCTAGG	200
5	TTTTACTACG	TTTGCTTTTG	AATTTGGTTT	TGCTGAGGGT	CAAATCATCA	250
	ATAACTGGAT	ACATGGACAA	GGAAGTACG	ATGAAATAGG	CAGATTCTTA	300
	AAACACTTCT	ATTATCCAGA	AGAGCTCAA	ACCACATTTC	TATGGCTAAG	350
	GGAGTACAAT	AAAGCAGCAA	AAGAAAAAAT	CACATTTCTT	GGCATTGATA	400
	TACCCAGAAA	TGGAGGTTCA	TACTTACCAA	ATATGGAGAT	AGTGCATGAC	450
10	TTTTTTAGAA	CAGCGGATAA	AGAAGCACTA	CACATTATCG	ATGATGCATT	500
	TAATATTGCA	AAAAAGATTG	ATTACTTCTC	CACATCACAG	GCAGCCTTAA	550
	ATTTACATGA	GCTAACAGAT	TCTGAGAAAT	GCCGTTTAAC	TAGCCAATTA	600
	GCTCGAGTAA	AAGTTCGCCT	TGAAGCTATG	GCTCCAATTC	ACATTGAAAA	650
	ATATGGGATT	GATAAATATG	AGACAATTCT	GCATTATGCC	AACGGTATGA	700
15	TATACTTGA	CTATAACATT	CAAGCTATGT	CGGGCTTTAT	TTCAGGAGGC	750
	GGAATGCAGG	GCGATATGGG	TGCAAAAAGAC	AAATACATGG	CAGATTCTGT	800
	GCTGTGGCAT	TTAAAAAACC	CACAAAGTGA	GCAGAAAGTG	ATAGTAGTAG	850
	CACATAATGC	ACATATTCAA	AAAACACCCA	TTCTGTATGA	TGGATTTCTA	900
	AGTTGCCTAC	CAATGGGCCA	AAGACTTAAA	AATGCCATTG	GTGATGATTA	950
20	TATGTCTTTA	GGTATTACTT	CTTATAGTGG	GCATACTGCA	GCCCTCTATC	1000
	CGGAAGTTGA	TACAAAATAT	GGTTTTTCGAG	TTGATAACTT	CCAACTGCAG	1050
	GAACCAAATG	AAGGTTCTGT	CGAGAAAGCT	ATTTCTGGTT	GTGGAGTTAC	1100
	TAATTCTTTT	GTCTTTTTTA	GAAATATTCC	TGAAGATTTA	CAATCCATCC	1150
	CGAACATGAT	TCGATTTGAN	TCTATTTACA	TGAAAGCAGA	ACTCGAGAAA	1200
25	GCTTTCGATG	GAATATTTCA	AATTGAAAAG	TCATCTGTAT	CTGAGGTCGT	1250
	TTATGAATAA					1260

30 2) INFORMATION FOR SEQ ID NO: 1536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536

AGATGTATTA ACTGGAAAAC AACAA

25

45

2) INFORMATION FOR SEQ ID NO: 1537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537

5 CTTTGTAATT AGTTTCTGAA AACCA

25

2) INFORMATION FOR SEQ ID NO: 1538

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538

20

TTAGAAGATA TAGGATACAA AATAGAAG

28

25 2) INFORMATION FOR SEQ ID NO: 1539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539

GAATGAAAAA GAAGTTGAGC TT

22

40

2) INFORMATION FOR SEQ ID NO: 1540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

45

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(C) ACCESSION NUMBER: M14039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540

	ATGAAAAATA	ATAATGTAAC	AGAAAAAGAA	TTATTTTATA	TTTTAGATTT	50
5	ATTTGAACAC	ATGAAAGTAA	CTTATTGGTT	AGATGGTGGC	TGGGGGGTAG	100
	ATGTATTAAC	TGGAAAACAA	CAAAGAGAAC	ACAGAGATAT	AGATATAGAT	150
	TTTGACGCTC	AACACACTCA	AAAAGTTATA	CAAAAATTAG	AAGATATAGG	200
	ATACAAAATA	GAAGTTCATT	GGATGCCTTC	ACGTATGGAA	CTTAAGCATG	250
	AAGAATATGG	GTATTTAGAT	ATTCATCCTA	TAAATCTAAA	TGATGATGGA	300
10	TCAATTACCC	AAGCAAACCC	AGAAGGTGGT	AATTATGTTT	TCCAAAATGA	350
	CTGGTTTTCA	GAAACTAATT	ACAAAGATCG	AAAAATACCA	TGTATTTCAA	400
	AAGAAGCTCA	ACTTCTTTT	CATTCTGGTT	ATGATTTAAC	AGAAACAGAC	450
	CATTTTGATA	TAAAAAATTT	AAAATCAATA	ACATAA		486

15

2) INFORMATION FOR SEQ ID NO: 1541

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541

	TGATAATCTT	ATACGTGGGG	AATTT	25
30				

2) INFORMATION FOR SEQ ID NO: 1542

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542

45	ATAATTTTCT	AATTGCCCTG	TTTCAT	26
----	------------	------------	--------	----

2) INFORMATION FOR SEQ ID NO: 1543

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543

GGGCAATTAG AAAATTATTT ATCAGA

26

10

2) INFORMATION FOR SEQ ID NO: 1544

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544

TTTTACTCAT GTTTAGCCAA TTATCA

26

25

2) INFORMATION FOR SEQ ID NO: 1545

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF110130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545

	ATGTTAAAAC	AAAAAGAATT	AATTGCAAAC	GTTAAGAATC	TTACTGAGTC	50
45	AGATGAACGA	ATTACAGCTT	GTATGATGTA	TGGATCGTTT	ACCAAAGGAG	100
	AAGGTGACCA	ATACTCTGAT	ATAGAGTTCT	ATATATTTTT	GAAACATAGT	150
	ATAACCTCGA	ACTTTGATTC	ATCCAACCTG	TTGTTTGACG	TAGCTCCGTA	200
	CTTGATGCTT	TATAAAAATG	AGTACGGAAC	AGAGGTAGTT	ATTTTTGATA	250
	ATCTTATACG	TGGGGAATTT	CATTTCTTTT	CTGAAAAGA	TATGAACATA	300
50	ATCCCCTCGT	TTAAAGATTC	AGGTTATATT	CCTGATACGA	AGGCTATGCT	350
	TATTTACGAT	GAAACAGGGC	AATTAGAAAA	TTATTTATCA	GAGATAAGTG	400
	GTGCAAGACC	AAATAGACTT	ACTGAAGAAA	ATGCTAATTT	TTTGTTGTGT	450
	AATTTCTCTA	ATCTATGGTT	GATGGGAATC	AACGTTCTAA	AAAGAGGAGA	500

ATATGCTCGT TCATTAGAAC TCTTATCACA ACTTCAAAAA AATACACTAC 550
 AACTTATACG TATGGCAGAA AAAAATGCTG ATAATTGGCT AAACATGAGT 600
 AAAAACCTTG AAAAAGAAAT TAGCCTTGAA AATTATAAAA AATTTGCAAA 650
 GACCACTGCT CGATTAGATA AGGTAGAATT ATTTGAAGCC TATAAAAATT 700
 5 CTTTGCTATT AGTTATGGAT TTGCAAAGTC ACCTTATTGA ACAATACAAC 750
 TTAAAAGTTA CACATGACAT TTTAGAAAGA TTGTTGAATT ACATTAGTGA 800
 ATAG 804

10

2) INFORMATION FOR SEQ ID NO: 1546

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546

CAAGAAGGAA TGGCTGTACT AC

22

25

2) INFORMATION FOR SEQ ID NO: 1547

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1547

TAATTCCCAA ATAACCCTAA TAATAGA

27

40

2) INFORMATION FOR SEQ ID NO: 1548

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(C) ACCESSION NUMBER: U70055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548

5
 ATGGAAAAAT ACAACAATTG GAAACTTAAG TTTTATACAA TATGGGCAGG 50
 GCAAGCAGTA TCATTAATCA CTAGTGCCAT CTTGCAAATG GCGATTATTT 100
 TTTACCTTAC AGAAAAAACT GGATCCGCGA TGGTCTTGTC TATGGCTTCA 150
 CTATTAGGTT TTTTACCCTA TGCGGTCTTT GGACCTGCAA TTGGTGTGCT 200
 10 AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCT GATTTAATTA 250
 TCGCAGCAGC TGGTTCGGTG CTTACTATTG TTGCATTCTA TATGGAGCTA 300
 CCTGTCTGGA TGGTTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC 350
 TTTTCACACC CCGGCTCTCA ATGCGGTAC GCCACTTTTA GTACCAGAAG 400
 AACAGCTTAC GAAATGTGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC 450
 15 TATATTGTTA GTCCGGCGGT TGCAGCACTC TTATACTCCG TTTGGGAACT 500
 AAATGCTATT ATTGCCATCG ATGTATTGGG TGCTGTGATT GCATCTATTA 550
 CGGTAGCAAT TGTACGTATT CCTAAGCTGG GTGATCGCGT GCAAAGTTTG 600
 GACCCAAATT TCATAAGAGA AATGCAAGAA GGAATGGCTG TACTACGGCA 650
 AAATAAAGGA TTATTTGCTT TATTACTCGT TGGAACATTA TATATGTTTG 700
 20 TTTATATGCC AATTAATGCA CTATTCCCTT TAATTAGCAT GGATTACTTT 750
 AATGGAACAC CTGTGCATAT TTCTATTACG GAAATTTCTT TTGCATCTGG 800
 AATGTTGATA GGGGGTCTAT TATTAGGGTT ATTTGGGAAT TACCAAAGC 850
 GAATCTTATT AATAACGGCA TCCATTTTTA TGATGGGGAT AAGCTTAACC 900
 ATTTCAGGAT TACTTCCCCA AAGTGGATTT TTCATTTTGT TAGTCTGCTG 950
 25 TGCAATAATG GGGCTTTCTG TTCCGTTTTA CAGCGGTGTG CAAACAGCTC 1000
 TTTTTCAGGA GAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTA 1050
 ACTGGAAGTA TCATGTCTCT TGCTATGCCA ATTGGATTAA TTCTTTCTGC 1100
 ACTCTTTGCT GATAGAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA 1150
 CTTTAATTAT TTGCATTGCA ATAGTTTGCC CAATGATAAA TGAGATTAGA 1200
 30 AAATTAGATT TAAAATAA 1218

2) INFORMATION FOR SEQ ID NO: 1549

35
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549

45
 GCTTATTATT AGGAAGATTA GGGGGC

26

50 2) INFORMATION FOR SEQ ID NO: 1550

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550

TAGCAAGTGA CATGATACTT CCGA

24

2) INFORMATION FOR SEQ ID NO: 1551

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: U83667

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551

	ATGGAAAAAT	ACAACAATTG	GAAACGAAAA	TTTTATGCAA	TATGGGCAGG	50
30	GCAAGCAGTA	TCATTAATCA	CTAGTGCCAT	CCTGCAAATG	GCGATTATTT	100
	TTTACCTTAC	AGAAAAAACA	GGATCTGCGA	TGGTCTTGTC	TATGGCTTCA	150
	TTAGTAGGTT	TTTTACCCTA	TGCGATTTTG	GGACCTGCCA	TTGGTGTGCT	200
	AGTGGATCGT	CATGATAGGA	AGAAGATAAT	GATTGGTGCC	GATTTAATTA	250
	TCGCAGCAGC	TGGTGCAGTG	CTTGCTATTG	TTGCATTCTG	TATGGAGCTA	300
35	CCTGTCTGGA	TGATTATGAT	AGTATTGTTT	ATCCGTAGCA	TTGGAACAGC	350
	TTTTCATACC	CCAGCACTCA	ATGCGGTTAC	ACCACTTTTA	GTACCAGAAG	400
	AACAGCTAAC	GAAATGCGCA	GGCTATAGTC	AGTCTTTGCA	GTCTATAAGC	450
	TATATTGTTA	GTCCGGCAGT	TGCAGCACTC	TTATACTCCG	TTTGGGATTT	500
	AAATGCTATT	ATTGCCATCG	ACGTATTGGG	TGCTGTGATT	GCATCTATTA	550
40	CGGTAGCAAT	TGTACGTATA	CCTAAGCTGG	GTAATCAAGT	GCAAAGTTTA	600
	GAACCAAATT	TCATAAGGGA	GATGAAAGAA	GGAGTTGTGG	TTCTGAGACA	650
	AAACAAAGGA	TTGTTTGCCT	TATTACTCTT	AGGAACACTA	TATACTTTTG	700
	TTTATATGCC	AATCAATGCA	CTATTTTCCT	TAATAAGCAT	GGAACACTTT	750
	AATGGAACGC	CTGTGCATAT	TTCTATTACG	GAAATTTCCCT	TTGCATTTGG	800
45	GATGCTAGCA	GGAGGCTTAT	TATTAGGAAG	ATTAGGGGGC	TTCGAAAAGC	850
	ATGTATTACT	AATAACAAGT	TCATTTTTTA	TAATGGGGAC	CAGTTTAGCC	900
	GTTTCGGGAA	TACTTCCTCC	AAATGGATTT	GTAATATTCG	TAGTTTGCTG	950
	TGCAATAATG	GGGCTTTTCG	TGCCATTTTA	TAGCGGTGTG	CAAACAGCTC	1000
	TTTTTTCAGGA	GAAAAATTAAG	CCTGAATATT	TAGGACGTGT	ATTTTCTTTG	1050
50	ATCGGAAGTA	TCATGTCACT	TGCTATGCCA	ATTGGGTTAA	TTCTTTCTGG	1100
	ATTCTTTGCT	GATAAAATCG	GTGTAAATCA	TTGGTTTTTA	CTATCAGGTA	1150
	TTTTAATTAT	TGGCATTGCT	ATAGTTTGCC	AAATGATAAC	TGAGGTTAGA	1200
	AAATTAGATT	TAAAATAA				1218

2) INFORMATION FOR SEQ ID NO: 1552

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552

GGCAAGCAGT ATCATTAATC ACTA

24

2) INFORMATION FOR SEQ ID NO: 1553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553

CAATGCTACG GATAACAAT ACTATC

26

2) INFORMATION FOR SEQ ID NO: 1554

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554

AGAAAATTAA GCCTGAATAT TTAGGAC

27

2) INFORMATION FOR SEQ ID NO: 1555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555

TAGTAAAAAC CAATGATTTA CACCG

25

10

2) INFORMATION FOR SEQ ID NO: 1556

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556

ACTGTACGCA CTTGCAGCCC GACAT

25

25

2) INFORMATION FOR SEQ ID NO: 1557

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557

GAACGGCAGG CGATTCTTGA GCAT

24

40

2) INFORMATION FOR SEQ ID NO: 1558

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558

GTGGTGGTGC ATGGCGATCT CT

22

5

2) INFORMATION FOR SEQ ID NO: 1559

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559

GCCGCAGCGA GGTACTCTTC GTTA

24

20

2) INFORMATION FOR SEQ ID NO: 1560

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: D16251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560

	ATGACCGTAG	TCACGACCGC	CGATACCTCC	CAACTGTACG	CACTTGCAGC	50
40	CCGACATGGG	CTCAAGCTCC	ATGGCCCCTG	GACTGTCAAT	GAGCTTGGGC	100
	TCGACTATAG	GATCGTGATC	GCCACCGTCG	ACGATGGACG	TCGGTGGGTG	150
	CTGCGCATCC	CGCGCCGAGC	CGAGGTAAGC	GCGAAGGTCG	AACCAGAGGC	200
	GCGGGTGCTG	GCAATGCTCA	AGAATCGCCT	GCCGTTTCGG	GTGCCGGAAT	250
	GGCGCGTGGC	CAACGCCGAG	CTCGTTGCCT	ATCCCATGCT	CGAAGACTCG	300
45	ACTGCGATGG	TCATCCAGCC	TGGTTCGTCC	ACGCCCCGCT	GGGTCGTGCC	350
	GCAGGACTCG	GAGGTCTTCG	CGGAGAGCTT	CGCGACCGCG	CTCGCCGCCC	400
	TGCATGCCGT	CCCCATTTCC	GCCGCCGTGG	ATGCGGGGAT	GCTCATCCGT	450
	ACACCGACGC	AGGCCCGTCA	GAAGGTGGCC	GACGACGTTG	ACCGCGTCCG	500
	ACGCGAGTTC	GTGGTGAACG	ACAAGCGCCT	CCACCGGTGG	CAGCGCTGGC	550
50	TCGACGACGA	TTCGTCGTGG	CCAGATTTCT	CCGTGGTGGT	GCATGGCGAT	600
	CTCTACGTGG	GCCATGTGCT	CATCGACAAC	ACGGAGCGCG	TCAGCGGGAT	650
	GATCGACTGG	AGCGAGGCCC	GCGTTGATGA	CCCTGCCATC	GACATGGCCG	700
	CGCACCTTAT	GGTCTTTGGT	GAAGAGGGGC	TCGCGAAGCT	CCTCCTCACG	750

TATGAAGCGG	CCGGTGGCCG	GGTGTGGCCG	CGGCTCGCCC	ACCACATCGC	800
GGAGCGCCTT	GCGTTCGGGG	CGGTACACCTA	CGCACTCTTC	GCCCTCGACT	850
CGGGTAACGA	AGAGTACCTC	GCTGCGGCGA	AGGCGCAGCT	CGCCGCAGCG	900
GAATGA					906

5

2) INFORMATION FOR SEQ ID NO: 1561

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: ATCC 18804

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1561

GATCATGGTA	AAACTACATT	GACTGCTGCT	ATCACCAAAG	TTTTAGCCGA	50
25	ACAAGGTGGT	GCCAACTTCT	TGGATTAYGG	TTCTATTGAT	100
AAGAAAGAGC	TAGAGGTATC	ACTATTTCCA	CTGCCCACGT	TGAATACGAA	150
ACCAAGAACA	GACACTATGC	CCACGTTGAT	TGTCCAGGAC	ACGCTGATTA	200
TATCAAAAAT	ATGATTACTG	GTGCCGCTCA	AATGGATGGT	GCTATCATTG	250
TTGTTGCTGC	CACTGATGGT	CAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
30	TTGGCCAGAC	AAGTTGGTGT	TCAAGACTTG	GTTGTGTTTG	350
CGATACTATT	GATGACCCTG	AAATGTTGGA	ATTAGTCGAA	ATGGAAATGA	400
GAGAATTGTT	ATCCACCTAC	GGTTTTGATG	GTGACAACAC	TCCAGTTATT	450
ATGGGATCTG	CTTTAATGGC	TTTGGAAGAC	AAGAAACCAG	AAATTGGTAA	500
GGAAGCTATC	TTGAAATTGT	TAGATGCTGT	CGATGAACAC	ATTCCAATC	550
35	CATCAAGAGA	CTTGGAACAA	CCATTTTTGT	TACCAGTTGA	600
TCCATCTCCG	GTAGAGGAAC	TGTTGTCAC	GGTAGAGTTG	AAAGAGGTGT	650
TTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTT	GACAAACCTT	700
ACAAGACTAC	TGTTACCGGT	ATTGAAATGT	TCAAAAAGA	ATTAGACTCT	750
GCTATGGCTG	GTGACAACTG	TGGTGTTTTG	TTAAGAGGTG	TTAAAAGAGA	800
40	TGAAATCAAG	AGAGGTATGG	TTTTGGCCAA	ACCAGGTACT	850
ACAAGAAGTT	CTTGGCTTCC	TTGTATATTT	TGACTTCCGA	AGAAGGTGGY	900
CGTTCCACTC	CATTTGGTGA	AGGTTACAAG	CCTCAATGCT	TCTTCAGAAC	950
TAACGATGTC	ACTACCACAT	TTTCATTCCC	AGAAGGAGAA	GGTGTGACC	1000
45	ATTCTCAAAT	GATCATGCCA	GGTGACAACA	TTGAAATGGT	1048
			TGGTGAAT		

2) INFORMATION FOR SEQ ID NO: 1562

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562

10
 TGATCACGGT AAAACCACAT TAACTGCTGC CATTACCAAA GTATTAGCTG 50
 AACAAAGGTGG TGCCAACCTT TTGGATTACG GTTCCATTGA TAGAGCTCCA 100
 GAAGAAAGAG CCAGAGGTAT CACTATTTCC ACTGCCCACG TTGAATACGA 150
 AACCAAGAAC AGACACTATG CCCACGTTGA TTGTCCAGGA CACGCTGATT 200
 15 ATATCAAAAA CATGATTACT GGTGCTGCTC AAATGGATGG TGCTATCATT 250
 GTTGTTGCTG CTACTGACGG TCAAATGCCA CAAACCAGAG AACATTTATT 300
 GTTGGAAGA CAAGTTGGTG TTCAAGACTT GGTTGTCTTT GTCAACAAAG 350
 TTGATACTAT TGATGACCCT GAGATGTTGG AATTAGTCGA AATGGAAATG 400
 AGAGAATTGT TGTCCACCTA CGGTTTTGAT GGTGACAACA CTCCTGTTAT 450
 20 TATGGGATCT GCTTTAATGG CCTTGGAAGG CAAAAACCA GAAATTGGTA 500
 AGGAAGCTAT TTTGAGATTG TTAGATGCTG TCGATGAACA CATTCCAAC 550
 CCATCAAGAG ACTTGAACA ACCATTTTTG TTGCCAGTTG AAGACGTGTT 600
 CTCCATCTCT GGTAGAGGAA CTGTTGTCAC CGGTAGAGTT GAAAGAGGTG 650
 TCTTGAAGAA GGGTGAAGAA ATCGAAATTG TTGGTGGTTT TGACAAACCA 700
 25 TACAAGACCA CTGTTACTGG TATTGAAATG TTCAAAAAGG AATTAGATTC 750
 TGCTATAGCT GGTGACAAC GTGGTGT TTTT GTTGAGAGGT GTTAAAAGAG 800
 ATGAAATCAA GAGAGGTATG GTTTTGGCCA AGCCAGGTAC TGCTACTTCT 850
 CACAAGAAAT TTTTAGCATC TTTGTATATT TTGACTTCAG AAGAAGGTGG 900
 TCGTTCCACT CCATTTGGAG AAGGTTACAA GCCTCAATGT TTCTTCAGAA 950
 30 CTAATGACGT CACTACCACA TTTTCATTCC CAGAAGGAGA AGGTGTTGAC 1000
 CACTCCCAA TGGTCATGCC AGGTGATAAC ATTGAAATGG TTGGTGAATT 1050
 GATCAAATCA TGTCCATTGG AAGT 1074

35

2) INFORMATION FOR SEQ ID NO: 1563

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1033 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida famata*

(B) STRAIN: ATCC 62894

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563

GATCACGGGA AGACTACTTT GACCGCTGCC ATCACCAAAG TTTTAGCCGA 50
 AAAAGGTGGT GCTAACTTCT TGGACTACGG TTCTATCGAT AAAGCTCCAG 100

	AAGAAAGAGC	CAGAGGTATT	ACTATTTCTG	CTGCCCATGT	TGAATACGAA	150
	ACTGACAAGA	GACACTATGC	CCATGTTGAT	TGTCCAGGTC	ACGCAGATTA	200
	TATCAAGAAT	ATGATTACTG	GTGCTGCTCA	AATGGATGGT	GCCATTATTG	250
	TTGTTGCTGC	TTCCGATGGT	CAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
5	TTGGCCAGAC	AAGTTGGTGT	TCAACACTTG	GTTGTTTTTCG	TCAACAAGGT	350
	CGACACCATT	GACGATCCAG	AAATGTTGGA	ATTGGTTGAA	ATGGAAATGA	400
	GAGATTTGTT	AACTACTTAC	GGTTTTGATG	GTGATAACAC	CCCAGTTATC	450
	ATGGGATCTG	CTTTGTGTGC	TTTGGAATCC	AGAGAACCAG	AAATTGGTCA	500
	AAAAGCCATT	GAAAAATTGT	TAGATGCCGT	CGATGAATAC	ATTCCAACCC	550
10	CAGTCAGAGA	CTTGGAACAA	CCATTCTTGA	TGCCAGTTGA	AGAAGTTTTTC	600
	TCCATTTCCG	GTAGAGGTAC	CGTTGTTGCT	GGTAGAGTCG	AAAGAGGTAC	650
	CTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTC	GACAAGCCAT	700
	TCAAGGCCAC	TGTTACTGGT	ATTGAAATGT	TCAAGAAGGA	ATTGGACTCC	750
	GCTCTTGCTG	GTGACAACTG	TGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
15	CGAAGTTAAG	AGAGGTATGG	TCTTGACCAA	GCCAAACACC	GTCATTCCC	850
	ACAAGAAGAT	CTTGGCCTCG	TTGTATATCT	TGACCAAGGA	AGAAGGTGGT	900
	AGACACTCTC	CATTTGGAGC	CAACTACAAG	CCCCAATTGT	TCATGAGAAC	950
	CACCGATGTT	ACCGGTACCA	TGACCTTCCC	AGAAGGTGCC	GACCAATCTG	1000
	CCATGGTCAT	GCCAGGTGAC	AACGTTGAAA	TGC		1033
20						

2) INFORMATION FOR SEQ ID NO: 1564

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564

	GATCACGGTA	AGACTACATT	GACAGCTGCT	ATCACCAAGA	CATTGGCCAA	50
40	GAACGGTGGT	GCTGATTTCT	TGGACTACTC	TTCCATTGAC	AAAGCTCCAG	100
	AGGAGAGAGC	CCGTGGTATC	ACTATCTCTA	CTGCCCATGT	CGAGTACGAG	150
	ACCGCCAAGA	GACATTACTC	CCACGTCGAC	TGTCCAGGTC	ACGCCGACTA	200
	CATCAAGAAC	ATGATTACTG	GTGCTGCCCA	AATGGACGGT	GCTATCATCG	250
	TTGTCGCCGC	CACCGATGGT	CAAATGCCAC	AAACTAGAGA	GCATTTGCTG	300
45	TTGGCCAGAC	AAGTCGGTGT	TCAACGTATC	GTTGTCTTTG	TCAACAAGGT	350
	GGACACCATC	GATGACCCTG	AAATGTTGGA	ATTAGTGGAA	ATGGAAATGA	400
	GAGAATTGTT	GAACGAATAC	GGTTTTGACG	GTGACAATGC	CCCTATCATT	450
	ATGGGTTCGG	CTTTGTGTGC	CCTAGAAGGT	CGTCAACCTG	AAATTGGTGA	500
	GCAAGCTATC	ATGAAACTAT	TGGACGCTGT	TGATGAATAC	ATTCCAACCC	550
50	CAGAAAGAGA	CTTGAACAAG	CCATTCTTGA	TGCCTGTTGA	AGACATCTTC	600
	TCCATCTCTG	GTAGAGGTAC	CGTCGTCACT	GGACGTGTCG	AAAGAGGTAA	650
	CTTGAAGAAG	GGTGAAGAAG	TTGAAATTGT	TGGTCACAAC	ACTACCCCAT	700
	TGAAGACCAC	CGTTACTGGT	ATCGAAATGT	TCAGAAAGGA	ATTGGACCAA	750

	GCTATGGCTG	GTGACAACGC	CGGTATCCTA	TTGAGAGGTA	TCAGAAGAGA	800
	CCAATTGAAG	AGAGGTATGG	TCATGGCCAA	GCCAGGTACC	GTCAAGGCTC	850
	ACACCAAGAT	TTTGGCTTCT	TTGTACATCT	TGTCTAAGGA	AGAAGGTGGT	900
	AGACATTCTG	GTTTCGGTGA	AAACTACAGA	CCTCAGATGT	TTATCAGAAC	950
5	CGCAGATGTC	ACTGTTGTGA	TGAAGTTCCC	AGAATCTGTG	GAAGACCACT	1000
	CTATGCAAGT	TATGCCAGGT	GACAACGTCG	AAATGGTCTG	TGAACTAGTC	1050
	CACCCA					1056

10

2) INFORMATION FOR SEQ ID NO: 1565

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1061 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
- (B) STRAIN: ATCC 6260

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565

	GATCATGGTA	AGACCACTTT	GACCGCTGCT	ATCACCAAGG	TTTTGTTCGGA	50
	AAAAGGAGGT	GCTAATTTCT	TGGATTACGG	CTCCATCGAC	AGAGCTCCAG	100
	AAGAGAGAGC	CAGAGGTATC	ACCATTTCCA	CTGCCCATGT	TGAGTACCAA	150
30	ACTGATAAGA	GACATTATGC	CCACGTTGAC	TGTCCAGGTC	ACGCCGATTA	200
	CATTAAGAAT	ATGATTACTG	GTGCCGCCCA	GATGGACGGT	GCCATTATTG	250
	TTGTTGCTGC	CACTGACGGT	CAAATGCCTC	AGACCAGAGA	GCACTTGTTG	300
	TTGGCCAGAC	AAGTTGGTGT	GCAACACTTG	GTAGTTTTTG	TGAACAAGGT	350
	GGACACCATT	GACGATCCCG	AGATGTTGGA	ATTGGTCGAG	ATGGAAATGA	400
35	GAGAATTGTT	GAGTCAGTAC	GGTTTCGATG	GTGACAACAC	CCCAGTTATC	450
	ATGGGATCTG	CTTTGTGTGC	TTTGGAAGT	AAGCAGCCAG	AAATTGGTGT	500
	GCAAGCCATT	GAAAAATTGT	TGGACGCTGT	CGATGAGCAC	ATTCCTACTC	550
	CTACCCGTGA	CTTGGAACAG	CCATTCTTGT	TGCCTGTTGA	AGATGTGTTC	600
	TCCATTTCTG	GTAGAGGAAC	TGTGGTACT	GGTAGAGTCG	AAAGAGGTTC	650
40	GTTGAAGAAG	GGTGAGGAAA	TCGAGATTGT	TGGTGACTTT	GACAAGCCAT	700
	TCAAGACCAC	TGTGACTGGA	ATTGAAATGT	TCAAGAAGGA	ATTGGATGCT	750
	GCTATGGCTG	GTGACAATGC	TGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
	CGATGTCAAG	AGAGGTATGG	TTTTGGCCAA	GCCTTCCACC	GTCACCTCTC	850
	ACAAGAAGGT	GTTGGCTTCC	TTGTACATCT	TGAGTAAGGA	AGAAGGTGGC	900
45	CGTCACTCTC	CTTTTGGTGA	GAACTACAAG	CCTCAATTGT	TCATCAGAAC	950
	TACTGACGTT	ACCGGTACTT	TAAGATTCCC	AGCCGGCGAG	GGTGTCGACC	1000
	ACTCGCAAAT	GGTTATGCCA	GGTGACAATG	TTGAGATGGA	AATTGAGCTT	1050
	GTGAGAAAGA	C				1061

50

2) INFORMATION FOR SEQ ID NO: 1566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566

```

15  GATCACGGTA AGACTACCTT GACTGCTGCT ATCACCAAGG TTTTGGCTTC      50
    TAAGGGTGGT GCTAGCTTCT TGGACTATGG TTCCATTGAC AGAGCCCCAG      100
    AGGAGAGAGC TAGAGGTATT ACTATTTCTA CTGCCCACGT TGAGTACCAA      150
    ACCGAAAAGA GACACTACGC CCACGTCGAC TGTCCAGGTC ACGCTGATTA      200
    CATTAGAAT  ATGATTACTG GTGCCGCCCA GATGGACGGT GCTATCATTTG      250
20  TTGTTGCTGC TTCTGATGGT CAGATGCCTC AGACCAGAGA GCACCTTTTG      300
    TTGGCCAGAC AGGTTGGTGT TCAGAACTTG GTTGTTTTCG TTAACAAGGT      350
    TGACACCATT GACGACCCTG AAATGTTGGA ATTGGTTGAG ATGGAAATGA      400
    GAGAATTGTT GACTACTTAC GGTTTTGACG GTGATGAGAC TCCTGTTATC      450
    ATGGGTTCTG CTTTGTGCGC TTTGGAAGAG AAGCAACCAG AGATTGGTGA      500
25  GCAGGCTATC ATGAAGTTGT TGGACGCTGT CGATGAGTAC ATTCCAACCC      550
    CACAGCGTGA CTTGGAGCAG CCATTCTTGA TGCCTGTTGA GGATGTTTTTC      600
    TCCATTTCTG GTAGAGGTAC TGTCGTTACT GGTAGAGTTG AGAGAGGTTT      650
    TTTGAAGAAG GGTGAGGAAA TCGAGATTGT CGGTGACTTC GCCAAGACTT      700
    TCAAGGCTAC CGTTACTGGT ATTGAGATGT TCAAGAAGGA ATTGGATGCT      750
30  GCTATGGCTG GTGACAACGC CGGTATCTTG TTGAGAGGTG TCAAGAGAGA      800
    TGAGATCTCC CGTGGTGATG TCTTGGCCAA GCCAGGTACT GTTACTCCAC      850
    ACAAGAAGAT CTTGGCTTCT TTGTACGTTT TGACCAAGGA AGAAGGTGGT      900
    CGTCACAACC CATTGCTGA  GAACTACAAG CCACAGTTGT TCCTCAGAAC      950
    CACCAACGTC ACTGGTACCA TGAGATTCCC AGAAGGTGAA GATGTTGACC      1000
35  ACTCTGCCAT GGTAAACCCA GGTGACAACG TTGAGATGGA AATCGAGTTG      1050
    GGTAGAAAGG CCCCACTTGA GTT                                1073
  
```

40 2) INFORMATION FOR SEQ ID NO: 1567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567

	CATGGTAAGA	CCACTTTGAC	TGCTGCCATC	ACCAAGACTC	TAGCTGAACG	50
	TGGTGGTGCT	GACTTTTGG	ACTACTCTTC	TATTGACAAG	GCTCCAGAAG	100
5	AAAGAGCYAG	AGGTATCACT	ATTTCTACTG	CTCATGTTGA	ATACGAGACT	150
	GAAAAGAGAC	ATTACTCCCA	CGTTGACTGT	CCAGGTCACG	CTGATTACAT	200
	CAAGAACATG	ATTACTGGTG	CTGCTCAAAT	GGACGGTGCT	ATTATTGTTG	250
	TTGCTGCTAC	TGATGGTCAA	ATGCCTCAAA	CCAGAGAGCA	TTTGTTGTTG	300
	GCCAGACAAG	TTGGTGTCCA	ACACATTGTT	GTTTTCGTTA	ACAAGGTTGA	350
10	CACCATCGAT	GATCCAGAAA	TGTTGGAATT	GGTTGAAATG	GAAATGAGAG	400
	AATTRTTGAC	TCAATATGGC	TTTGACGGTG	ACAACACTCC	AGTGATCATG	450
	GGTTCTGCTT	TGTGTGCCTT	GGAAGGTAAG	CAACCAGAAA	TTGGTGAGCA	500
	AGCCATCATG	AAGTTGTTGG	ACGCTGTTGA	CGAATACATC	CCAACCCAG	550
	CCCGTGACTT	GGAAA VCCA	TTCTTGATGC	CTGTTGAAGA	TATCTTCTCC	600
15	ATTTCCGGTA	GAGGTACTGT	CGTCACTGGT	AGAGTTGAAC	GTGGTAACTT	650
	GAAGAAGGGT	GAAGAAATCG	AAATTGTTGG	TCACAACACC	ACTCCTTTCA	700
	AGACTACTGT	TACTGGTATT	GAAATGTTCA	GAAAGGAATT	GGACCAAGCC	750
	ATGGCTGGTG	ACAACGCTGG	TGTCCTTTTG	AGAGGTGTCA	GAAGAGACCA	800
	ATTGAAGAGA	GGTATGGTTT	TGGCTAAGCC	AGGTACTGTT	AAGGCCCACA	850
20	CCAAGTTCTT	GGCTTCCTTG	TACATTTTGA	CCAAGGAAGA	AGGTGGTAGA	900
	CACTCCGGTT	TCGGTGAAAA	CTACAGACCA	CAAATCTACG	TCAGAACTGC	950
	TGACGTTACC	GTGCTCTTGA	AGTTCCCAGA	ATCTGTTGAA	GACCATTCCA	1000
	TGCAAGTCAT	GCCAGGTGAC	AATGTCGAAA	TGGAGTGTGA	ATTGGTTCAC	1050
	CCAACCTCCAT	TG				1062
25						

2) INFORMATION FOR SEQ ID NO: 1568

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
 (B) STRAIN: ATCC 66035

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568

	CGGAAAGACC	ACCTTGACCG	CCGCCATTAC	CAAGGTTTTG	GCTGACAAGG	50
45	GTGGCGCCAA	CTTCTTGAC	TACGGTGCCA	TTGACAAGGC	TCCTGAAGAA	100
	AGAGCACGTG	GTATCACCAT	TTCCACTGCC	CACGTTGAAT	ACGAGACCGA	150
	CAACAGACAC	TACGCCACG	TTGACTGTCC	AGGTCACGCC	GATTACATCA	200
	AGAACATGAT	CACGGGTGCC	GCTCAAATGG	ACGGTGCCAT	TATTGTTGTT	250
	GCAGCCACCG	ACGGCCAAAT	GCCTCAAACC	AGAGAGCACT	TGTTGTTGGC	300
50	CAGACAAGTT	GGTGTGCAAC	ACTTGTTTGT	TTTCGTGAAC	AAGGTTGATA	350
	CCATCGACGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGAGAA	400
	TTGTTGACTC	AATACGGATT	TGACGGCGAT	GAAACCCCTG	TTGTTATGGG	450
	CTCTGCTCTT	TGCGCTTTGG	AAGGTAGAGA	ACCAGAGATT	GGTGAGCAAG	500

	CCATCACCAA	GTTGTTGGAG	GCTGTTGACG	AGTACATCCC	AACCCACAA	550
	CGTGACTTGG	AACAACCAATT	CTTGATGCCT	GTTGAAGATG	TTTTCTCCAT	600
	TTCTGGTAGA	GGTACTGTTG	TCACTGGTAG	AGTGGAGAGA	GGTTCCTTGA	650
	AGAAGGGTGA	GGAGATCGAG	ATTGTTGGTG	ACTTTGACAA	GCCTTTCAAG	700
5	ACTACTGTTA	CTGGTATTGA	GATGTTCAAG	AAGGAATTGG	ACGCTGCTAT	750
	GGCTGGTGAC	AATGCTGGTA	TCTTGTGAG	AGGTGTCAAG	AGAGAACAAG	800
	TTTCCCGTGG	TATGGTTTTG	GCCAAGCCAG	GCACTGTGAC	CTCGCACAAAG	850
	AAGGTTTTTG	CTTCTTTGTA	CATTTTGTCT	AAGGAAGAAG	GTGGTCGTCA	900
	CTCTCCATTT	GGCGAGAACT	ACAAGCCTCA	ATTGTTTCCTT	AGAACTACCG	950
10	ATGTCACTGG	TACTTTGAGA	TTCCCAGCAG	GTGAGGACGT	TGACCACTCC	1000
	GCTATGGTTT	CTCCAGGTGA	CAATGTCGAG	ATGGAAATCG	AGTTGGTCAG	1050
	AAAGACTCCT	CT				1062

15 2) INFORMATION FOR SEQ ID NO: 1569

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 990 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida sphaerica*

(B) STRAIN: ATCC 2504

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569

	TCACCAAGAC	TTTGGCTGAA	CGTGGTGGTG	CTGATTTCTT	GGACTACTCT	50
35	TCCATTGACA	AGGCTCCAGA	AGAAAGAGCR	AGAGGTATCA	CTATTTCTAC	100
	TGCACATGTT	GAATATGAAA	CTGACAAGAG	ACATTACTCT	CACGTCGACT	150
	GTCCAGGTCA	TGCTGATTAC	ATCAAGAATA	TGATTACTGG	TGCTGCCCAA	200
	ATGGATGGTG	CTATCATTGT	TGTTGCTGCT	ACAGATGGTC	AAATGCCTCA	250
	AACCAGAGAA	CATTTGTTGT	TGGCTAGACA	AGTTGGTGTT	CAACAYATCG	300
40	TTGTTTTTCGT	TAACAAGGTT	GACACTATCG	ATGACCCCTGA	AATGTTAGAA	350
	TTGGTTGAAA	TGGAAATGAG	AGAATTATTG	ACCCAATACG	GTTTCGATGG	400
	TGACAACACT	CCAGTCATCA	TGGGTTCCTGC	TTTGTGTGCT	TTAGAAGGTA	450
	AGCAACCAGA	AATTGGTGAA	CAAGCAATCA	TGAAGTTATT	GGACGCTGTT	500
	GACGAATACA	TCCCAACTCC	AGCTCGTGAT	TTGGAAAAGC	CTTTCTTGAT	550
45	GCCTGTTGAA	GATATCTTCT	CCATCTCCGG	TAGAGGTACC	GTCGTAAGT	600
	GTAGAGTTGA	ACGTGGTAAC	TTGAAKAAGG	GTRAAGAAAT	CGAAATCGTT	650
	GGTCACAACA	CCACTCCATT	CAAGACCACT	GTTACTGGTA	TTGAAATGTT	700
	CAGAAAGGAA	TTGGACCAAG	CTATGGCTGG	TGATAACGCT	GGTGTCWTGT	750
	TGAGAGGTGT	CAGAAGAGAC	CAATTAAAGA	GAGGTATGGT	CTTGGCCAAG	800
50	CCAGGTACTG	TCAAGGCTCA	CACCRAATTC	TTGGCCTCTT	TGTATATCTT	850
	GACCAAGGAA	GAAGGTGGTA	GACATTCCGG	TTTCGGTGAA	AATTACAGAC	900
	CTCAAATCTA	CGTTAGAACT	GCTGATGTCA	CCGTTGTTTT	GAAGTTCCCA	950
	GAAGCTGTTG	AAGATCACTC	TATGCAAGTC	ATGCCAGGTG		990

2) INFORMATION FOR SEQ ID NO: 1570

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1184 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570

	GATCATGGTA	AAACCACTTT	GACTGCTGCC	ATTACTAAAG	TCTTGGCTGA	50
	TAAAGGTCAA	GCTAACTTCT	TAGATTACGG	TTCTATTGAT	AGAGCTCCAG	100
	AAGAAAGAGC	CAGAGGTATC	ACCATCTCTA	CTGCCCACGT	TGAATATGAA	150
20	ACCGAAAAAA	GACATTACGC	CCATGTTGAG	TATGTATACT	TTTTTTTGT	200
	GTGTAATTGT	TTTAAAGATT	TTCTTTAAAG	CTGAAGAAGT	CAAATCAGTT	250
	CTTTGATAAC	TTCTATTAAA	AAAAGGGAAA	AATTAACAAG	ATATACTAAC	300
	ACTATAACAG	TTGTCCTGGA	CATCAAGATT	ATATCAAGAA	TATGATTACC	350
	GGTGCCGCTC	AAATGGATGG	TGCTATTATT	GTTGTTGCTG	CCACTGATGG	400
25	TCAAATGCCA	CAAACCAGAG	AACATTTGTT	GTTGGCTAGA	CAAGTCGGTG	450
	TTCAAGATTT	GGTTGTCTTT	GTTAACAAAG	TCGACACTAT	TGATGACCCA	500
	GAAATGTTGG	AATTGGTTGA	AATGGAAATG	AGAGAATTAT	TGACTACTTA	550
	CGGTTTTGAT	GGTGATAACA	CTCCTGTTAT	CATGGGTTCT	GCTTTGATGG	600
	CCTTGCAAGG	TAAACAACCA	GAAATTGGTG	AACAAGCTAT	CATGAAATTG	650
30	ATGGACGCTA	TTGATGAACA	CATTCCAACC	CCAACCAGAG	ACTTGGAACA	700
	ATCTTTCTTG	ATGCCAGTTG	AAGATGTTTT	CTCCATTTCT	GGTAGAGGTA	750
	CTGTTGTTAC	TGGTAGAGTC	GAAAGAGGTG	TCTTAAAGAA	GGGTGAAGAA	800
	ATTGAAATTG	TTGGTGGTTT	CGAAAAACCA	TTCAAGACCA	CTGTTACTGG	850
	TATTGAAATG	TTCAAGAAAG	AATTAGATGC	TGCTATGGCT	GGTGACAAC	900
35	GTGGTGTCTT	GTTGAGAGGT	GTCAAGAGAG	ACGAAATCAA	GAGAGGTATG	950
	GTTTTGGCTA	AACCAGGTAC	TGCTACTTCC	CACAAGAAAT	TCTTGGCTTC	1000
	CATGTATATC	TTAACTGCTG	AAGAAGGTGG	TCGTTCCACT	CCATTCGGTG	1050
	AAGGTTACAA	GCCACAATGT	TTCTTCAGAA	CTAACGATGT	TACCACTTCC	1100
	TTCTCTTTCC	CAGAAGGTGA	AGGTGTTGAC	CACTCCCAA	TGGTTATGCC	1150
40	AGGTGACAAC	ATTGAAATGG	TCGGTGAATT	GATT		1184

2) INFORMATION FOR SEQ ID NO: 1571

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida viswanathii*

(B) STRAIN: ATCC 28269

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571

```

CGATCACGGT AAGACCACCT TGACCGCCGC CATCACCAAG GTCTTGCCCG      50
ACAAGGGTCA GGCTAACTTC TTGGACTACG GATCCATTGA CAGAGCCCCT      100
GAAGAAAGAG CAAGAGGTAT CACTATCTCC ACTGCCCACG TTGAATACGA      150
10 GACTGATAAG AGACACTATG CCCACGTTGA TTGCCCGGGC CATCAAGATT      200
ATATCAAGAA TATGATCACT GGTGCTGCCC AAATGGACGG TGCTATCATT      250
GTTGTTGCTG CTA CTGACGG TCAGATGCCA CAAACCAGAG AACACTTGTT      300
GTTGGCTAGA CAAGTTGGTG TCCAAGACTT GGTGTTTTTC GTTAACAAGG      350
TTGACACTAT CGATGACCCA GAAATGTTGG AATTGGTTGA AATGGAAATG      400
15 AGAGAATTAT TATCTTCTTA YGGCTTTGAC GGTGACAACA CCCAGTTGT      450
CATGGGTTCC GCTTTGATGG CTTTGCAAGG TAAGCAACCA GAAATTGGTG      500
AACAAGCTAT TATTAAGTTG ATGGACGCTA TTGATGAACA CATYCCAACC      550
CCAACCAGAG ACTTGGAACA ACCATTCTTG TTGCCAGTTG AAGATGTCTT      600
TTCTATTTCC GGTAGAGGTA CCGTCGTCAC TGGTAGAGTC GAAAGAGGTG      650
20 TCTTGAAGAA GGGTGAAGAA ATTGAAATTG TCGGTAAGT TGAAGAGCCA      700
TTCAAGACCA CCGTACTGG TATTGAAATG TTCAAGAAGG AATTGGATGC      750
TGCTATGGCT GGTGACAACT GTGGTGCTCTT GTTGAGAGGT GTCAAGAGAG      800
ACGAAATCAG CAGAGGTATG GTTTTGGCCA AGCCAGGTAC CGTCACTTCC      850
CACAAGAAGT TCTTGGCCTC CATGTACATC TTGACTGGTG AAGAAGGTGG      900
25 TCGTCGTACC CCATTCGGTG AAGGTTACAA GCCACAATGT TTCTTCAGAA      950
CCAATGACAT CACCACCACT TTCACTTTCC CAGAAGGTGA AGGTGTCGAC      1000
CACTCCCAA TGGTTATGCC AGGTGACAAC ATCGAAATGG TTGGTGAATT      1050
GTACAAGGCT TGTCCTTGA A                                1071

```

30

2) INFORMATION FOR SEQ ID NO: 1572

(i) SEQUENCE CHARACTERISTICS:

```

35 (A) LENGTH: 817 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*

(B) STRAIN: ATCC 8750

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572

```

TATCTTGGTT WGCTCGGCCG CTGACGGCCC AATGCCTCAG ACTCGCGAGC      50
ACATCCTGCT GAGCCGTCAG GTTGGCGTTC CTTACATCAT CGTGTTCCCTG      100
50 AACAAAGGCCG ACATGGTTGA TGACGAAGAG CTGATCGAAC TGGTTGAAAT      150
GGAAGTTCGC GAGCTGTTGT CCAAGTACGA CTTCCCTGGC GACGACACCC      200
CGATCATCAA GGGTTCGGCC AAAGTGGCTC TGGAAGGCCG CGAAGGCCCA      250
CTGGGCAGCC AAGCCGTTCT GGCTCTGGCC GAAGCGCTGG ACAACTACAT      300

```

	TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	G TTCCTGATG	CCTGTTGAAG	350
	ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
	CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
	CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
	CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
	GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
10	GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
	TCGCCATGGA	AGAAGGT				817

15 2) INFORMATION FOR SEQ ID NO: 1573

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573

30	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTT	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAAC TTCTTG	AGCAATACGA	ATTCGAAGAG	GATACTCCAA	200
35	TCGTTTCGTGG	TTCTGCACTG	GGTGCAATTGA	ATGGTGTTGA	CAAGTGGGTT	250
	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAACAG	GACGTATTGA	GACTGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450
40	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACTTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
45	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GGCGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	GTAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

50 2) INFORMATION FOR SEQ ID NO: 1574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574

	GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
	GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
15	TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
	ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
	TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
	GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTG	ATACATTCCA	300
	GAGCCAAAGC	GTGATATCGA	TGATCCATTG	CTATTACCAA	TCGAAGATAT	350
20	CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
	GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
	ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
	AGGTCGTGCA	GGTGATAACG	TTGGTGTCT	ACTACGTGGT	ACCAAGCGTG	550
	ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
25	CACACCAAGT	TCAGTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
	TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
	CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
	ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
30	TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 1575

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
- (B) STRAIN: ATCC 33315

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575

	GGTAGTGTCT	GCAGCTGACG	GCCCAATGCC	ACAAACTCGT	GAACATATCC	50
50	TATTGTCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGACGATGA	AGAATTACTT	GAATTAGTTG	AAATGGAAGT	150
	ACGTGATCTA	TTAAGTGAAT	ACGACTTCCC	AGGTGATGAT	ACTCCTGTTA	200
	TTTCTGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	ATATGAACAA	250

	AAAGTCTTAG	ACTTAATGGC	AGCTGTAGAT	GATTTTCATCC	CAACTCCTGA	300
	ACGTGACCAT	GACAAACCGT	TCATGATGCC	GATTGAAGAT	GTTTTCTCAA	350
	TCACTGGTCG	TGGAAGTGT	GCTACAGGTC	GTGTTGAACG	TGGAAGTATT	400
	AAAGTCGGTG	ATGAAGTTGA	TATCATCGGT	ATTCATGAAA	ATGTTAAAAA	450
5	GACAACTGTT	ACGGGTGTAG	AAATGTTCCG	TAAATTGTTG	GATTACGCTG	500
	AAGCTGGCGA	TAACATCGGT	ACATTATTGC	GTGGTGTTTC	TCGTGATGAT	550
	ATCGAACGTG	GTCAAGTGTT	GGCTAAACCA	GGCACAATCA	CACCACATAC	600
	AAAATTCTCA	GCTGAAGTTT	ATGTATTAAC	AAAAGAAGAA	GGCGGACGTC	650
	ATACTCCATT	CTTCTCAAAC	TATCGCCCAC	AATTTTACTT	CCGTACAAC	700
10	GACATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	TGGTTATGCC	750
	AGGTGATAAC	GTAGCAATGG	AAGTTGAATT	AATTCACCCT	GTTGCTATTG	800
	AAA					803

15

2) INFORMATION FOR SEQ ID NO: 1576

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576

	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	GCGAAGGAAA	AAAACATAAA	50
	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	GATAATAGAG	TTAGAACTAT	100
	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	GGGCTTAAAA	GCTGAGGCTT	150
35	TAGGTGCTCC	TATTAGTGTT	CCTGTTGGTG	AGAAAGTTTT	AGGAAGAATT	200
	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	GGTGAAGAAA	TTTCTTTTGA	250
	TAAAAAATGG	GCAATTCATA	GAGATCCGCC	AGCTTTTGAA	GATCAAAGCA	300
	CAAAAAGTGA	GATTTTTGAA	ACAGGGATTA	AAGTTGTAGA	TTTGCTTGCT	350
	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	TTTGGTGGTG	CAGGTGTTGG	400
40	TAAAACTGTT	ATTATTATGG	AGCTTATTCA	CAATGTTGCA	TTTAAGCATA	450
	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	AGAGAACTCG	TGAAGGAAAT	500
	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	GTTTTAGACA	AAGTTGCTCT	550
	ATGTTATGGA	CAAATGAATG	AACCACCAGG	AGCAAGAAAT	CGTATTGCTT	600
	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	GAGATGAAAT	GGGTCTTGAT	650
45	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	TTTTCACAAT	CAGGTTCTGA	700
	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	AGCTGTGGGT	TATCAACCAA	750
	CCCTAGCAAG	TGAAATGGGT	AAATTCCAAG	AAAGAATTAC	TTCAACTAAA	800
	AAAGG					805

50.

2) INFORMATION FOR SEQ ID NO: 1577

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*
 (B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577

15	ATTTACCCAA	GATCAACGAA	GCCGTCGAAG	TAAATTTCTGA	GGTTGAGGGC	50
	AAGCAAAACA	GACTTGTGTT	AGAGGTTGCC	GCACACCTTG	GCGATAACCG	100
	CGTAAGAACG	ATCGCTATGG	ATATGAGCGA	AGGCTTAACC	AGAGGCCTTG	150
	AGGCTACGGC	TCTTGCGCG	CCTATTAGCG	TTCCGGTCGG	CGAAAAAGTT	200
	TTGGGAAGGA	TTTTTAACGT	CGTCGGCGAT	CTGATCGACG	AGGGTGAAGG	250
20	CATAGAATTT	GATAAAAAAT	GGTCTATCCA	CCGCGATCCT	CCGCCGTTTG	300
	AAGAGCAAAG	CACGAAGAGT	GAAATTTTTG	AAACGGGTAT	AAAAGTGGTC	350
	GATCTTCTAG	CCCCTTATGC	AAAAGGCGGT	AAGGTCGGAT	TATTCGGCGG	400
	TGCCGGCGTC	GGTAAGACGG	TTATTATCAT	GGAGCTTATC	CACAACGTTG	450
	CATTTAAGCA	TAGCGGTTAT	TCCGTGTTTG	CCGGCGTGGG	CGAGCGAACC	500
25	CGCGAAGGAA	ACGACCTTTA	TCACGAGATG	AAAGAGAGTA	ACGTTTTTGA	550
	CAAAGTCGCC	TTGTGCTACG	GCCAGATGAA	CGAGCCGCCG	GGAGCAAGAA	600
	ACCGCATCGC	TCTAACAGGC	CTAACGATGG	CTGAATACTT	CCGCGACGAG	650
	ATGGGACTTG	ACGTTTTGAT	GTTTATAGAC	AACATCTTCC	GTTTCTCTCA	700
	GTCTGGCGCT	GAGATGTCGG	CGCTTCTTGG	ACGTATCCCG	TCAGCCGTTG	750
30	GTTATCAGCC	GACTTTGGCG	AGCGAAATGG	GCAAATTCCA	AGAGAGAATT	800
	ACATCAACC					809

2) INFORMATION FOR SEQ ID NO: 1578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578

50	AATCGAAGTG	CAACGTTTCAT	TGCGTGTA	CTTGATGGT	GCTGTAACT	GTGT	50
	TGGACTCACA	ATCAGGTGTA	GAACCTCAA	AAGAGAA	ACAGTTGG	GCGTCAA	100
	GCGACAGATT	ACCGCGTACC	GCGTGTTGTA	TTCTGTAACA	AAATGGACAA		150

	AATTGGTGCA	GACTTCTTAT	ACTCTGTATC	AACTTTACAT	GATCGTTTAC	200
	AAGCAAATGC	TCACCCAATC	CAATTACCAA	TTGGTGCGGA	AGATGACTTT	250
	ACTGGTATTA	TCGACTTAGT	AAAAATGAAA	GCTGAAATCT	ACACAAATGA	300
	CTTAGGAACT	GAAATCCAAG	AGACTGAAAT	TCCTGAAGAA	TACGTAGAAT	350
5	TAGCTGAAGA	ATGGCGCGAA	AAATTAATTG	AAGCTGTTGC	TGATACTGAT	400
	GAAGAACTAA	TGATGAAATT	CTTGGAAGGT	GAAGAAATCA	CTGAAGAAGA	450
	ATTGAAAGCT	GGTATTCGTC	AAGCAACATT	GACTGTTGAC	TTTTTCCCTG	500
	TTCTTTGCGG	ATCTGCCTTT	AAAAACAAAG	GGGTTCAATT	GATGTTGGAT	550
	GCAGTCATCG	ACTACTTGCC	TTCACCACTT	GATGTTCCCTG	CGATTAAAGG	600
10	GATCAATCCT	AAAACAGACG	AAGAACTGA	TCGTCCGGCT	GACGATGAAG	650
	CACCATTTCG	TTCATTAGCA	TTTAAAGTAA	TGACTGACCC	ATTCGTARGT	700
	CGTTTGACAT	TCTTYCGTGT	GTATTCARGT	ATCTTGAAC	CTGGATCATA	750
	CGTATTGAAT	GCTTCAAAAG	GCAAACGCGA	ACGTATCGGT	CGGATCCTAC	800
	AAATGCACGC	CAACACTCGT	GCTGAAATCC	AAACAGTATA	CTCAGGCGAT	850
15	ATCGCCGCTG	CTGTTGGTTT	GAAAGACACA	ACAACAGTATA	ATCCACTATG	900
	TGATGAAAAA	TCCCCAGTAA	TCCTTGAATC	AATCGAATTC	CCAGAACCAG	950
	TTATCGAAGT	CGCTGTTGAG	CTTAAATCAA	AAGCTGACCA	AGATAAAATG	1000
	GGGGTTGCTT	TACAAAAACT	TGCTGAAGAA	GATCCATCAT	TCCGTGTGGA	1050
	AMCAAACGCT	GAAACAGGCG	AACTGTTAT	CGCTGGTATG	GGAGAACTTC	1100
20	ACTTGGACGT	CTTAGTTGAC	CGTATGCGTC	GCGAATTTAA	AGTTGAAGCA	1150
	AACGTAGGTG	CGCCTCAAGT	TTCTTATCGT	GAAACATTCC	GTGCAGCAAC	1200
	ACAAGCGGAA	GGTAAATTTG	TACGTCAGTC	TGGTGGTAAA	GGTCAATACG	1250
	GTCACGTATG	GGTCGAATTT	ACACCAAACG	AAGAAGGTAA	AGGCTTCGAA	1300
	TTCGAAAACG	CGATTGTCGG	TGGTGTGGTT	CCTCGTGAAT	ACATCCCAGC	1350
25	AGTTGAAAAA	GGACTTGAAG	AATCAATGGC	GAACGGTGTC	TTAGCCGGTT	1400
	ACCCATTAGT	AGACATCAAA	GCAAACTTTT	ATGATGGTTC	ATACCATGAT	1450
	GTCGATTCAA	GTGAAACTGC	CTTCCGTGTT	GCAGCTTCTA	TGGCTTTACG	1500
	TGCTGCAGCG	AAGAAAGCAA	ACCCAGTAAT	TCTTGAACCA	ATGATGAAAG	1550
	TAGTTATCAC	TGTACCAGAA	GATTACTTAG	GTGATGTTAT	GGGTCACGTA	1600
30	ACTGCTCGTC	GTGGACGCGT	AGAAGGAATG	GAAGCACWCG	GTAAC TCACA	1650
	AATCGTGAAC	GCAATCGTGC	C			1671

35 2) INFORMATION FOR SEQ ID NO: 1579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579

50	GAAGTACAAC	GTTCACTACG	GGTTCTTGAC	GGWGCTGTAA	CAGTATTGGA	50
	CTCACAATCT	GGTGTAGAAC	CACAACTGA	AACAGTTTGG	CGTCAAGCGA	100
	CAGATTACCG	CGTACCACGT	ATCGTATTCT	GTAACAAAAT	GGATAAAATC	150

	GGTGCAGACT	TCTTATACTC	TGTATCTACT	TTACATGATC	GCTTGCAAGC	200
	AAATGCTCAT	CCAATCCAAT	TACCAATTGG	TGCGGAAGAT	GACTTTACTG	250
	GTATCATCGA	TCTAGTAAAA	ATGAAAGCTG	AGATCTATAC	AAACGATTTA	300
	GGAACAGAGA	TTCAAGAAAC	TGAAATTCCT	GAAGAGTACA	AAGAATTAGC	350
5	TGAAGAATGG	CGCGAAAAAT	TAGTTGAAGC	TGTTGCAGAT	ACTGACGAAG	400
	AGCTAATGAT	GAAATTCTTG	GAAGGTGAAG	AAATCACTGA	AGAAGAATTG	450
	AAAGCTGGTA	TCCGTCAAGC	GACATTGACT	GTTGAATTTT	TCCCAGTTCT	500
	TTGTGGTTCA	GCCTTCAAAA	ACAAAGGGGT	TCAATTGATG	TTGGATGCAG	550
	TCATCGACTA	CCTTCCTTCA	CCACTTGATG	TTCCTGCAAT	CAAAGGGATC	600
10	AATCCTAAAA	CTGACGAAGA	AACTGATCGT	CCTGCTGACG	ATGAAGCGCC	650
	TTTTGCTTCA	CTAGCATTTA	AAGTAATGAC	TGACCCATTC	GTAGGTCGTT	700
	TGACATTCTT	CCGTGTGTAT	TCAGGTGTCT	TGAACTCTGG	ATCATATGTC	750
	TTGAATGCTT	CAAAAGACAA	ACGCGAACGT	ATCGGTCGTA	TTCTGCAAAT	800
	GCACGCGAAC	ACTTGTGCAG	AAATCCAAAC	AGTTTATTCA	GGCGATATCG	850
15	CTGCAGCTGT	TGGTTTGAAA	GATTCCACAA	CAGGGGATAC	ATTGTGTGCG	900
	AAAAATCACC	CAGTAATCCT	TGAATCAATC	GAATTCCCAG	AMCCAGTTAT	950
	CGAAGTAGCT	GTTGAACYTA	AATCAAAAAGC	TGACCAAGAT	AAAATGGGTG	1000
	TGGCTTTACA	AAAACCTGCT	GAAGAAGATC	CTTCATTCCG	TGTAGAAMCA	1050
	AACGCTGAAA	CTGGCGAAAC	TGTTATCGCA	GGGATGGGTG	AACTTCACTT	1100
20	GGACGTCCTT	GTTGACCGTA	TGCGTCGCGA	ATTTAAAGTT	GAAGCAAACG	1150
	TTGGTGCGCC	TCAAGTTTCT	TACCGCGAAA	CATTCCGTGC	TTCTACGCAA	1200
	GCCGAAGGTA	AATTTGTACG	TCAGTCTGGT	GGTAAAGGTC	AATACGGTCA	1250
	CGTATGGATC	GAATTTACAC	CAAACGAAGA	AGGTAAAGGC	TTCGAATTCT	1300
	AAAACGCAAT	TGTCGGTGGT	GTGGTTCCAC	GTGAATACAT	CCCAGCAGTT	1350
25	GAAAAAGGAC	TTGAAGACTC	AATGGCTAAC	GGTGTCTAG	CTGGTTATCC	1400
	ATTGGTTGAC	ATCAAAGCCA	AGCTTTACGA	TGGTTCATAC	CATGATGTCT	1450
	ATTCAAGTGA	AACAGCCTTC	CGTGTGGCAG	CTTCAATGGC	TTTACGTGCT	1500
	GCAGCGAAGA	AAGCTAATCC	AGTGATTCTT	GAACCAATGA	TGAAAGTTGT	1550
	TATCACTGTT	CCTGAAGATT	ACTTAGGTGA	TATTATGGGA	CACGTAACCTG	1600
30	CTCGTCGTGG	ACGTGTTGAA	GGTATGGAAG	CGCATGGTAA	CTCACAAATC	1650
	GTTAACGCGA	TT				1662

35 2) INFORMATION FOR SEQ ID NO: 1580

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580

50	CAATCGAAGT	ACAACGTTCT	CTTCGTGTAT	TGGATGGTGC	TGTTACCGTT	50
	CTTGACTCAC	AATCAGGTGT	TGAGCCTCAA	ACTGAAACAG	TTTGGCGTCA	100
	AGCAACTGAG	TATGGAGTTC	CACGTATCGT	ATTGCCAAC	AAAATGGACA	150

	AAATCGGTGC	TGACTTCCTT	TACTCTGTAA	GCACACTTCA	CGATCGTCTT	200
	CAAGCAAATG	CACACCCAAT	CCAATTGCCA	ATCGGTCTTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGACA	TCCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGATC	GAAGCAGTTG	CTGAAACTGA	400
	CGAAGAATTG	ATGATGAAAT	ACCTCGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGGTATCCGT	AAAGCGACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GCTCTGCCTT	CAAGAACAAA	GGTGTTCAAT	TGATGCTTGA	550
	TGCGGTTATT	GACTACCTTC	CAAGCCCCTT	TGACATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGATGAA	650
	GAGCCATTTG	CAGCTCTTGC	CTTCAAGATC	ATGACAGACC	CATTGTAAG	700
	TCGTTTGACA	TTCTTCCGTG	TTTACTCARG	TGKTCTTCAA	TCAGGTTTCA	750
	ACGTATTGAA	CACTTCTAAA	GGKAAACGTG	AGCGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CCAACAGCCG	TCAAGAAATT	GACACTGGTT	ACTCAAGAGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TCCAACGGT	GACTCATTGC	900
	CAGATGAAAA	AGCTAAAATC	ATTCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGCCAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCTGGTAT	GGGTGAGCTT	1100
20	CACCTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTTGAAGC	1150
	AAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAC	GAAGAAGGTA	AAGGATTCGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	ACTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	TGCGGCTTCA	CTTGCTCTTA	1500
	AAGAAGCTGC	TAAATCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACAATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTCG	TGCTTACGT				1669

35 2) INFORMATION FOR SEQ ID NO: 1581

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581

AATTGGGGAC TACACCTATT ATGATG

26

50

2) INFORMATION FOR SEQ ID NO: 1582

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582

10 GGCAAATCAG TCAGTTCAGG AGT

23

2) INFORMATION FOR SEQ ID NO: 1583

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583

25

CGATTGGCAA CAATACACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1584

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584

40

TCACCTATTT TTACGCCTGG TAGGAC

26

2) INFORMATION FOR SEQ ID NO: 1585

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

5 (C) ACCESSION NUMBER: AF139725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585

```

10 ATGACTATAC CTGACGCAAA TGCAATCTAT CCTAACTCAG CCATCAAAGA      50
   GGTGTGCTTT ATCAAGAACG TGATCAAAAG TCCCAATATT GAAATTGGGG      100
   ACTACACCTA TTATGATGAC CCAGTAAATC CCACCGATTG TGAGAAACAC      150
   GTTACCCATC ACTATGAATT TCTAGGCGAC AAATTAATCA TCGGTAAATT      200
   TTGTTCTATC GCCAGTGGCA TTGAATTTAT CATGAACGGT GCCAACCACG      250
   TAATGAAAGG TATTTGCGACT TATCCATTTA ATATTTTAGG TGGCGATTGG      300
15 CAACAATACA CTCCTGAACT GACTGATTTG CCGTTGAAAG GTGATACTGT      350
   AGTCGGAAAT GACGTGTGGT TTGGGCAAAA TGTGACCGTC CTACCAGGCG      400
   TAAAAATAGG TGACGGTGCC ATTATCGGAG CAAATAGTGT TGTAACAAAA      450
   GACGTCGCTC CATATACAAT TGTCGGTGGC AATCCAATTC AACTCATCGG      500
   ACCAAGATTT GAACCGGAAG TTATTCAAGC ATTAGAAAAT CTGGCATGGT      550
20 GGAATAAAGA TATTGAATGG ATAAGTCTA ATGTTCTCTAA ACTAATGCAA      600
   ACAACACCCA CACTTGAATT GATAAACAGT TTAATGGAAA AATAA          645

```

25 2) INFORMATION FOR SEQ ID NO: 1586

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586

ATTCCCACAA TCTTTTTTAT CAATAA

26

40

2) INFORMATION FOR SEQ ID NO: 1587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587

CATTGTTCAG ATTCGGTAAA GTTC

24

2) INFORMATION FOR SEQ ID NO: 1588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588

GTTTTTGAAG TTAAATAGTG TTCTT

2) INFORMATION FOR SEQ ID NO: 1589

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589

CTTCCATTG TACTTTCCT A

2) INFORMATION FOR SEQ ID NO: 1590

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Cloning vector pFW16
- (C) ACCESSION NUMBER: U50983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1590

ATGAAAATTA	TTAATATTGG	AGTTTTAGCT	CATGTTGATG	CAGGAAAAAC	50
TACCTTAACA	GAAAGCTTAT	TATATAACAG	TGGAGCGATT	ACAGAATTAG	100
GAAGCGTGGA	CAAAGGTACA	ACGAGGACGG	ATAATACGCT	TTTAGAACGT	150
CAGAGAGGAA	TTACAATTCA	GACAGGAATA	ACCTCTTTTC	AGTGGGAAAA	200
TACGAAGGTG	AACATCATAG	ACACGCCAGG	ACATATGGAT	TTCTTAGCAG	250

	AAGTATATCG	TTCATTATCA	GTTTTAGATG	GGGCAATTCT	ACTGATTTCT	300
	GCAAAAGATG	GCGTACAAGC	ACAAACTCGT	ATATTATTTT	ATGCACTTAG	350
	GAAATGGGG	ATTCCCACAA	TCTTTTTTAT	CAATAAGATT	GACCAAAATG	400
	GAATTGATTT	ATCAACGGTT	TATCAGGATA	TTAAAGAGAA	ACTTTCTGCC	450
5	GAAATTGTAA	TCAAACAGAA	GGTAGAACTG	TATCCTAATG	TGTGTGTGAC	500
	GAACCTTTACC	GAATCTGAAC	AATGGGATAC	GGTAATAGAG	GGAAACGATG	550
	ACCTTTTAGA	GAAATATATG	TCCGGTAAAT	CATTAGAAGC	ATTGGAACCTC	600
	GAACAAGAGG	AAAGCATAAG	ATTTCAGAAT	TGTTCTCTGT	TCCCTCTTTA	650
	TCATGGAAGT	GCAAAAAGTA	ATATAGGGAT	TGATAACCTT	ATAGAAGTTA	700
10	TTACTAATAA	ATTTTATTCA	TCAACACATC	GAGGTCCGTC	TGAACTTTGC	750
	GGAAATGTTT	TCAAATTTGA	ATATACAAAA	AAAAGACAAC	GTCTTGACATA	800
	TATACGCCTT	TATAGTGGAG	TACTACATTT	ACGAGATTCTG	GTTAGAGTAT	850
	CAGAAAAGGA	AAAAATAAAA	GTTACAGAAA	TGTATACTTC	AATAAATGGT	900
	GAATTATGTA	AGATTGATAG	AGCTTATTCT	GGAGAAATTG	TTATTTTGCA	950
15	AAATGAGTTT	TTGAAGTTAA	ATAGTGTTCT	TGGAGATACA	AAACTATTGC	1000
	CACAGAGAAA	AAAGATTGAA	AATCCGCACC	CTCTACTACA	AACAACCTGTT	1050
	GAACCGAGTA	AACCTGAACA	GAGAGAAATG	TTGCTTGATG	CCCTTTTGGA	1100
	AATCTCAGAT	AGTGATCCGC	TTCTACGATA	TTACGTGGAT	TCTACGACAC	1150
	ATGAAATTAT	ACTTTCTTTC	TTAGGGAAAG	TACAAATGGA	AGTGATTAGT	1200
20	GCACTGTTGC	AAGAAAAGTA	TCATGTGGAG	ATAGAAATAA	CAGAGCCTAC	1250
	AGTCATTTAT	ATGGAGAGAC	CGTTAAAAAA	TGCAGAATAT	ACCATTACACA	1300
	TCGAAGTGCC	GCCAAATCCT	TTCTGGGCTT	CCATTGGTCT	ATCTGTATCA	1350
	CCGCTTCCGT	TGGGAAGTGG	AATGCAGTAT	GAGAGCTCGG	TTTCTCTTGG	1400
	ATACTTAAAT	CAATCATTTT	AAAATGCAGT	TATGGAAGGG	ATACGCTATG	1450
25	GTTGTGAACA	AGGATTGTAT	GGTTGGAATG	TGACGGACTG	TAAAATCTGT	1500
	TTTAAGTATG	GCTTATACTA	TAGCCCTGTT	AGTACCCAG	CAGATTTTTCG	1550
	GATGCTTGCT	CCTATTGTAT	TGGAACAAGT	CTTAAAAAAA	GCTGGAACAG	1600
	AATTGTTAGA	GCCATATCTT	AGTTTTTAAA	TTTATGCGCC	ACAGGAATAT	1650
	CTTTCACGAG	CATACAACGA	TGCTCCTAAA	TATTGTGCGA	ACATCGTAGA	1700
30	CACTCAATTG	AAAAATAATG	AGGTCATTCT	TAGTGGAGAA	ATCCCTGCTC	1750
	GGTGTATTCA	AGAATATCGT	AGTGATTTAA	CTTTCTTTAC	AAATGGACGT	1800
	AGTGTGTTGTT	TAACAGAGTT	AAAAGGGTAC	CATGTTACTA	CCGGTGAACC	1850
	TGTTTGCCAG	CCCCGTCGTC	CAAATAGTCG	GATAGATAAA	GTACGATATA	1900
	TGTTCAATAA	AATAACTTAG				1920
35						

2) INFORMATION FOR SEQ ID NO: 1591

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591

50 ATGAGGTAAT AGAACGGATT

20

2) INFORMATION FOR SEQ ID NO: 1592

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592

CAGTATTTCA GTAAGCGTAA A

21

2) INFORMATION FOR SEQ ID NO: 1593

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593

CCGAGCGATT TACCGGATAC TTGGCTGCIC GCTCGG

36

2) INFORMATION FOR SEQ ID NO: 1594

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: N97-330
(C) ACCESSION NUMBER: AF175293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594

ATGTTTAGAA	TTAAAGTTGC	AGTTCGTGTT	GGGGGCTGTT	CAGAGGAACA	50
TAATGTTTCG	ATAAAATCTG	CGATGGAGAT	TGCCGCAAAC	ATAGATACAA	100
AAAAGTATCA	GCCTTATTAT	ATTGGAATCA	CAAAATCCGG	CGTTTGGAAA	150
ATGTGTGAAA	AACCTTGTTT	GGAGTGGGAA	CAATATGCGG	GGGATCCGGT	200
TGTTTTTTCA	CCGGACAGAA	GTACGCATGG	TCTGCTGATA	CAAAAAGACA	250

	CTGGGTATGA	AATCCAGCCT	GTGGATGTGG	GATTACCGAT	GATTCATGGC	300
	AAGTTTGGCG	AGGATGGCTC	CATACAAGGC	TTGCTTGAAT	TGTCAGGCAT	350
	TCCGTATGTG	GGATGCGATA	TTCAAAGCTC	CGTGACCTGC	ATGGATAAGG	400
	CGCTTGATA	TACCGTTGTG	AAAAATGCGG	GTATCGCTGT	GCCTGGGTTC	450
5	CGGATCCTTC	AGGAGGGGGA	TCGCCTGGAA	ACAGAGGATT	TCGTATATCC	500
	CGTTTTTGTA	AAGCCTGCCC	GTTCCGGCTC	ATCCTTTGGC	GTAAACAAGG	550
	TATGCAAGGC	AGAAGAACTG	CAGGCAGCAA	TCGAAGATGC	AAGAAAATAT	600
	GACAGCAAGA	TTTTGATTGA	AGAGGCCGTT	ACCGGGAGTG	AGGTAGGCTG	650
	CGCCATACTG	GGAAACGGAA	ATGATCTCAT	GGCTGGCGAG	GTGGATCAGA	700
10	TTGAGCTGAG	ACACGGCTTT	TTTAAGATTC	ATCAGGAAGC	ACAGCCGGAG	750
	AAAGGATCTG	AAAATGCAGT	CATCCGAGTT	CCAGCCGCCT	TACCGGATGA	800
	GGTAATAGAA	CGGATTCAGA	AAACAGCAAT	GAAGATTTAC	CGGATACTTG	850
	GCTGCAGAGG	ATTGGCCCGC	ATTGACCTGT	TTTTGCGGGA	GGACGGCTGC	900
	ATTGTGTTGA	ATGAAGTGAA	TACCATGCCG	GGTTTTACTT	CCTACAGCCG	950
15	TTATCCCCGC	ATGATGACAG	CAGCCGGTTT	TACGCTTACT	GAAATACTGG	1000
	ATCGCTTGAT	TGAACTTTCA	CTTAGGAGGT	AA		1032

20 2) INFORMATION FOR SEQ ID NO: 1595

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595

AAATAATGCT CCATCAATTT GCTGA

25

35 2) INFORMATION FOR SEQ ID NO: 1596

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596

ATAGTCGAAA AAGCCATCCA CAAG

24

50 2) INFORMATION FOR SEQ ID NO: 1597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597

GATGAATTTG CGAAAATACA TGGA

24

2) INFORMATION FOR SEQ ID NO: 1598

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598

CAGCCAATTT CTACCCCTTT CAC

23

2) INFORMATION FOR SEQ ID NO: 1599

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: BM4405
 (C) ACCESSION NUMBER: AF136925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599

CAGGGAGTAT	TTGAGTTATT	AGATATTCCA	TATGTAGGTT	GTGGTATCGG	50
AGCTGCAGCA	ATTTCCATGA	ATAAAATAAT	GCTCCATCAA	TTTGCTGAAA	100
TAGTTGGTGT	AAAAAGCACT	CCTAGTATGA	TTATAGAAAA	GGGACAAGAC	150
CTACAAAAAG	TCGATGAATT	TGCGAAAATA	CATGGATTTC	CTTTATATAT	200
CAAACCGAAT	GAGGCAGGCT	CATCAAAAGG	AATTAGCAAG	GTAGAACAAA	250
AAAGTGATTT	ATATAAAGCA	ATAGACGAAG	CTTCAAAATA	TGATAGCCGT	300

	ATTTTAATTC	AAAAGGAAGT	GAAAGGGGTA	GAAATTGGCT	GTGGGATTTT	350
	AGGGAATGAA	CAATTGGTCG	TTGGAGAATG	TGATCAAATT	AGTCTTGTGG	400
	ATGGCTTTTT	CGACTATGAA	GAGAAATACA	ATTTAGTAAC	AGCAGAAATT	450
	TTGTTACCAG	CTAAACTATC	AATAGACAAA	AAAGAAGACA	TCCAGATAAA	500
5	AGCAAAAAAA	CTATACAGAC	TATTAGGGTG	CAAAGGATTA	GCGAGAATCG	550
	ACTTTTCTT	AACGGATGAC	GGAGAAATTT	TATTAAATGA	GATCAACACC	600
	CTCC					604

10

2) INFORMATION FOR SEQ ID NO: 1600

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 805 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
- (B) STRAIN: ATCC 49349

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600

	ACCTCAAATT	AATGAAGCAA	TTGTTGTAAA	TTTTGAAAGC	GAAGGAAAAA	50
	AACATAAACT	TGTTTTAGAA	GTAGCAGCTC	ATTTAGGAGA	TAATAGAGTT	100
	AGAACTATTG	CTATGGATAT	GACAGATGGT	TTGGTAAGGG	GCTTAAAAGC	150
30	TGAGGCTTTA	GGTGCTCCTA	TTAGTGTTC	TGTTGGTGAG	AAAGTTTTAG	200
	GAAGAATTTT	CAATGTTACT	GGAGATTTGA	TCGATGAAGG	TGAAGAAATT	250
	CCTTTTGATA	AAAAATGGGC	AATTCATAGA	GATCCGCCAG	CTTTTGAAGA	300
	TCAAAGCACA	AAAAGTGAGA	TTTTTGAAAC	AGGGATTAAA	GTTGTAGATT	350
	TACTTGCTCC	TTATGCAAAA	GGTGGTAAAG	TAGGTCTTTT	TGGTGGTGCA	400
35	GGTGTGTA	AAACTGTTAT	TATTATGGAG	CTTATTCACA	ATGTTGCATT	450
	TAAGCATAGC	GGCTATTCTG	TATTTGCAGG	TGTGGGTGAG	AGAACTCGTG	500
	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	AAAGTAATGT	TTTAGACAAA	550
	GTTGCTCTAT	GTTATGGACA	AATGAATGAA	CCACCAGGAG	CAAGAAATCG	600
	TATTGCTTTA	ACAGGTTTAA	CAATGGCTGA	GTATTTTAGA	GATGAAATGG	650
40	GTCTTGATGT	GCTTATGTTT	ATTGATAATA	TCTTTAGATT	TTCAACAATCA	700
	GGTTCTGAAA	TGTCAGCACT	TTAGGAAGA	ATTCCATCAG	CTGTGGGTTA	750
	TCAACCAACC	CTAGCAAGTG	AAATGGGTAA	ATTCCAAGAA	AGAATTACTT	800
	CAACT					805

45

2) INFORMATION FOR SEQ ID NO: 1601

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601

```

10 CTCCTTACCA GATATCAACA ATGCGCTGGT TGTATATAAA AATGATGCCA      50
   ATAAACAAA AGTTGTTTTA GAAGCAGCGT TAGAATTAGG TGACGGAATC      100
   ATTCGTGCGA TTGCAATGGA ATCGACTGAT GGATTGCAAC GTGGGATGGA      150
   AGTTGTGCGAT ATGGGAGAAT CTATTTCTGT ACCAGTTGGA ACAGAACTT      200
   TAGGACGTGT GTTTAATGTA TTAGGAGATA CGATTGACTT AGAAGCTCCT      250
15 TTTCTTAAAG ATGCACCGCG TAGTGGAATC CATAAAAAG CCCCTAATTT      300
   TGATGAATTA AGTACAAGCA CAGAAATTCT AGAAACAGGG ATCAAAGTCA      350
   TCGATCTATT AGCCCCTTAT TAAAAGGTG GTAAAGTTGG ATTGTTTGGG      400
   GGAGCCGGTG TAGGAAAAAC GGTATTGATT CAAGAGTTGA TTCACAATAT      450
   CGCACAAGAA CACGGTGCGA TTTCTGGTCTT TACTGGTGTT GGTGAGCGTA      500
20 CACGTGAAGG AAACGATTTG TATTATGAAA TGAAAGATTC AGGAGTCATT      550
   GAAAAACAG CGATGGTGTT TGGACAAATG AATGAGCCAC CTGGTGACAG      600
   GATGCGTGTA GCCTTGACTG GATTAACGAT TGCTGAATAT TTCCGTGATG      650
   TTGAAGGACA GGATGTACTG TTGTTTATCG ACAATATCTT CCGTTTTACA      700
   CAAGCTGGTT CTGAAGTGTC TGCCTTGTTA GGTCGTATGC CATCAGCTGT      750
25 GGGATATCAA CCAACATTAG CTACCGAAAT GGGGCAATTG CAAGAGCGGA      800
   TCACGTCAAC GAAAAAAGGA TCGATC      826

```

30 2) INFORMATION FOR SEQ ID NO: 1602

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602

```

45 TGATACTTTA CCAGATATTA ATAATGCATT AGTAGTATAT AAAAAGGACG      50
   AGGACAAGAC ACGCGTTGTC TTAGAAGCCA CTTTGGAAC TGGAGATGGC      100
   ATGATTCGTG CAATCTCTAT GGGATCGACT GATGGCTTGC AACGGGGAAT      150
   GGAAGTTGTG GACACACAAG CACCTATTTT TGTTCCAGTA GGAAATGAAA      200
50 CCTTAGGACG TGTTTTTAAT GTCTTAGGAG AAACGATTGA TAAACAGGCA      250
   CCGTTTCCTG AAGATGCCAA AAAAAGTGGT ATTCATAAAA AAGCACCCGC      300
   TTTTGATGAA TTAAGTACCA GTTCTGAAAT ATTGAAACC GGGATTAAAG      350
   TAATCGATTT GCTAGCTCCT TATTTACGAG GTGGTAAAGT TGGATTATTT      400

```

```

GGCGGTGCTG GCGTGGGTAA AACGGTATTA ATTCAAGAAT TAATTCATAA      450
CGTTGCCCAA GAACATGGGG GAATTTCTGT TTTTACGGGT GTCGGAGAGC      500
GTACTCGTGA AGGAAATGAC CTATATTATG AAATGCAGGA TTCAGGCGTT      550
ATTGAAAAAA CGGCTATGGT ATTTGGACAA ATGAACGAAC CCCCTGGTGC      600
5  ACGTATGCGT GTAGCGTTAA CTGGTTTGAC ACTTGCTGAG TACTTCCGTG      650
ATGTACAAGG TCAAGACGTA TTATTATTTA TAGATAATAT TTTCCGCTTT      700
ACTCAAGCAG GAACAGAAGT ATCTGCTTTA TTAGGACGGA TGCCGTCTGC      750
CGTTGGTTAC CAACCAACTC TAGCAACGGA AATGGGACAG TTGCAAGAAC      800
GAATCACATC GACAGATAAA GGATCAATTA CCT                          833
10

```

2) INFORMATION FOR SEQ ID NO: 1603

```

15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 806 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Campylobacter sputorum subsp. sputorum
25  (B) STRAIN: ATCC 35980

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603

```

30  ATCAGCCTAA AATTAACGAA GCAATAGAAG TTAATTATGA ATTAGATGGT      50
      AAAAAAATAA GACTTATTCT TGAAGTAGCT GGACATCTTG GCGATAATAG      100
      AGCAAGAACC ATTGCTATGG ATATGAGTGA TGGTTTACAA AGAGGATTAG      150
      AAGTTACGGC TCTTGGTGCT CCTATAACAG TTCCTGTTGG AGATAAAGTT      200
      TTAGGTAGAA TGTTTAATGT TGTAGGTGAC TTAATAGATG AAGGTGAAGT      250
      AACAGATTTT GATAAAAGAT GGGCTATCCA TAGAGATCCT CCTTCGTTTG      300
35  AAGATCAAAG TACAAAAAGT GAAATTTTGG AAACAGGTAT AAAAGTAGTT      350
      GATCTTCTTG CACCTTATGC AAAAGGTGGT AAAGTTGGCT TATTTGGTGG      400
      TGCTGGCGTT GGAAAAACAG TTATCATAAT GGAGCTTATA CATAATGTTG      450
      CATTTAAACA CAGCGGTTAT TCAATTTTGG CCGGTGTTGG AGAGAGAACA      500
      AGAGAGGGAA ATGATCTTTA TAATGAGATG AAAGAGTCTG GTGTTTGGGA      550
40  TAAAGTTGCC TTATGTTATG GACAAATGAA TGAACCACCA GGAGCAAGAA      600
      ACCGTATAGC ATTAACAGGT CTTACAATGG CTGAATATTT CCGTGATGAA      650
      ATGGGGCTTG ATGTGTTGAT GTTTATAGAT AATATTTTGA GATTTTCTCA      700
      ATCAGGTTCT GAAATGTCAG CGCTGCTTGG TAGAATTCCA TCTGCTGTTG      750
      GTTATCAACC AACATTAGCA AGTGAGATGG GAAAACCTCA AGAAAGAATT      800
45  ACTTCC                          806

```

2) INFORMATION FOR SEQ ID NO: 1604

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 738 bases
      (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604

	GGTGTATATCC	GCACAATCGC	TATGGAATCT	ACAGATGGAT	TGCAACGGGG	50
	GATGGAAGTT	GTCGATACCG	GCAAACCAAT	CTCTGTTCTT	GTAAGGTAAAG	100
	AAACATTAGG	TCGTGTGTTT	AACGTATTAG	GTGAAACGAT	CGACAAAGAA	150
15	GCACCTTTTC	CAGAAGATGT	AGAAAAGAGC	GGTATTACAC	AAAAGGCCCC	200
	CGCTTTTGAA	GACCTTAGCA	CCAGTAATGA	GATTTTAGAA	ACTGGGATCA	250
	AGGTTATCGA	CTTATTAGCC	CCTTACTTAA	AAGGTGGTAA	AGTTGGACTA	300
	TTCGGTGGTG	CCGGTGTGTT	TAAACCGTC	TTAATTCAAG	AACTGATTCA	350
	TAATATCGCC	CAAGAACACG	GTGGGATTTC	TGCTTTTACC	GGGGTTGGGG	400
20	AACGGACTCG	TGAAGGGAAC	GACCTTTATT	ATGAAATGAA	AGAATCCGGC	450
	GTTATTGAAA	AAACAGCGAT	GGTCTTCGGA	CAAATGAATG	AGCCACCAGG	500
	TGCGCGGATG	CGCGTTGCCT	TGACTGGTTT	GACATTAGCT	GAATATTTCC	550
	GTGATGAAGA	AGGTCAAGAT	GTGTTGCTAT	TTATCGATAA	CATTTTCCGC	600
	TTCACACAAG	CCGGATCAGA	AGTTTCGGCG	CTATTAGGTC	GGATGCCATC	650
25	TGCCGTTGGT	TATCAACCAA	CCTTGGCAAC	AGAAATGGGT	CAATTACAAG	700
	AACGAATCAC	TTCAACGAAA	AAAGGCTCAA	TTACATCG		738

30 2) INFORMATION FOR SEQ ID NO: 1605

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605

ATYATYGAAR TITAYGCICC

20

45

2) INFORMATION FOR SEQ ID NO: 1606

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606

5 CCRAACATIA YICCIAC TTT TTC

23

2) INFORMATION FOR SEQ ID NO: 1607

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607

25	CTGGATTATG CGATGTCGGT CATTGTTGGC CGTGCGCTGC CGGATGTCCG	50
	AGATGGCCTG AAACCGGTAC ACCGTCGCGT ACTTTACGCC ATGAACGTAT	100
	TGGGCAATGA CTGGAACAAA GCCTATAAAA AATCCGCCCG TGTCGTTGGT	150
	GACGTAATCG GTAAATACCA CCCTCATGGT GATACGCCCG TTTATGACAC	200
	CATTGTACGT ATGGCACAGC CATTCTCCTT GCGTTATATG CTGGTCGATG	250
30	GCCAGGGTAA CTTTCGGTTCT GTCGATGGCG ACTCCGCCCG AGCGATGCGT	300
	TATACGGAAA TCCGTATGTC GAAAATCGCC CACGAG	336

35 2) INFORMATION FOR SEQ ID NO: 1608

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608

50

CTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG CTGCCGGATG	50
TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTATA CGCCATGAAC	100
GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCTG CCCGTGTCGT	150

GGGTGACGTC	ATCGGTAAAT	ACCACCCTCA	TGGTGATACT	GCCGTATACG	200
ACACCATTGT	ACGTATGGCG	CAGCCATTCT	CCCTGCGTTA	CATGCTGGTA	250
GATGGCCAGG	GTAAC TTTGG	TTCGGTCGAC	GGCGACTCCG	CCGCAGCGAT	300
GCGTTATACG	GAAATCCGTA	TGTCGAAGAT	CGCCCATGAA	C	341

5

2) INFORMATION FOR SEQ ID NO: 1609

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609

20 GCCCTGATCC AAATAGCATA TA

22

2) INFORMATION FOR SEQ ID NO: 1610

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610

35

CCTGGCATAA CAGTAACATT CTG

23

40 2) INFORMATION FOR SEQ ID NO: 1611

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611

TGGGAAAAAG CAACTCCATC TC

22

2) INFORMATION FOR SEQ ID NO: 1612

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612

ACAACTGAAT TCGCAGCAAC AAT

23

2) INFORMATION FOR SEQ ID NO: 1613

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: U19459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613

ATGAAATATG	GCCCTGATCC	AAATAGCATA	TATCCACATG	AAGAAATAAA	50
AAGTGTTTGT	TTTATTAAAA	ATACAATTAC	CAATCCAAAT	ATTATAGTTG	100
GAGATTATAC	TTACTATTCC	GATGTTAACG	GAGCTGAAAA	ATTTGAAGAA	150
CATGTGACAC	ATCATTATGA	ATTTAGGGGT	GATAAACTTG	TAATTGGCAA	200
GTTTTGTGCA	ATAGCTGAAG	GTATAGAATT	TATTATGAAT	GGAGCAAACC	250
ATAGAATGAA	TTCAATAACA	ACTTATCCTT	TTAATATAAT	GGGAAATGGT	300
TGGGAAAAAG	CAACTCCATC	TCTTGAAGAT	TTACCATTTA	AGGGAGATAC	350
TGTTGTTGGA	AATGATGTGT	GGATTGGTCA	GAATGTTACT	GTTATGCCAG	400
GAATTCAAAT	AGGAGATGGA	GCAATTGTTG	CTGCGAATTC	AGTTGTTACA	450
AAAGATGTAC	CACCATATCG	TATTATTGGT	GGAAATCCGA	GTAGAATTAT	500
AAAGAAAAGG	TTTGAAGATG	AATTGATAGA	TTATTTATTG	CAAATAAAAT	550
GGTGGGATTG	GTCAGCACAA	AAAATATTTT	CTAATCTTGA	AACACTTTGT	600
AGCTCTGATT	TAGAGAAAAT	AAAATCTATT	CGAGATTAG		639

2) INFORMATION FOR SEQ ID NO: 1614

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614

CCAATCCAGA AGAAATATAC CC

22

10

2) INFORMATION FOR SEQ ID NO: 1615

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615

ATTAGTTTAT CCCCAATCAA TTCA

24

25

2) INFORMATION FOR SEQ ID NO: 1616

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616

40

ATAATGAATG GGGCTAATCA TCGTAT

26

2) INFORMATION FOR SEQ ID NO: 1617

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617

GCCAACAACCT GAATAAGGAT CAAC

24

5

2) INFORMATION FOR SEQ ID NO: 1618

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 639 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
(C) ACCESSION NUMBER: AF015628

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618

	ATGAAATGGC	AAAATCAGCA	AGGCCCCAAT	CCAGAAGAAA	TATACCCTAT	50
	AGAAGGTAAT	AAACATGTTC	AATTTATTAA	ACCATCTATA	ACAAAGCCCA	100
25	ATATTTTAGT	TGGGGAATAT	TCATATTACG	ATAGTAAAGA	TGGTGAATCT	150
	TTTGAAAGCC	AAGTTCTTTA	TCACTATGAA	TTGATTGGGG	ATAAACTAAT	200
	ATTAGGGAAG	TTTTGTTCTA	TTGGACCCGG	AACGACATTT	ATAATGAATG	250
	GGGCTAATCA	TCGTATGGAT	GGTTCAACAT	TTCCATTCAA	TCTTTTCGGA	300
	AATGGTTGGG	AGAAGCATAAC	CCCTACATTG	GAAGACCTTC	CTTATAAGGG	350
30	TAACACGGAA	ATTGGGAACG	ATGTTTGGAT	TGGACGAGAT	GTGACAATTA	400
	TGCCCCGGTGT	AAAAATAGGA	AACGGGGCTA	TTATTGCAGC	AAAATCGGTT	450
	GTGACAAAGA	ACGTTGATCC	TTATTCAAGT	GTTGGCGGTA	ATCCTTCACG	500
	ATTAATTAAG	ATAAGGTTTT	CCAAGGAAAA	AATCGCAGCA	TTACTAAAAG	550
	TAAGGTGGTG	GGACCTAGAG	ATAGAGACGA	TAAATGAAAA	TATTGATTGC	600
35	ATCCTGAATG	GTGATATAAA	AAAGGTTAAA	AGAAGTTAG		639

2) INFORMATION FOR SEQ ID NO: 1619

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619

50

AAGGCAAAAT AAAAGGAGCA AAGC

24

2) INFORMATION FOR SEQ ID NO: 1620

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620

TGTACCCGAG ACATCTTCAC CAC

23

2) INFORMATION FOR SEQ ID NO: 1621

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621

AATTGAAGGA CGGGTATTGT GGAAAG

26

2) INFORMATION FOR SEQ ID NO: 1622

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622

CGATTTTGAC AGATGGCGAT AATGAA

26

2) INFORMATION FOR SEQ ID NO: 1623

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M90056

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623

	ATGAAAATAA	TGTTAGAGGG	ACTTAATATA	AAACATTATG	TTCAAGATCG	50
	TTTATTGTTG	AACATAAATC	GCCTAAAGAT	TTATCAGAAT	GATCGTATTG	100
	GTTTAATTGG	TAAAAATGGA	AGTGGAAAAA	CAACGTTACT	TCACATATTA	150
15	TATAAAAAAA	TTGTGCCTGA	AGAAGGTATT	GTAAAACAAT	TTTCACATTG	200
	TGAACCTATT	CCTCAATTGA	AGCTCATAGA	ATCAACTAAA	AGTGGTGGTG	250
	AAGTAACACG	AAACTATATT	CGGCAAGCGC	TTGATAAAAA	TCCAGAACTG	300
	CTATTAGCAG	ATGAACCAAC	AACTAACTTA	GATAATAACT	ATATAGAAAA	350
	ATTAGAACAG	GATTTAAAAA	ATTGGCATGG	AGCATTTTATT	ATAGTTTCAC	400
20	ATGATCGCGC	TTTTTTTAGAT	AACTTGTGTA	CTACTATATG	GGAAATTGAC	450
	GAGGGAAGAA	TAAGTGAATA	TAAGGGGAAT	TATAGTAACT	ATGTTGAACA	500
	AAAAGAATTA	GAAAGACATC	GAGAAGAATT	AGAATATGAA	AAATATGAAA	550
	AAGAAAAGAA	ACGATTGGAA	AAAGCTATAA	ATATAAAAGA	ACAGAAAGCT	600
	CAACGAGCAA	CTAAAAAACC	GAAAAACTTA	AGTTTATCTG	AAGGCAAAAT	650
25	AAAAGGAGCA	AAGCCATACT	TTGCAGGTAA	GCAAAAGAAG	TTACGAAAAA	700
	CTGTAAAATC	TCTAGAAACC	AGACTAGAAA	AACTTGAAAG	CGTCGAAAG	750
	AGAAACGAAC	TTCCTCCACT	TAAAATGGAT	TTAGTGAACT	TAGAAAGTGT	800
	AAAAAATAGA	ACTATAATAC	GTGGTGAAGA	TGTCTCGGGT	ACAATTGAAG	850
	GACGGGTATT	GTGGAAAGCA	AAAAGTTTTA	GTATTTCGCG	AGGAGACAAG	900
30	ATGGCAATTA	TCGGATCTAA	TGGTACAGGA	AAGACAACGT	TTATTAAAAA	950
	AATTGTGCAT	GGGAATCCTG	GTATTTTCATT	ATCGCCATCT	GTCAAAATCG	1000
	GTTATTTTAT	CCAAAAAATA	GATACATTAG	AATTAGATAA	GAGCATTTTA	1050
	GAAAATGTTC	AATCTTCTTC	ACAACAAAAT	GAAACTCTTA	TTCGAACTAT	1100
	TCTAGCTAGA	ATGCATTTTT	TTAGAGATGA	TGTTTATAAA	CCAATAAGTG	1150
35	TCTTAAGTGG	TGGAGAGCGA	GTTAAAGTAG	CACTAACTAA	AGTATTCTTA	1200
	AGTGAAGTTA	ATACGTTGGT	ACTAGATGAA	CCAACAAACT	TTCTTGATAT	1250
	GGAAGCTATA	GAGGCGTTTG	AATCTTTGTT	AAAGGAATAT	AATGGCAGTA	1300
	TAATCTTTGT	ATCTCACGAT	CGTAAATTTA	TCGAAAAAGT	AGCCACTCGA	1350
	ATAATGACAA	TTGATAATAA	AGAAATAAAA	ATATTTGATG	GCACATATGA	1400
40	ACAATTTAAA	CAAGCTGAAA	AGCCAACAAG	GAATATTAAA	GAAGATAAAA	1450
	AACTTTTACT	TGAGACAAAA	ATTACAGAAG	TACTCAGTCG	ATTGAGTATT	1500
	GAACCTTCGG	AAGAATTAGA	ACAAGAGTTT	CAAAACTTAA	TAAATGAAAA	1550
	AAGAAATTTG	GATAAATAA				1569

45

2) INFORMATION FOR SEQ ID NO: 1624

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624

5 TTCTTTAATG CTCGTAGATG AACCTA 26

10 2) INFORMATION FOR SEQ ID NO: 1625

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1625

TTTTCGTATT CTTCTTGTTG CTTTC 25

25 2) INFORMATION FOR SEQ ID NO: 1626

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626

AGGAATGATT AAGCCCCCTT CAAAAA 26

40 2) INFORMATION FOR SEQ ID NO: 1627

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627

TTACATTGCG ACCATGAAAT TGCTCT

26

2) INFORMATION FOR SEQ ID NO: 1628

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: U82085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628

20	ATGCTTAAAA	TCGACATGAA	GAATGTAAAA	AAATATTATG	CAGATAAATT	50
	AATTTTAAAT	ATAAAAGAAC	TAAAGATTTA	TAGTGGGGAT	AAAATAGGTA	100
	TTGTAGGTAA	GAATGGAGTT	GGCAAAACAA	CACTTTAAAA	AATAATAAAA	150
	GGACTAATAG	AGATTGACGA	AGGAAATATA	ATTATAAGTG	AAAAAACAAC	200
	TATTAAATAT	ATCTCTCAAT	TAGAAGAACC	ACATAGTAAG	ATAATTGATG	250
25	GAAAATATGC	TTCAATATTT	CAAGTTGAAA	ATAAGTGGAA	TGACAATATG	300
	AGTGGTGGTG	AAAAAACTAG	ATTTAAACTA	GCAGAGGGAT	TTCAAGATCA	350
	ATGTTCTTTA	ATGCTCGTAG	ATGAACCTAC	AAGTAATTTA	GATATCGAAG	400
	GAATAGAGTT	GATAACAAAT	ACTTTTAAAG	AGTACCGTGA	TACTTTTTTG	450
	GTAGTATCTC	ATGATAGAAT	TTTTTTAGAT	CAAGTTTGTA	CAAAAATTTT	500
30	TGAAATTGAA	AATGGATATA	TTAGAGAATT	CATCGGTAAT	TATACAAACT	550
	ATATAGAGCA	AAAAGAAATG	CTTCTACGAA	AGCAACAAGA	AGAATACGAA	600
	AAGTATAATT	CTAAAAGAAA	GCAATTGGAG	CAAGCTATAA	AGCTAAAAGA	650
	GAATAAGGCG	CAAGGAATGA	TTAAGCCCCC	TTCAAAAACA	ATGGGAACAT	700
	CTGAATCTAG	AATATGGAAA	ATGCAACATG	CTACTAAACA	AAAAAAGATG	750
35	CATAGAAATA	CGAAATCGTT	GGAAACACGA	ATAGATAAAT	TAAATCATGT	800
	AGAAAAAATA	AAAGAGCTTC	CTTCTATTAA	AATGGATTTA	CCTAATAGAG	850
	AGCAATTTCA	TGGTCGCAAT	GTAATTAGTT	TAAAAAACTT	ATCTATAAAA	900
	TTTAATAATC	AATTTCTTTG	GAGAGATGCT	TCATTTGTCA	TTAAAGGTGG	950
	AGAAAAGGTT	GCTATAATTG	GTAACAATGG	TGTAGGAAAA	ACAACATTGT	1000
40	TGAAGCTGAT	TCTAGAAAAA	GTAGAATCAG	TAATAATATC	ACCATCAGTT	1050
	AAAATTGGAT	ACGTCAGTCA	AAACTTAGAT	GTTCTACAAT	CTCATAAATC	1100
	TATCTTAGAA	AATGTTATGT	CTACCTCCAT	TCAAGATGAA	ACAATAGCAA	1150
	GAATTGTTCT	AGCAAGATTA	CATTTTTTATC	GCAATGATGT	TCATAAAGAA	1200
	ATAAATGTTT	TGAGTGGTGG	AGAACAAATA	AAGGTTGCTT	TTGCCAAGCT	1250
45	ATTTGTTAGC	GATTGTAATA	CATTAATTCT	TGATGAACCA	ACAAACTATT	1300
	TGGATATCGA	TGCTGTTGAG	GCATTAGAAG	AATTGTTAAT	TACCTATGAA	1350
	GGTGTGTGTG	TATTTGCTTC	CCATGATAAA	AAATTTATAC	AAAACCTAGC	1400
	TGAACAATTG	TTAATAATAG	AAAATAATAA	AGTGAAAAAA	TTCGAAGGAA	1450
	CATATATAGA	ATATTTAAAA	ATTAAAGATA	AACCAAATTT	AAATACAAAT	1500
50	GAAAAAGAAC	TCAAAGAAAA	AAAGATGATA	CTAGAAATGC	AAATTTTCATC	1550
	ATTATTAAAGT	AAAATCTCAA	TGGAAGAAAA	TGAAGAAAAA	AACAAAGAAT	1600
	TAGATGAAAA	GTACAAATTG	AAATTAAAAAG	AATTGAAAAAG	CCTAAATAAA	1650
	AATATTTA					1658

2) INFORMATION FOR SEQ ID NO: 1629

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629

AAGGGGAAAG TTTGGATTAC ACAACA

26

2) INFORMATION FOR SEQ ID NO: 1630

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630

GAACCACAGG GCATTATCAG AACC

24

2) INFORMATION FOR SEQ ID NO: 1631

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631

CGACGATGCT TTATGGTTTG T

21

2) INFORMATION FOR SEQ ID NO: 1632

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632

GTTAATTTGC CTATCTTGTC AACTC

26

10

2) INFORMATION FOR SEQ ID NO: 1633

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M36022

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633

	ATGGAATTTA	AATTACAAGA	ATTAAATCTT	ACTAACCAAG	ATACAGGACC	50
	ATATGGTATA	ACCGTTTCAG	ATAAGGGGAA	AGTTTGGATT	ACACAACATA	100
	AAGCAAATAT	GATAAGTTGC	ATCAATTTAG	ATGGAAAAAT	TACAGAGTAC	150
30	CCACTACCGA	CACCAGATGC	AAAAGTCATG	TGTTTAACTA	TATCCTCAGA	200
	TGGGGAAGTT	TGGTTTACTG	AGAATGCAGC	AAACAAAATA	GGGAGGATTA	250
	CAAAAAAAGG	GATTATTAAG	GAATATACAT	TGCCTAACCC	AGATTCAGCA	300
	CCCTACGGTA	TTACAGAAGG	ACCAAATGGA	GATATATGGT	TTACAGAAAT	350
	GAATGGCAAC	CGTATTGGAC	GTATTACGGA	CGACGGTAAA	ATTCGTGAAT	400
35	ACGAGCTGCC	TAATAAAGGA	TCTTACCCTT	CTTTTATCAC	TTTGGGTTCT	450
	GATAATGCCC	TGTGGTTCAC	AGAAAATCAA	AATAATGCTA	TTGGTAGAAT	500
	TACAGAAAGT	GGGGATATTA	CAGAGTTTAA	AATTCCTACA	CCTGCATCAG	550
	GACCAGTTGG	TATTACAAAG	GGGAACGACG	ATGCTTTATG	GTTTGTGGAA	600
	ATTATCGGTA	ATAAGATAGG	GCGAATAACT	CCTCTGGGGG	AAATTACCGA	650
40	ATTCAAAATT	CCAACGCCAA	ACGCTCGACC	TCATGCAATT	ACTGCTGGAG	700
	CAGGAATTGA	TTTATGGTTT	ACTGAATGGG	GGGCTAATAA	AATAGGAAGG	750
	CTGACAAGCA	ATAATATAAT	TGAGGAATAC	CCAATTCAAA	TCAAAAGTGG	800
	TGAACCACAT	GGCATTGTGTT	TCGATGGTGA	AACAATTTGG	TTTGCAATGG	850
45	AGTGTGACAA	GATAGGCAAA	TTAACTCTCA	TTAAGGATAA	TATGGAGTGA	900

2) INFORMATION FOR SEQ ID NO: 1634

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634

TTAACTTGTC TATTCCCGAT TCAGG

25

10

2) INFORMATION FOR SEQ ID NO: 1635

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635

GCTGTGGCAA TGGATATTCT GTA

23

25

2) INFORMATION FOR SEQ ID NO: 1636

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636

TTCCTACCCC TGATGCTAAA GTGA

24

40

2) INFORMATION FOR SEQ ID NO: 1637

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637

CAAAGTGCGT TATCCGAACC TAA

23

5

2) INFORMATION FOR SEQ ID NO: 1638

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 527 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: WSA-172

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638

	GGTGGGGAAG	ACTGTCTTCA	TCCAGGAATT	GATTGTGAGT	CGTTCCACAT	50
	GCTCACCTAG	TTTTCGCTCG	ATCTTTTCAC	TAACGCAAAC	CATGTAGAAC	100
	AACATTGCCA	AGGCCACGG	TGGTTACTCC	GTCTTCACTG	GTGTTGGTGA	150
25	GCGTACTCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	GAGACTGGTG	200
	TCATTACAGCT	CGAGGGTGAA	TCCAAGGTCG	CACTGGTGTT	CGGACAGATG	250
	AACGAGCCCC	CCGGTGCCCG	TGCCCGTGTC	GCCCTTACCG	GTCTGACCAT	300
	TGCCGAGTAC	TTCCGTGACG	AGGAGGGTCA	GGACGTGCTG	CTCTTCATTG	350
	ACAACATTTT	CCGTTTCACC	CAGGCCGGTT	CTGAGGTGTC	TGCCCTTCTC	400
30	GGTCGTATCC	CCTCTGCCGT	CGGTTACCAG	CCCACCCTGG	CCGTCGACAT	450
	GGGTGGTATG	CAGGAGCGTA	TCACCACCAC	CAAGAAGGGT	TCTATTACCT	500
	CCGTCCARGC	CGTCTACGTC	CCCGCGA			527

35

2) INFORMATION FOR SEQ ID NO: 1639

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 452 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 64746

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639

	ACTGTCTTGA	TTCAAGAACT	TATTAACAAC	ATTGCTAAAG	CCCATGGTGG	50
	TTACTCTATT	TTCTGTGGTG	TTGGTGAACG	TACTCGTGAA	GGTAACGATT	100

	TATACCACGA	AATGATGGAA	ACTGGTGTCA	TTAAACTTGA	AGGTGACTCC	150
	AAGTGTGCTC	TTGTATTTCGG	TCAAATGAAC	GAACCTCCTG	GTGCTCGTGC	200
	CCGTGTTGCT	TTAACTGGTT	TAACCATTGC	TGAATACTTC	CGTGATGAAG	250
	AAGGTCAAGA	TGTGTTACTT	TTCATTGATA	ACATTTTCCG	TTTCACTCAA	300
5	GCTGGTTCTG	AAGTATCTGC	CCTTTTAGGT	CGTATTCCAT	CTGCTGTAGG	350
	TTACCAACCC	ACTTTATCTA	CTGATATGGG	TGGTATGCAA	GAACGTATTA	400
	CTACTACCAA	GAATGGTTCC	ATTACCTCTG	TACARGCCGT	CTACGTCCCC	450
	GC					452

10

2) INFORMATION FOR SEQ ID NO: 1640

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 783 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462
 25 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640

	ACGCCCTTAC	GGTAAAACAA	AGCAACGAAA	ACGGAAGCAT	GAACCTTAACA	50
30	TTTGAAGTTG	CACTTCATTT	AGGTGATGAT	ACAGTTCGTA	CAGTTGCGAT	100
	GTCTTCCACA	GATGGACTTG	TTCGTGGCAC	AGAAGTAGAA	GATACTGGTA	150
	AAGCAATCTC	TGTACCAGTT	GGTGATGCAA	CACTTGGTCG	TGTATTCAAC	200
	GTATTAGGTG	ATGCAATTGA	CTTAGATGGT	GAACCTCCTG	CGGATGTACA	250
	CCGTGATCCA	ATTCACCGTC	AAGCACCTGC	ATTCGAAGAA	TTATCTACTA	300
35	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	ACTTGCTCCT	350
	TACATTAAGG	GTGGTAAGAT	CGGCCTATTC	GGTGGTGCCG	GCGTAGGTAA	400
	AACAGTATTA	ATTCAGAAGT	TAATTAACAA	CATCGCACAA	GAGCACGGTG	450
	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTAATCGTGA	GGGTAATGAC	500
	TTATACCATG	AAATGAGCGA	TTCTGGCGTA	ATCAAGAAAA	CTGCGATGGT	550
40	ATTCGGACAA	ATGAATGAGC	CACCTGGAGC	ACGTCAACGT	GTTGCATTAA	600
	CAGGTTTAAC	AATGGCTGAG	CATTTCCGTG	ATGAGCAAGG	ACAAGACGTA	650
	CTTCTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	GTTCTGAAGT	700
	ATCTGCCCTT	CTTGGTTCGT	TGCCATCTGC	GGTAGGTTAC	CAACCAACAC	750
	TTGCAACAGA	AATGGGTCAA	TTACAAGAGC	GTA		783

45

2) INFORMATION FOR SEQ ID NO: 1641

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL NRS-319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641

10 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT 50
 TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA 100
 CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA 150
 GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG 200
 15 TGTATTCAAC GTATTAGGTG ATGCAATTGA CTTAGATGGT GATGTTCTTG 250
 CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA 300
 CTATCTACTA AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT 350
 ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG 400
 GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA 450
 20 GAACACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA 500
 GGGTAACGAC TTATACCATG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA 550
 CTGCGATGGT ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT 600
 GTTGCAATTAA CAGGTTTAAC AATGGCTGAA CATTTCCGTG ATGAGCAAGG 650
 ACAAGACGTA CTATTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCAG 700
 25 GTTCTGAAGT ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC 750
 CAACCAACAC TTGCAACAGA AATGGGTCAA TTACAAGAGC GTATTACATC 800
 TACAAATAAA GGATCTATCA CGT 823

30

2) INFORMATION FOR SEQ ID NO: 1642

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL BD-15

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642

50 GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAAAG 50
 CAACGAAAAC GGAGCAAACA TTAACCTAAC ATTTGAAGTT GCACTTCATT 100
 TAGGTGATGA TACAGTTCGT ACAGTTGCGA TGTCTTCCAC AGATGGACTT 150
 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
 TGGTGATGTA AACTTGGTC GTGTATTCAA CGTATTAGGT GATGCAATTG 250
 ACTTAGATGG TGAAGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
 CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350

	TTGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAAG	GGTGGTAAGA	400
	TTGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACAGTATT	AATTCAGGAA	450
	TTAATTAACA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCCGG	500
	TGTAGGTGAG	CGTACTCGTG	AAGGTAACGA	CTTATACCAC	GAAATGAGCG	550
5	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCATTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCGGT	GATGAGCAAG	GACAAGACGT	ACTACTGTTC	ATCGATAACA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	750
	ATGCCATCTG	CGGTAGGTTA	CCAGCCAACA	CTTGCAACAG	AAATGGGTCA	800
10	ATTACAAGAG	CGTATTACAT	CTACAAATA			829

2) INFORMATION FOR SEQ ID NO: 1643

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycooides*
 (B) STRAIN: NRRL BD-10

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643

30	AATCTACAAT	GCCCTTACGG	TAAAACAAAG	CAACGAAAAC	GGAGCAAGCA	50
	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	TAGGTGATGA	CACAGTTCGT	100
	ACAGTTGCGA	TGTCTTCCAC	AGATGGACTT	GTTTCGTGGCA	CAGAAGTAGA	150
	AGATACTGGT	AAACCAATCT	CTGTACCGGT	TGGTGATGCA	ACACTTGGTC	200
	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	ACTTAGATGG	TGAAGTTCCT	250
35	GCGGATGTAC	GCCGTGATCC	AATTCACCGT	CAAGCACCTG	CGTTCGAAGA	300
	GTTATCTACG	AAAGTAGAAA	TTCTTGAAAC	TGGTATTAAA	GTAGTAGACT	350
	TACTTGCTCC	TTACATTAAA	GGTGGTAAAA	TCGGTCTATT	CGGTGGTGCC	400
	GGTGTAGGTA	AAACAGTATT	AATCCAGGAA	TTAATTAACA	ACATCGCACA	450
	AGAGCACGGT	GGTATTTCTG	TATTCGCTGG	TGTAGGTGAG	CGTACTCGTG	500
40	AAGGTAATGA	CTTATACCAC	GAAATGAGCG	ATTCTGGCGT	AATCAAGAAA	550
	ACAGCGATGG	TATTCGGACA	AATGAACGAG	CCACCTGGTG	CACGTCAACG	600
	TGTTGCATTA	ACAGGATTAA	CAATGGCTGA	ACATTTCCGT	GATGAGCAAG	650
	GACAAGACGT	ACTATTGTTC	ATCGATAACA	TCTTCCGTTT	CACGCAAGCG	700
	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	ATGCCATCTG	CGGTAGGTTA	750
45	CCAACCAACT	CTTGCAACAG	AAATGGGTCA	ATTACAAGAG	CGTATTACAT	800
	CTACAAATAA	AGGATCTATC	ACG			823

50 2) INFORMATION FOR SEQ ID NO: 1644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644

	GGAAAGCTAC	CTGAAATCTA	CAATGCCCTT	AGAATTAAAC	AAGACGCAGT	50
	TAACTTAACT	TTAGAAGTTG	CACTTCACTT	AGGTGATGAT	ACAGTTCGTA	100
15	CAGTTGCGAT	GTCTTCCACA	GACGGACTTG	TTCGTGGTAC	TGCAGTAGAA	150
	GATACTGGCA	AAGCGATTTC	TGTTCCAGTT	GGTGATGCAA	CACTTGGTTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGT	GAGGTTCCAG	250
	CAGATGTACG	CCGTGATCCA	ATTCACCGTC	AAGCACCTGC	ATTCGAAGAG	300
	TTATCTACAA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
20	ACTTGCTCCT	TACATTAAAG	GTGGTAAAAT	CGGTCTATTC	GGTGGTGCCG	400
	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTACTCGTGA	500
	AGGTAACGAC	TTATACCATG	AAATGAGCGA	TTCTGGCGTA	ATCAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGTGC	ACGTCAACGT	600
25	GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
	ACAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
	GTTCTGAA					708

30

2) INFORMATION FOR SEQ ID NO: 1645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
- (B) STRAIN: ATCC 35567

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645

	GTACGATGCG	CTTGAAGTTC	AAAACGATGT	CAAAC TAGTG	CTGGAAGTTC	50
	AACAGCAGCT	CGGTGGTGGT	GTCGTTCTGT	GTATCGCTAT	GGGTACCTCA	100
	GATGGCCTAA	GCCGCGGTCT	GAAAGTACTT	GATTTAGAAC	ACCCTATCGA	150
50	AGTTCCTGTC	GGTGTGGCAA	CTCTGGGCCG	TATTATGAAC	GTGCTTGGTG	200
	AGCCTATCGA	TATGAAGGGT	GACATTGGTG	AAGAAGAGCG	TTGGGCTATC	250
	CATCGCGCTG	CACCAAGCTA	CGAAGATTTA	TCCAGTGCTA	ACGAACTGCT	300
	GGAAACGGGC	ATCAAGGTTA	TCGACCTGAT	TTGTCCGTTT	GCCAAAGGCG	350

```

GTAAAGTTGG TCTGTTTGGT GGTGCCGGCG TAGGTAAAAC GGTAAACATG 400
ATGGAGCTGA TTCGTAATAT TGCGACTGAG CACTCAGGTT ACTCTGTATT 450
TGCCGGCGTT GGTGAGCGTA CTCGTGAGGG TAATGACTTC TACCACGAAA 500
TGACAGAATC TAACGTATTA GACAAAGTAT CTCTGGTTTA TGGCCAAATG 550
5 AATGAGCCAC CGGGAAACCG TCTGCGCGTT GCGTTAACCG GCCTGACCAT 600
GGCGGAAAAA TTCCGTGATG AAGGCCGTGA CGTTCTGCTG TTTATCGATA 650
ACATTTATCG TTATACCTTA GCCGGTACAG AAGTATCAGC ACTGTTAGGT 700
CGTATGCCAT CAGCGGTAGG TTACCAACCA ACGCTGGCGG AAGAGATGGG 750
TACACTGCAA GAACGTATCA CYTCAACC 778
10

```

2) INFORMATION FOR SEQ ID NO: 1646

```

15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 806 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Buttiauxella agrestis
25 (B) STRAIN: ATCC 33320

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646

```

GATGCCGTAC CAAAAGTGTA CGACGCTCTT GAGGTTACAA ATGGTAAAGA 50
30 CCGTCTGGTG CTGGAAGTTC AGCAACAGTT AGGTGGTGGC GTAGTGCGTA 100
CTATCGCCAT GGGTACTTCT GATGGTTTGC GTCGTGGTCT GGAAGTTTCT 150
AACCTCGATC ACCCAATTGA AGTGCCAGTA GGTAAAGCAA CTCTGGGCCG 200
TATCATGAAC GTCCTGGGCG AGCCTATCGA CATGAAAGGC GATATCGGCG 250
AAGAAGAGCG TTGGGCGATT CACCGTGCTG CTCCTAGCTA CGAAGAACTG 300
35 TCTAGCTCCC AGGATCTGCT GGAAACCGGC ATCAAAGTAA TGGACCTGAT 350
TTGCCCGTTC GCTAAGGGTG GTAAAGTCGG TCTGTTTCGGT GGTGCGGGTG 400
TGGGTAAAAC TGTAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCAGTGTT TGCAGGCGTG GGGGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCATGAAA TGACCGATTC CAACGTTCTG GACAAAGTAT 550
40 CACTGGTTTA TGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
GCGTTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
CGTTCTGCTG TTCGTTGATA ACATTTACCG TTATACCCTG GCCGGTACAG 700
AAGTATCTGC GCTGCTGGGT CGTATGCCAT CTGCGGTAGG TTACCAGCCA 750
ACTCTGGCAG AAGAGATGGG TGTTTTGCAG GAGCGTATTA CCTCCACCAA 800
45 AACTGG 806

```

2) INFORMATION FOR SEQ ID NO: 1647

```

50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1122 bases
    (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
(B) STRAIN: ATCC 36586

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647

	GAAACCGTTG	TTGACACTGG	TTCCCCAATC	ACCGTCCCAG	TTGGTCGTGA	50
	AACCTTGGGT	CGTATCATTA	ACGTTATCGG	TGAACCAATC	GATGAACGTG	100
	GTCCAATCAA	CACCAAGCAA	AGAAACCCAA	TCCATGCTGA	TCCTCCTTCA	150
15	TTTGCTGAAC	AATCCACTTC	TGCTGAAGTT	TTAGAAACCG	GTATTAAAGT	200
	TGTCGATTTA	TTGGCTCCTT	ATGCCAGAGG	TGGTAAAATT	GGTTTATTCG	250
	GTGGTGCCGG	TGTCGGTAAA	ACCGTCTTTA	TCCAAGAATT	GATTAACAAC	300
	ATTGCTAAAG	CTCATGGTGG	TTTCTCAGTC	TTCACCGGTG	TCGGTGAAAG	350
	AACCAGAGAA	GGTAACGATT	TATACCGTGA	AATGAAAGAA	ACCGGTGTCA	400
20	TTAACTTGGA	AGGTGACTCT	AAAGTCGCTT	TAGTCTTCGG	TCAAATGAAC	450
	GAACCTCCAG	GTGCTAGAGC	CCGTGTTGCC	TTAACCGGTC	TAACCATTGC	500
	TGAATACTTC	AGAGATGAAG	AAGGTCAAGA	TGTCTTGTTA	TTCGTTGATA	550
	ACATTTTCAG	ATTCACCCAA	GCTGGTTCAG	AAGTCTCTGC	CTTATTAGGT	600
	CGTATTCCAT	CTGCTGTCGG	TTATCAACCA	ACCTTGGCCA	CTGATATGGG	650
25	TTTGTTGCAA	GAACGTATCA	CCACCACCAG	AAAAGGTTCC	GTCACTTCTG	700
	TCCAAGCTGT	TTATGTCCCA	GCTGATGATT	TGACTGATCC	TGCCCCAGCC	750
	ACCACTTTCG	CGCATTTGGA	TGCTACTACT	GTCTTGTCTC	GTGGTATCTC	800
	AGAATTGGGT	ATCTACCCAG	CTGTGCATCC	ATTGGATTCC	AAATCAAGAT	850
	TATTAGATGC	CGCTGTTGTT	GGTCAAGAAC	ATTACGATGT	TGCTACTCAA	900
30	GTTCAACAAA	CTTTACAAGC	CTACAAATCT	TTACAAGATA	TTATCGCTAT	950
	TTTAGGTATG	GATGAATTAT	CAGAACAAGA	TAAATTGACC	GTTGAAAGAG	1000
	CTAGAAAGAT	CCAACGTTTC	TTATCTCAAC	CATTTGCTGT	CGCTGAAGTT	1050
	TTCAGGTGTA	TTCCAGGTAG	ATTAGTTAGA	TTGAAAGAAA	CCGTTGCTTC	1100
	ATTCAGAGAC	GTTTTAGCTG	GT			1122

35

2) INFORMATION FOR SEQ ID NO: 1648

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: ATCC 700677

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648

	TACGTCTCTT	ACCCTGACGA	TGATTTGCAA	GTCGCATCTA	CGGTCGTAGA	50
	TGTTTCAAAT	GGTAAAGTCA	TCGCCCAACT	TGGAGCTCGT	CACCAAGCAA	100
	GTAACGTTTC	ATTTGGTACC	AACCAAGCTG	TGGAAACCAA	TCGTGACTGG	150
	GGATCAACTA	TGAAACCAAT	CACAGACTAT	GCTCCTGCCT	TGGAGTACGG	200
5	TGTCTACGAT	TCAACTGCTA	CTATCGTTCA	CGATGAGCCC	TATAACTACC	250
	CTGGGACAGA	TATCCCTCTC	TATAACTGGG	ATCGAGCATA	TTTCGGTAAT	300
	ATTACTCTGC	AATATGCCCT	TCAACAATCT	CGTAACGTAC	CTGCCGTTGA	350
	AACACTAAAC	AAGGTCGGTC	TAGATAAGGC	TAAAACCTTC	CTTAATGGTC	400
	TTGGTATCGA	CTATCCAAGC	ATGCATTATG	CAAACGCCAT	TTCAAGTAAT	450
10	ACAACTGAAT	CCAACAAAAA	ATATGGTGCA	AGTAGTGAAA	AAATAGCTAC	500
	CGCCTATGCC	GCATTCGCAA	ATGGTGGTAT	TTACCACAAA	CCAATGTACA	550
	TCAATAAAGT	TGTCTTTAGC	GATGGTAGCG	AAAAAGAATT	TTCTGACCCT	600
	GGCACAAGAG	CCATGAAAGA	AACGACTGCT	TACATGATGA	CAGAAATGAT	650
	GAAAACAGTC	TGGACGTACG	GAAC TGGTCG	TGGTGCCTAC	CTGCCTTGGC	700
15	TTCCTCAAGC	TGGTAAAACA	GGTACCTCTA	ACTATACTGA	CGAAGAAATT	750
	GAAAAGTATA	TCAAGAACAC	TGGTTACGTA	GCTCCAGATG	AAATGTTTGT	800
	GGGTTATACC	CGT				813

20

2) INFORMATION FOR SEQ ID NO: 1649

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649

	ATTAATGAAG	CTATTGTTGT	TAATTATGAA	TTAGAAGGAA	AAGAATGCAA	50
	GCTAGTTCTT	GAAGTAGCTG	CACATTTAGG	CGATAATAAA	GTAAGAACCA	100
	TCGCTATGGA	TATGACAGAT	GGTCTTGTTA	GAGGTTTAAC	AGCCGTCGCA	150
40	ACTGGAAATC	CAATTAGTGT	TCCAGTAGGC	GAAAAAGTTC	TTGGAAGAAT	200
	TTTTAATGTA	ACGGGTGATT	TGATTGATGA	GGGCGAAGAA	ATCAATTTTG	250
	ATAAGCACTG	GTCAATTCAT	AGAGATCCAC	CTCCATTTGA	AGAACAAAGT	300
	ACAAAAAGCG	AAATCTTTGA	AACAGGTATA	AAGTTTGTTG	ATTTGCTAGC	350
	TCCTTATGCT	AAAGGTGGAA	AAGTTGGTCT	TTTTGGTGGT	GCAGGTGTTG	400
45	GTAAAACCGT	TATTATTATG	GAATTAATTC	ACAATGTTGC	ATTTAAACAT	450
	AGCGGATATT	CTGTTTTTGC	AGGTGTTGGC	GAAAGAAGTC	GTGAGGGTAA	500
	TGACCTTTAC	AATGAAATGA	AAGAAAGTAA	TGTATTAGAT	AAAGTTGCAT	550
	TGTGTTATGG	TCAAATGAAT	GAACCACCAG	GGGCAAGAAA	TCGTATAGCT	600
	TTAACAGGTC	TTACTATGGC	TGAGTATTTT	AGAGATGAAA	TGGGACTTGA	650
50	TGTTTTAATG	ATTATTGATA	ATATTTTTCAG	ATTTTCTCAA	TCAGGCTCAG	700
	AAATGTCAGC	ACTTTTtagga	AGAATTCCTT	CAGCTGTTGG	TTATCAACCA	750
	ACCTTAGCTA	GTGAAATGGG	TAAGTTCCAA	GAAAGAATTA	CTTCAACCAA	800
	GAAAGGATCT	ATT				813

2) INFORMATION FOR SEQ ID NO: 1650

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650

GGTGGGGAAG	ACTGTGTTCA	TTCAGGAATT	GATTGTAAGT	TCTGTTATCA	50
ACTAAAGCCG	ACAGCGGTTG	CTGATATGCT	CTAGAACAAC	ATTGCTAAGG	100
CTCACGGTGG	TTACTCCGTG	TTCAGTGGTG	TCGGTGAGCG	TACCCGTGAG	150
GGTAACGATT	TGTACCATGA	AATGCAAGAG	ACCCGTGTCA	TTCAACTCGA	200
CGGAGAGTCC	AAGGTCGCTC	TTGTCTTCGG	TCAAATGAAC	GAGCCCCCTG	250
GTGCCCCGTG	CCGTGTTGCC	CTTACCGGTT	TGACCATTGC	TGAATACTTC	300
CGTGACGAGG	AAGGCCAAGA	CGGTAGGCTT	CATGCTTCTA	TCGCTAGGGG	350
CGTGTGATAC	AGGAGGCTAA	TCGCTTTTCT	AGTGCTTCTC	TTTATTGACA	400
ACATTTTCCG	TTTCACTCAA	GCTGGTTCTG	AAGTGTCTGC	CTTGCTCGGT	450
CGTATTCCTT	CCGCTGTCGG	TTACCAACCT	ACTCTCGCCG	TCGACATGGG	500
TGTTATGCAG	GAACGTATCA	CCACCACCAC	CAAGGGATCC	ATTACTTCAG	550
TGCARGCCGT	CTACGTCCCC				570

2) INFORMATION FOR SEQ ID NO: 1651

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651

TGTCTTCATC	CAGGAGTTAA	TTGTACGTTT	TTTGTCTGCC	TACTATAATA	50
GACGAAGAAA	TATTTTGATT	TATTTTCTA	ATAATTCAA	TAGAACAACA	100
TTGCCAAAGC	CCACGGTGGT	TACTCTGTCT	TCAGTGGTGT	TGGCGAGCGG	150
ACCCGTGAAG	GAAACGATCT	GTACCACGAA	ATGCAGGAGA	CCCGTGTCAT	200
CCAGCTCGAT	GGCGAGTCCA	AGGTCGCCCT	CGTCTTCGGT	CAAATGAACG	250
AACCCCCCGG	AGCCCGTGCC	CGTGTTGCCC	TCAGTGGTCT	GACCGTTGCT	300

	GAATACTTCC	GTGACGAGGA	AGGTCAAGAT	GGTGCGTATA	TATATATTTCG	350
	CCAGTAATTT	GACTCGAAGC	TCCACTCACA	CATATATTAG	TGCTCCTCTT	400
	CATCGACAAC	ATTTTCCGCT	TCACCCAGGC	AGGTTCCGAA	GTGTCCGCCC	450
	TGCTCGGCCG	TATCCCCTCC	GCCGTCGGTT	ACCAGCCCAC	CCTCGCTGTC	500
5	GACATGGGTA	TGATGCAGGA	ACGTATCACC	ACCACCACCA	AGGGCTCCAT	550
	CACCTCCGTG					560

10 2) INFORMATION FOR SEQ ID NO: 1652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652

25	CCACAAGTGT	ACAGCGCCCT	TGAGGTTAAA	AATGGTGATG	CTCGTCTGGT	50
	GCTGGAAGTT	CAGCAGCAGC	TGGGCGGTGG	CGTGGTTCGT	ACCATCGCCA	100
	TGGGTTCTTC	AGACGGCCTT	AAGCGTGGTC	TGGAAGCCGT	TGACCTTCAG	150
	CACCCAATTG	AAGTACCGGT	AGGTACTGCC	ACACTTGGCC	GTATCATGAA	200
30	CGTGCTGGGT	GAGCCGATCG	ATATGAAAGG	CGACATTGGC	GAAGAAGAGC	250
	GCTGGGCGAT	TCACCGCTCT	GCACCTTCTT	ACGAAGATCA	GTCGAACTCT	300
	CAGGATCTGC	TGGAAACCGG	CATCAAGGTG	ATTGACCTGA	TGTGTCCGTT	350
	CGCCAAGGGC	GGTAAAGTCG	GCTTGTTTCG	TGGTGCGGGC	GTAGGTAAAA	400
	CCGTCAACAT	GATGGAGCTT	ATTCGTAACA	TTGCGGCTGA	GCACTCAGGT	450
35	TTCTCGGTAT	TTGCCGGTGT	GGGTGAGCGT	ACCCGTGAAG	GTAACGACTT	500
	CTACCACGAA	ATGACCGACT	CCAACGTTAT	CGACAAAGTT	TCGCTGGTCT	550
	ATGGTCAGAT	GAACGAGCCA	CCGGGTAACC	GTCTGCGCGT	TGCGCTGACC	600
	GGTCTGACCA	TGGCGGAGAA	GTTCCGTGAC	GAAGGTCGTG	ACGTACTGCT	650
	GTTTATCGAT	AACATCTATC	GTTACACCCT	GGCCGGTACT	GAAGTCTCCG	700
40	CTCTGCTGGG	TCGTATGCCT	TCTGCGGTAG	GTTACCAGCC	AACGCTGGCG	750
	GAAGAGATGG	GCGTTCTGCA	GGAACGTATC			780

45 2) INFORMATION FOR SEQ ID NO: 1653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653

	TGTGTTTCATT	CAGGAGCTGA	TTGTGAGTAC	CCCGGAGATT	TTCCTGCGAT	50
	TGCGCATGAA	GCAAGCGCTG	ACGTCCATCT	AGAACAACAT	CGCCAAGGCT	100
10	CACGGTGGTT	ACTCCGTGTT	CTGCGGTGTC	GGCGAGCGTA	CTCGTGAGGG	150
	TAACGATTTG	TACCACGAAA	TGCAGGAGAC	CGGTGTCATC	AACCTCGAGG	200
	GCGAGTCCAA	GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCCGGGA	250
	GCCCGTGCCC	GTGTCGCCCT	TACTGGTCTT	ACCGTCGCTG	AGTAAGTTTT	300
	GACAACCAGA	AGCGAGTATT	GCCACAATTA	CTGACTAAAA	ATCAAGATAT	350
15	TTCCGTGACG	AGGAGGGCCA	GGATGTGCTT	CTCTTCATTG	ACAACATTTT	400
	CCGTTTCACC	CAGGCCGGTT	CTGAGGTGTC	CGCTCTTCTC	GGCCGTATTC	450
	CCTCTGCCGT	CGGTTACCAG	CCCACTCTCG	CCGTCGACAT	GGGTATGATG	500
	CAGGAGCGTA	TCACCACCAC	CCAGAAGGGT	TCCATCACTT	CCGTC	545

20

2) INFORMATION FOR SEQ ID NO: 1654

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 564 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium moniliiforme*

(B) STRAIN: WSA-213

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654

	TGTGTTTATT	CAGGAGCTCA	TCAACAACAT	CGCCAAGGCC	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CCCGTGAGGG	TAACGATCTG	100
40	TACCACGAAA	TGCAGGAGAC	TTCCGTTATT	CAGCTTGATG	GCGAGTCCAA	150
	GGTTGCCCTG	GTTTTTCGGTC	AGATGAACGA	GCCCCCTGGA	GCTCGTGCCC	200
	GTGTCGCTCT	TACCGGGTAA	GTTGATAGAT	AGTGCCTTCC	CTTCCTGTTT	250
	CAACACCTCA	ACACCACCAC	TCCCCAAGAC	ATTGCTACTC	ATACTGCACC	300
	ATGATATTAT	ATTTACGCCT	CTTGGACGCT	AGCTAATGTT	GTATCGACAG	350
45	TTTGACTGTT	GCTGAGTACT	TCAGAGACGA	GGAGGGTCAG	GACGTGCTGC	400
	TTTTTCATTGA	CAACATTTTC	CGATTCACTC	AGGCCGGTTC	CGAGGTGTCT	450
	GCCCTTCTCG	GTCGTATCCC	CTCTGCCGTC	GGTTACCAGC	CCACTCTGGC	500
	CGTCGACATG	GGTGGTATGC	AGGAGCGTAT	TACCACCACC	ACCAAGGGTT	550
	CCATTACCTC	AGTC				564

50

2) INFORMATION FOR SEQ ID NO: 1655

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655

15	CGTACCGCGC	GTGTACGAGG	CTCTTGAGGT	ACAAAATGGT	AGTGAGAATC	50
	TGGTGCTGGA	AGTTCAGCAG	CAGCTCGGCG	GCGGTATTGT	TCGTACCATC	100
	GCCATGGGTT	CTTCCGACGG	TCTGCGTCGC	GGTCTGGAAG	TCAAAGACCT	150
	CGAGCATCCG	ATCGAAGTCC	CGGTAGGTAA	AGCAACGCTG	GGTCGTATCA	200
20	TGAACGTACT	GGGCCAACCG	GTAGACATGA	AAGGCGACAT	CGGCGAAGAA	250
	GAGCGTTGGG	CGATTCACCG	CGCAGCGCCT	TCCTACGAAG	AGTTGTCAAA	300
	CTCTCAGGAA	CTGCTGGAAA	CCGGCATCAA	AGTTATCGAC	CTGATGTGTC	350
	CGTTTGCGAA	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	400
	AAAACCGTAA	ACATGATGGA	GCTGATCCGT	AACATCGCGA	TCGAGCACTC	450
25	CGGTTACTCC	GTGTTTGCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	500
	ACTTCTACCA	CGAAATGACC	GACTCCAACG	TTATCGATAA	AGTATCCCTG	550
	GTGTATGGCC	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCGCT	600
	GACCGGCCTG	ACCATGGCTG	AGAAGTTCCG	TGACGAAGGT	CGTGACGTTT	650
	TGCTGTTCGT	CGATAACATC	TATCGTTACA	CCCTGGCCGG	TACTGAAGTA	700
30	TCCGCACTGC	TGGGTCGTAT	GCCTTCAGCG	GTAGGTTACC	AGCCGACTCT	750
	GGCGGAAGAG	ATGGGCGTTC	TGCAGG			776

2) INFORMATION FOR SEQ ID NO: 1656

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
(B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656

50	GTGTTTCATCC	AGGAGTTGAT	TGTAAGTGAT	TATATTCCCC	TAGAAAGAAA	50
	TGTTTTGAAC	AAAAGTCTCG	AATTAGAAAA	TTCTTTTCAG	ATACTAATTT	100
	ACTATAGAAC	AACATTGCCA	AGGCTCACGG	TGGTTACTCC	GTCTTCACCG	150

	GTGTCGGAGA	GCGAACCCGT	GAAGGAAACG	ATCTGTACCA	TGAAATGCAG	200
	GAAACTCGTG	TCATCCAAC	TGATGGCGAG	TCCAAGGTCG	CCCTGGTCTT	250
	CGGTCAGATG	AACGAGCCCC	CAGGTGCCCC	TGCCCCGTGT	GCTCTTACTG	300
	GTTTGACCAT	TGCTGAGTAC	TTCCGTGATG	AGGAAGGTCA	AGACGGTATG	350
5	TTCTTTAAAT	TAGATATCTT	CTGGAGAAAC	AGCGTCTAAC	AAATTCTTCC	400
	AGTGCTTCTC	TTCATCGACA	ACATCTTCCG	TTTCACTCAG	GCTGGTTCCG	450
	AAGTGTCTGC	CCTGCTTGGT	CGTATTCCAT	CTGCCGTCGG	TTACCAACCC	500
	ACTCTTGCCG	TCGACATGGG	TGGTATGCAG	GAACGTATTA	CCACCACCAA	550
	GAAGGGATCC	ATTACCTCCG	TC			572

2) INFORMATION FOR SEQ ID NO: 1657

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
- (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657

	GCCTAAAGTG	TATAACGCAC	TTGAGGTGAA	AGGCGGTGCC	ACTAAACTGG	50
30	TACTGGAAGT	TCAGCAGCAG	CTAGGCGGCG	GCGTTGTACG	CTGTATCGCT	100
	ATGGGTACTT	CTGACGGTCT	GCGTCGCGGA	CTGGACGTTG	TTGACCTGGA	150
	GCACCCGATT	GAAGTCCAG	TAGGTAAAGC	GACCTTAGGC	CGCATTATGA	200
	ACGTACTGGG	TGAGCCAATT	GATATGAAGG	GTGATATCGG	CGAAGAAGAT	250
	CGCTGGGCTA	TTCACCGTGA	AGCTCCAAGC	TACGAAGAAC	TGTCTAACTC	300
35	GCAAGAACTG	CTGGAAACCG	GTATCAAGGT	AATGGACTTG	ATTTGTCCGT	350
	TCGCTAAGGG	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCGGG	TGTTGGTAAA	400
	ACAGTAAACA	TGATGGAGCT	GATCCGTAAAC	ATCGCGATCG	AGCACTCAGG	450
	TTACTCTGTA	TTTGCCGGCG	TGGGTGAACG	TACTCGTGAG	GGTAACGACT	500
	TCTACCACGA	AATGACCGAC	TCCAACGTAT	TGGACAAAGT	ATCACTGGTT	550
40	TATGGCCAGA	TGAACGAGCC	ACCAGGAAAC	CGTCTGCGCG	TTGCGCTGAC	600
	CGGTCTGACT	ATGGCTGAGA	AGTTCCGTGA	CGAAGGTCGT	GACGTACTGC	650
	TGTTTCATCGA	TAACATCTAC	CGTTATACCT	TGGCCGGTAC	CGAAGTATCT	700
	GCACTGCTGG	GTCGTATGCC	TTCTGCGGTA	GGTTATCAGC	CAACGCTGGC	750
	GGAAGAGATG	GGTGTCTGTC	AAGAACGTAT	CACCTCTACC		790

2) INFORMATION FOR SEQ ID NO: 1658

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658

```

10 TGTCTTCATT CAGGAGCTTA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
   ACTCCGTCTT CACTGGTGTG GGAGAGCGCA CTCGTGAGGG AAACGACTTG      100
   TATCACGAGA TGCAAGAGAC TTCCGTTATC CAGCTCGAAG GCGAATCCAA      150
   GGTGCCCCTC GTCTTCGGTC AAATGAACGA GCCTCCGGGT GCTCGTGCTC      200
15 GTGTTGCTCT CACCGGTCGT AAGTGCTCCT TCCCAGATTT CTCTTCCCCA      250
   GTTCTGAC CCACCTTTTTC CTTCCACCAC CATTCTACTG GGTAGGACCA      300
   AGATAGCACT GCCTATTCTG GTGCCTTCCT ACCGCCTACT CTACTGCCTA      350
   TTCCACCACC TTTTCTACCG CCTCTTCTAC TTGCTATTGT ATACTAACTT      400
   ACTCAAACAG TTACTATTGC TGAGTACTTC CGTGACGCTG AGGGCCAGGA      450
20 TGTGCTTCTC TTCATCGACA ACATTTTCCG TTTCACCCAG GCCGGTTCCG      500
   AGGTGTCCGC TCTTCTCGGT CGTATCCCCT CCGCCGTCGG TTACCAGCCC      550
   ACCCTTGCCG TCGACATGGG TGGTATGCAG GAGCGTATCA CCACCACCAA      600
   GAAGGGATCC ATTACCTCCG TC                                     622

```

25

2) INFORMATION FOR SEQ ID NO: 1659

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 794 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659

```

   GACGCTGTAC CTCAGGTGTA CGATGCACTG ACAGTTGAGG GTGCTGAGCT      50
   GGTACTGGAA GTGCAGCAGC AGCTGGGTGG TGGTGTGTT CGCTGTATCG      100
45 CGATGGGTGC CTCTGATGGC CTCAAGCGCG GTCTGAAAGC GCACAATACT      150
   GGTGCTCCTA TCACTGTACC GGTGGGTGTG GAAACACTGG GCCGGATCAT      200
   GGATGTGTTG GGTAACCCGA TTGACCAGAA AGGTCCAATC GGTGAACAAG      250
   ATCGCTGGGT GATCCACCGT GAAGCACCAA GCTACGAAGA TCAGGCTAAC      300
   AGCACTGAAC TGCTGGAAAC CGGTATCAAG GTTATCGACC TGGTATGCCC      350
50 GTTTGCGAAA GCGGGTAAAG TCGGTCTGTT CGGTGGTGCC GGTGTAGGTA      400
   AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC      450
   GGTTATTCCG TGTTTGCGGG CGTGGGTGAG CGTACCCGTG AAGGTAACGA      500
   CTTCTACCAC GAAATGACAG ACTCCAACGT ACTGGACAAA GTATCCCTGG      550

```

	TGTACGGTCA	GATGAACGAG	CCGCCAGGTA	ACCGTCTGCG	CGTAGCACTG	600
	ACCGGCCTGA	CCATTGCGGA	GAAATTCCGT	GATGAAGGTC	GTGACGTACT	650
	GCTGTTCATC	GATAACATCT	ACCGTTATAC	CCTGGCGGGG	ACCGAAGTAT	700
	CGGCACTGCT	GGGCCGTATG	CCTTCTGCGG	TAGGTTATCA	GCCAACGCTG	750
5	GCGGAAGAGA	TGGGTGTACT	GCAAGAGCGT	ATTACCTCTA	CCCG	794

2) INFORMATION FOR SEQ ID NO: 1660

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
 (B) STRAIN: ATCC 8071

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660

25	AGGTATATGA	CGCTSTGAAG	ATCACAGGTG	AAGGCGCCTG	TAATGGTTTG	50
	GTGCTGGAAG	TTCAGCAACA	GCTAGGCGGT	GGTGTAGTTC	GTACTATCGC	100
	TATGGGTTCT	TCTGATGGTC	TGCGTCGTGG	TCTTGAGGTT	GTAACTCAG	150
	GTTACCTAT	TTCTGTTTCT	GTTGGTACCG	CCACGCTTGG	CCGTATCATG	200
	AACGTATTAG	GTGAGCCTAT	TGATGAAGCG	GGTCCAATCG	GTGAAGAAGA	250
30	GCGTTATGTT	ATTCACCGTG	CAGCACCTTC	ATATGAAGAT	CAATCGAACA	300
	CTACTGAACT	GTTAGAGACA	GGTATCAAGG	TTATTGACCT	TGTTTGTTCCA	350
	TTGCTAAGG	GTGGTAAAGT	AGGTCTGTTC	GGTGGTGCGG	GTGTTGGTAA	400
	AACAGTTAAC	ATGATGGAAC	TGATTAACAA	CATCGCTAAA	GCTCACTCGG	450
	GTCTTTCCGT	GTTGCGCCGT	GTGGGTGAAC	GTACTCGTGA	AGGTAACGAC	500
35	TTCTACTACG	AGATGAAAGA	TTCTGGCGTT	CTCGACAAAG	TGGCCATGGT	550
	TTATGGTCAG	ATGAACGAGC	CACCAGGAAA	CCGTTTACGC	GTAGCACTGT	600
	CAGGTCTGAC	AATGGCTGAG	AAGTTCCGTG	ACGAAGGTCG	TGACGTATTG	650
	TTGTTTCGTT	ACAACATCTA	CCGTTATACC	TTAGCCGGTA	CTGAAGTATC	700
	TGCACTGTTA	GGCCGTATGC	CTTCTGCGGT	AGGTTATCAA	CCAACATTGG	750
40	CTGAAGAAAT	GGGCGTTCTG	CAAGAGCGTA	TTACTTCAAC	TAAGACGGG	799

2) INFORMATION FOR SEQ ID NO: 1661

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661

TGGGAAGCGA AAATCCTG

18

5.

2) INFORMATION FOR SEQ ID NO: 1662

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 774 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662

	CTATGCCTCA	AACTAGAGAG	CATATCTTGC	TATCTCGCCA	AGTAGGCGTT	50
	CCATATATCG	TTGTATTTAT	GAACAAAGCC	GATATGGTCG	ATGACGCTGA	100
25	GCTTCTTGAG	CTAGTCGAGA	TGGAAATTCG	CGAGCTTCTT	AACGAGTACA	150
	ACTTCCCTGG	CGATGATACT	CCTATCATAT	CAGGTTCTGC	TCTTAAAGCC	200
	CTCGAAGAGG	CTAAAGCAGG	CGTTGATGGC	GAGTGGTCAG	CAAAAGTTCT	250
	TGAGCTTATG	GATAAAGTCG	ATGAGTATAT	CCCAACTCCA	GTTCGTGCTA	300
	CCGATAAAGA	CTTCCTGATG	CCTATCGAAG	ACGTTTTCTC	TATCTCAGGT	350
30	CGTGGAACGG	TCGTTACTGG	TAGGATCGAA	AAAGGTGTCG	TAAAAGTTGG	400
	CGATACTATC	GAGATCGTTG	GTATCAAACC	TACTCAAAC	ACGACAGTTA	450
	CTGGCGTTGA	GATGTTTAGG	AAAGAGATGG	AACAAGCGCA	GGCCGGTGAT	500
	AACGTAGGTG	TTCTTTTAAG	AGGTACTAAA	AAAGAAGACG	TCGAGCGCGG	550
	CATGGTTCTT	TGTAAGCCAA	AATCAATCAC	TCCTCATACA	AAATTTGAGG	600
35	GTGAGGTTTA	TATCCTAACA	AAAGAGGAAG	GCGGACGCCA	CACTCCATTC	650
	TTTAACAAC	ATAGACCACA	ATTTTATGTA	AGAACAACAG	ACGTTACAGG	700
	TTCTATCACA	CTTCAGAAAG	GAAGTGAAG	GGTTATGCCT	GGAGATAATG	750
	TCAGAATTTT	CGTTGAACTC	ATCG			774

10

2) INFORMATION FOR SEQ ID NO: 1663

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*

(B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663

5	TTCTGCGGCT	GACGGCCCAA	TGCCACAAAC	TAGAGAGCAC	ATCTTGCTAT	50
	CTCGCCAAGT	AGGCGTTCCG	TATATCGTTG	TTTTTATGAA	CAAAGCCGAT	100
	ATGGTCGATG	ATGCCGAGCT	TCTTGAGCTG	GTTGAGATGG	AGATTCGCGA	150
	GCTTCTAAAC	GAGTATGATT	TCCCTGGTGA	CGATACTCCA	ATCGTAGCAG	200
	GCTCTGCTCT	TCAAGCTCTT	AATGAAGCCA	AAGCCGGAAC	AGAAGGCGAG	250
10	TGGTCTGCAA	AAATTCTTGA	GCTTATGGCT	AAAGTTGACG	AGTATATCCC	300
	GACTCCGGTT	CGTGCAACGG	ATAAAGACTT	CTTGATGCCT	ATTGAGGACG	350
	TTTTCTCTAT	CTCCGGTCGC	GGCACCGTCG	TTACCGGCAG	AATCGAAAAA	400
	GGTATCGTAA	AAGTCGGTGA	TACTATCGAG	ATCGTAGGTA	TCCGCGATAC	450
	TCAAACAAC	ACCGTTACCG	GCGTTGAGAT	GTTTCAGAAAA	GAGATGGATC	500
15	AAGGCGAAGC	GGGCGATAAC	GTAGGCGTTC	TTCTAAGAGG	CACTAAAAAA	550
	GAAGACGTTG	AGCGCGGTAT	GGTTCTTTGC	AAACCTAAAT	CAATCACTCC	600
	TCACACTAAA	TTTGAGGGAG	AGGTTTATAT	CTTAACATAA	GAGGAAGGCG	650
	GACGCCATAC	TCCATTCTTT	AATAACTATA	GACCGCAGTT	TTATGTAAGA	700
	ACTACCGACG	TTACCGGTTT	TATCACTCTT	CCGGAAGGAA	CAGAGATGGT	750
20	TATGCCTGGC	GATAACTTAA	AGATAAGCGT	TGAGCTTATC	G	791

2) INFORMATION FOR SEQ ID NO: 1664

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664

40	CGACGGACAG	ATGCCCCAGA	CCAGGGAGCA	CTTGCTCCTC	GCCCGCCAGG	50
	TCGGTGTCAA	GCGCATTGTC	GTCTTCGTCA	ACAAGGTCGA	TGCCATTGAG	100
	GACAAGGAGA	TGTTGGAGCT	CGTCGAGATG	GAGATGCGTG	AGCTTCTCTC	150
	CAGCTACGGC	TTCGAGGGTG	ACGACACTCC	CATCGTCATG	GGTTCCGCCC	200
	TTTGCGCCAT	TGAGGGCCGC	GAGCCCGACA	TTGGTGTCGA	GAAGATTGAC	250
45	GAGCTCCTCG	AGCACGTCGA	CACCTGGATC	CCCACCCCCG	AGCGTGACAT	300
	CGCCAAGCCT	TTCTTCATGT	CCGTTGAGGA	CGTCTTCTCC	ATTCCCGGCC	350
	GTGGTACCGT	CGCTTCTGGC	CGTGTCGAGC	GTGGTGTCCT	GAAGAAGGAT	400
	TCCGAAGTCG	AGCTTGTCGG	CAAGAACAAG	AACCCCATCA	AGACCAAGGT	450
	TACCGACATC	GAGACCTTCA	AGAAGTCTTG	CGACGAGTCC	CGCGCTGGTG	500
50	ACAACCTCCGG	TCTCCTTCTC	CGTGGTGTCA	AGCGTGACGA	TGTCCTCCGT	550
	GGCATGGTTCG	TTGTCCAGCC	CGGCACCACC	AAGGCCACA	AGAAGTTCCT	600
	TGCCTCCATG	TACGTCCTCA	CCAAGGAGGA	GGGTGGCCGC	CACACTGGTT	650
	TCGCCAACAA	CTACAAGCCC	CAGATGTTCA	TCCGTACCGC	CGATGAGGCC	700

GCCACTCTTA	CCTGGCCCGA	GGGTACCGAG	GAGGACAAGA	TGGTCATGCC	750
CGGTGACAAT	GTCGAGATGA	TCTGCGAGAT	CCACAAGCCC	ATTGCCGTCG	800
AGCAAGGCCA					810

5

2) INFORMATION FOR SEQ ID NO: 1665

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665

CAGTACAGGT AGACTTCTG

19

20

2) INFORMATION FOR SEQ ID NO: 1666

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Microsporum audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666

ATGATTGCGA	AACCTACTTG	CTGTGGAAGA	ATTTGGATAT	TCTAACATTT	50
CTCTAGGCCT	CAAACCAGAG	AGCATCTGCT	CCTTGCCCGC	CAGGTCGGTG	100
TTCAGAAGCT	CGTCGTTTTT	GTAAACAAGG	TCGACGCTGT	TGAGGACCCA	150
GAGATGTTGG	AACTTGTCGA	GCTAGAGATG	CGTGAGCTGC	TCAGCCACTA	200
TGGTTTCGAG	GGTGAGGAGA	CCCCAATCAT	TTTTGGCTCT	GCTCTCTGCG	250
CCCTTGAATC	TCGACGACCA	GAATTGGGTG	TTGAGAAGAT	CGATGAGCTA	300
45 TTGAACGCTG	TGGATACCTG	GATTCCCACC	CCAGAGCGTG	CCACTGATAA	350
GCCTTTCCTT	ATGTCCATTG	AGGAAGTTTT	CTCCATCTCT	GGTCGTGGTA	400
CCGTCGTTTT	CGGTCGTGTC	GAGCGTGGTA	TCCTCAAGAA	GGACTCTGAT	450
GTCGAAATTG	TGGGTGGATC	TGATACACCC	ATCAAGACGA	AGGTCACCGA	500
CATTGAAACC	TTCAAGAAGT	CTTGTGACGA	ATCCCGAGCT	GGTGACAACT	550
50 CCGGTCTACT	TCTCCGAGGT	GTCAAGCGTG	AGGACTTGAG	ACGTGGAATG	600
GTTGTTGCTG	CTCCCGGATC	GACCAAGGCT	CATACCGACT	TCATGGTCTC	650
CCTTTATGTT	CTGACCGAGG	CTGAGGGTGG	CCGTTCCAAT	GGATTCACCC	700
ACAAGTACCG	CCCACAGATG	TTCATCCGTA	CTGCCGGTAT	GTAAACCCTT	750

TTTCTACCAT	TCACTTTGTT	TCACCACTGA	CTTGTATACT	TTACCGCAGA	800
CGAAGCCGCA	TCTTTCAGCT	GGCCTGGAGA	GGATCAAGAC	AAGAAGGCCA	850
TGCCTGGTGA	CAATGTCGAG	ATGATTTGCA	AGACCCTC		888

5

2) INFORMATION FOR SEQ ID NO: 1667

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667

ATGCCGCAGA	CCCGCGAGCA	CTTGCTGCTC	GCCCGTCAGG	TCGGTGTCCA	50
GAAGATCGTT	GTTTTTCGTCA	ACAAGGTTGA	TGCTATCGAC	GACCCGGAGA	100
25 TGCTGGAGCT	TGTCGAGATG	GAGATGCGTG	AACTTCTCAG	CACATACGGT	150
TTCGAGGGTG	ACGAGACCCC	TGTTATTATG	GGCTCCGCGC	TCATGGCTCT	200
CAACAACCAG	CGCCCCGAGA	TTGGTCAACA	GAAGATTGAT	GAACTCATGG	250
CCGCTGTCGA	CGAGTGGATC	CCTACTCCCC	AGCGTGACCT	CGACAAGCCT	300
TTCCTGATGT	CTGTTGAGGA	TGTCTTCTCC	ATTGCTGGCC	GTGGTACCGT	350
30 TGTGTCCGGC	CGTGTGGAGC	GCGGTACCCT	CAAGCGTGAT	GAGGAAGTCG	400
AGCTTGTCGG	CAAGGGTGTC	GACCCCATCA	AGACCAAGGT	CACCGATATC	450
GAGACTTTCA	AGAAGTCCTG	CGAGGAGGCT	CAGGCTGGTG	ACAACCTCTGG	500
TCTTCTGATC	CGTGGTGTCC	GCCGCGAGGA	TGTTTCGTCG	GGTATGGTTG	550
TCTCCAAGCC	CGGCACCGTC	AAGTCTCACA	CTCAGTTCCT	GGCCTCGCTT	600
35 TACGTTCTCA	CCAAGGAGGA	GGGTGGTCGC	CACACTGGTT	TCGGCGAGCA	650
CTACCGTCCC	CAGCTCTACC	TCCGTACCTC	AGACGAGTCT	GTCGATCTGA	700
CCTTCCCCGA	GGGAACTGAG	GATCACCCT	CCAAGATCGT	CATGCCTGGT	750
GACAACATCG	AGATGGTTCG	CACGATGACT	CACGCCAACG	CTA	793

40

2) INFORMATION FOR SEQ ID NO: 1668

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 KL1699
(C) ACCESSION NUMBER: J01717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668

```

5  AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC      50
   TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC      100
   GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG      150
   GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG TTCGTGAACT      200
10  TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC GTTCGTGGTT      250
   CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG      300
   GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT      350
   TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC      400
   GTGGTACCGT TGTTACCGGT CGTGTAGAAG GCGGTATCAT CAAAGTTGGT      450
15  GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT CTACCTGTAC      500
   TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT GCTGGTGAGA      550
   ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
   CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC      650
   TGAAGTGATC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT      700
20  TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA CGTGACTGGT      750
   ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG GCGACAACAT      800
   CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC GACGGTCTGC      850
   GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

```

25

2) INFORMATION FOR SEQ ID NO: 1669

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 805 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

     (A) ORGANISM: Saksenaea vasiformis
     (B) STRAIN: ATCC 60625

```

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669

```

   TCCTCGTGGT CGCCGCCACC GACGGCCCGA TGCCGCAGAC CAAGGAGCAC      50
   GTGCTCCTGG CCCGCCAGGT CGGCGTTCCG TACATCGTCG TCGCCCTCAA      100
45  CAAGGCCGAC ATGGTGACG ACGAGGAGAT CCTGGAGCTC GTCGAGCTCG      150
   AGGTCCGTGA GCTCCTCTCC GAGTACGAGT TCCCGGGCGA CGACGTTCCC      200
   GTCGTCAAGG TCTCCGCTCT GAAGGCCCTC GAGGGCGACA AGGAGTGGGG      250
   CAACTCGGTT CTCGAGCTCA TGAACGCCGT CGACACGGCG ATCCCCGAGC      300
   CCGAGCGTGA CGTCGACAAG CCGTTCCTCA TGCCGATCGA GGACGTCTTC      350
50  ACGATCACCG GTCGCGGTAC GGTCGTCACC GGCCGTATCG AGCGTGGTGT      400
   CCTGAAGGTC AACGAGACCG TCGACATCAT CGGCATCAAG ACCGAGAAGA      450
   CCACCACCAC GGTCACCGGC ATCGAGATGT TCCGGAAGCT CCTCGACGAG      500
   GGCCAGGCCG GTGAGAACGT CGGTCTGCTC CTCCGTGGCA TCAAGCGCGA      550

```

	GGACGTCGAG	CGCGGGCCAGG	TCATCATCAA	GCCGGGCTCG	GTCACGCCGC	600
	ACACGGAGTT	CGAGGCGCAG	GCCTACATCC	TGTCCAAGGA	CGAGGGTGGC	650
	CGCCACACGC	CGTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGTAC	700
	GACGGACGTG	ACCGGCGTGG	TGACCTCC	CGAGGGCACC	GAGATGGTCA	750
5	TGCCGGGTGA	CAACACCGAG	ATGAAGGTGG	AGCTCATCCA	GCCCGTCGCC	800
	ATGGA					805

10 2) INFORMATION FOR SEQ ID NO: 1670

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 935 bases
	(B) TYPE: Nucleic acid
15	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Trichophyton tonsurans</i>
(B)	STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670

25	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACA	GATGAAAGGA	50
	TTTGACGTTT	CTAACATCAG	TCTAGGCCTC	AGACCAGAGA	ACATTTGCTC	100
	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	TTAACAAGGT	150
	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	CTTGAAATGC	200
30	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	CCCCATCATT	250
	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	AGCTTGGTGT	300
	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	ATCCCCACCC	350
	CAGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	GGAAGTGTTT	400
	TCTATCTCTG	GTGCTGGTAC	CGTCGTCTCC	GGTCGTGTTG	AGCGTGGTAT	450
35	CCTCAAGAAG	GATTCGGACG	TCGAAATTGT	TGGTGGCTCT	ACCACCCCTA	500
	TCAAGACCAA	GGTCACCGAT	ATCGAAACCT	TCAAGAAGTC	CTGCGATGAA	550
	TCTCGAGCTG	GTGACAACTC	TGGTCTCCTT	CTCCGAGGTA	TCAAGCGTGA	600
	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	ACCAAGGCTC	650
	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	TGAGGGTGGT	700
40	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	TCATCCGTAC	750
	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	ATCATTGCTA	800
	ACTTGATTTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	TGGCCTGGAG	850
	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	GATGATTTGC	900
	AAGACCCTCC	ACCCATTGCT	TGCCGAGGCT	GGCCA		935
45						

2) INFORMATION FOR SEQ ID NO: 1671

50 (i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH: 772 bases
(B)	TYPE: Nucleic acid
(C)	STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter aerogenes*

(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671

10
 ACGATGCCCT TGAGGTACAG AATGGTAATG AGAGCCTGGT GCTGGAAGTT 50
 CAGCAGCAGC TCGGCGGTGG CGTAGTCCGT GCTATCGCCA TGGGTTCTTC 100
 CGACGGTCTG CGTCGTGGTC TGGAAGTTAA AGACCTTGAG CACCCGATCG 150
 AAGTCCCGGT AGGTAAAGCG ACTCTGGGCC GTATCATGAA CGTCCTGGGT 200
 15 CAGCCGATCG ACATGAAAGG CGACATCGGC GAAGAAGAAC GTTGGGCTAT 250
 CCACCGCGCG GCGCCTTCCT ATGAAGAGCT GTCCAGCTCT CAGGAACTGC 300
 TGGAAACCGG CATCAAAGTT ATCGACTTGA TGTGTCCGTT CGCTAAGGGC 350
 GGTAAAGTTG GTCTGTTCGG TGGTGCGGGT GTAGGTAAAA CCGTAAACAT 400
 GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT TACTCCGTGT 450
 20 TTGCGGGCGT TGGTGAGCGT ACTCGTGAGG GTAACGACTT CTATCACGAA 500
 ATGACCGACT CCAACGTTCT GGATAAAGTA TCCCTGGTTT ACGGCCAGAT 550
 GAACGAGCCG CCGGGAAACC GTCTGCGCGT TGCCTGACC GGCCTGACCA 600
 TGGCTGAGAA ATTCCGTGAC GAAGGTCGTG ACGTTCTGCT GTTCGTCGAT 650
 AACATCTATC GTTACACCCT GGCCGGTACT GAAGTATCTG CACTGCTGGG 700
 25 CCGTATGCCT TCAGCGGTAG GTTATCAGCC GACTCTGGCG GAAGAGATGG 750
 GCGTTCTGCA GGAACGTATC AC 772

30 2) INFORMATION FOR SEQ ID NO: 1672

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(B) STRAIN: Tohama 1

(C) ACCESSION NUMBER: Genome project

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1672

ATGAGCAACG GAACCATCGT TCAGTGCATC GGCGCCGTGG TGGATATTCA 50
 GTTCCCCCGC GATAACATGC CCAAGATCTA CGAAGCGCTC ACCCTGGTGC 100
 ACGAGGGTTC CTCGTTCGCC GAGAAGGGCT TGACGCTGGA AGTGCAACAA 150
 50 CAGCTGGGCG ACGGCGTGGT GCGTACCATC GCGCTGGGTT CCAGCGACGG 200
 GCTGCGCCGC GGCATGCAAG TGGCCGGCAC CGGCGCACC GATCTCGGTGC 250
 CCGTGGGCCA CGGCACCCTG GGCCGCATCA TGGACGTGCT GGGCCGTCCC 300
 ATCGACGAAG CCGGTCCCAT CGCCTCCGAC GAGAAGCGCG CCATCCACCA 350

	GCCCCGCGCCC	CGTTTTCGACG	AGCTGTTCGCC	GTCGGTTCGAG	CTGCTGGAAA	400
	CCGGCATCAA	GGTTATCGAC	CTGGTGTGCC	CGTTCGCCAA	GGGCGGCAAG	450
	GTCGGCCTGT	TCGGCGGCGC	CGGCGTGGGC	AAGACCGTCA	ACATGATGGA	500
	ACTGATCAAC	AACATCGCCA	AGCAGCACAG	CGGCTTGTCG	GTGTTTCGCCG	550
5	GCGTGGGCGA	GCGTACCCGC	GAAGGCAACG	ACTTCTACCA	CGAAATGGAA	600
	GAGTCGAACG	TTCTGGACAA	GGTGGCCATG	GTGTTTCGGCC	AGATGAACGA	650
	GCCCCCGGGC	AACCGCCTGC	GCGTGGCGCT	GACCGGCCTG	ACCATGGCCG	700
	AGAAGTTCCG	CGACGAAGGC	CGTGACATCC	TGTTCTTCGT	CGACAACATC	750
	TACCGCTACA	CCCTGGCCGG	TACCGAAGTG	TCGGCGCTGC	TGGGCCGTAT	800
10	GCCGTCGGCG	GTGGGCTACC	AGCCTACGCT	GGCCGAGGAA	ATGGGCGTGC	850
	TGCAAGAGCG	CATCACCTCG	ACCAAGACCG	GTTTCGATCAC	CTCGATCCAG	900
	GCCGTGTACG	TGCCTGCCGA	CGACTTGACC	GACCCGTTCG	CCGCCACGAC	950
	CTTCCAGCAC	TTGGACTCGA	CCGTCGTGCT	GTCGCGTGAC	ATCGCTGCGC	1000
	TGGGCATCTA	TCCCGCCGTG	GACCCGCTGG	ATTCCTCCAG	CCGCCAGCTC	1050
15	GACCCGCAAG	TCGTGGGCGA	AGAGCACTAC	CAGGTGGCCC	GTGGCGTGCA	1100
	GCAGACGCTG	CAGCGCTACA	AGGAACTGCG	CGACATCATC	GCGATTCTGG	1150
	GCATGGACGA	ACTGTCGCCG	GAAGACAAGC	AGGCCGTGGC	CCGCGCGCGC	1200
	AAGATCCAGC	GCTTCCTGTC	GCAGCCCTTC	TACGTGGCCG	AAGTGTTTAC	1250
	CGGCTCGCCG	GGCAAGTACG	TGTCGCTGGC	CGAAACGATC	CGTGGCTTCA	1300
20	AGATGATCGT	CGACGGCGAG	TGCGACGCGC	TGCCCAGGCA	GGCGTTCTAC	1350
	ATGGTCGGCA	CGATCGACGA	GGCCTTCGAG	AAGGCCAAGA	AACTCCAATA	1400
	A					1401

25

2) INFORMATION FOR SEQ ID NO: 1673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*
 (B) STRAIN: ATCC 9345

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673

	CAGCTACCGA	CGGTCCAATG	GCTCAGACCC	GCGAGCACGT	TCTTCTTGCT	50
	CGCCAGGTTG	GCGTTCCACA	GATCATCGTT	GCTCTCAACA	AGGCTGACAT	100
	GGTTGACGAC	GAGGAAATCC	TCGAACTCGT	CGAAATGGAA	GTTTCGTGAGC	150
45	TTCTCTCTTC	CCAGGAGTAC	CCAGGTGACG	ACCTCCCAGT	CGTCAAGATC	200
	TCGGCACTCA	AGGCTCTCGA	AGGCGATGCC	GAATGGAGCA	AGGCAATCGA	250
	AGATCTCATG	GAAGCTGTCT	ATACCTACTT	CGACGATCCA	GTGCGTGACC	300
	TCGATAAGCC	ATTCTCATG	CCAATCGAAG	ACGTCTTCAC	CATCACCGGT	350
	CGTGGCACCG	TTGTTACCGG	CCGTGCAGAG	CGCGGTATGC	TCAACTTGAA	400
50	CGAAGAAGTT	GAAATCCTCG	GTATCCGTGC	ACCACAGAAG	ACAACCGTTA	450
	CCGGTATCGA	AATGTTCCAC	AAGTCGATGG	ATCACGCAGA	TGCAGGCGAA	500
	AACTGTGGTC	TTCTCCTCCG	TGGCACCAAG	CGCGAAGATG	TTGAACGTGG	550
	TCAGGTTGTT	GCCAAGCCAG	GCACCATCAC	CCCACACACC	AACTTCGAAG	600

CTCAGGTCTA	CGTGCTCGGT	AAGGAAGAAG	GTGGCCGTCA	CAACCCATTC	650
TTCTCCAAC	ACCGTCCACA	GTTCTACTTC	CGTACCACGG	ATGTTACCGG	700
CGTGATCACC	CTTCCAGAGG	GCACCGAAAT	GGTTATGCCA	GGCGACAACA	750
CCGACATGAC	AGTTGAGCTC	ATCCAGCCAA	TCGCTATGGA	AGAGGGC	797

5

2) INFORMATION FOR SEQ ID NO: 1674

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Butyrivibrio fibrisolvens*
- (B) STRAIN: ATCC 19171

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674

CTGATGGTCC	TATGCCACAG	ACCCGTGAGC	ACATCCTATT	AGCACGTCAG	50
25 GTAGGCGTAC	CATACATCAT	CGTATTCCTA	AACAAGTGCG	ATATGGTTGA	100
CGACGAGGAA	TTATTAGAGT	TAGTTGAGAT	GGACGTACGT	GATCTATTAA	150
ATCAGTACCA	GTTCCCAGGC	GACGACACTC	CAATCATCCG	TGGTTCAGCA	200
CTAGGTGCAT	TAAACGGCGA	AGAGAAGTGG	AAAGAGGCAA	TCTATCAGTT	250
AGCAGACACT	CTAGATTTCAT	ACATTCCAGA	GCCAAAGCGT	GATATCGATG	300
30 ATCCATTCCCT	ATTACCAATC	GAAGATATCT	TCTCAATCTC	AGGTCGTGGT	350
ACTGTAGTAA	CCGGCCGTGT	AGAGCGTGGT	ATTGTACACG	TAGGTGACGA	400
AGTTGAAATC	GTTGGTATTC	GTCCAACCAC	CAAGACCACT	GTAAGTGGCG	450
TTGAAATGTT	CCGTAAGTTA	CTAGACGAAG	GTCGTGCAGG	TGATAACGTT	500
GGTGTTCCTAC	TACGTGGTAC	CAAGCGTGAT	GAGGTTGAGC	GTGGTCAGGT	550
35 TCTAGCTGCT	CCAGGCACAA	TCACTCCACA	CACCAAGTTC	ACTGGTCAGG	600
TTTACGTACT	AAGCAAGGAT	GAAGGTGGTC	GTCACACTCC	ATTCTTCAAG	650
GGCTACCGTC	CACAGTTCTT	CTTCCGTACA	ACCGATATTA	CCGGTTCTAT	700
CGATCTGAAA	GAGGGCGTAG	AGATGGTAAT	GCCAGGTGAT	AACACCGACA	750
40 TGACCGTAAC	CCTAATCCAC	CCAGTAGCTA	TGGCT		785

40

2) INFORMATION FOR SEQ ID NO: 1675

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
 (B) STRAIN: ATCC 49349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675

5
 TGGGGCGATC TTGGTTGTTT CTGCTGCAGA TGGTCCTATG CCACAAACTA 50
 GAGAGCACAT TCTTCTTTCT CGTCAAGTAG GCGTTCCATA TATTGTTGTT 100
 TTTATGAATA AAGCAGATAT GGTTGATGAT GCTGAGCTTT TAGAGTTAGT 150
 TGAAATGGAA ATTAGAGAAT TATTAAGCTC TTATGATTTT CCAGGCGATG 200
 10 ATACACCTAT TATTTCTGGT TCTGCTTTAA AAGCTCTTGA AGAAGCTAAA 250
 GCTGGACAAG ATGGTGAATG GTCAGCAAAA ATTATGGATC TTATGGCTGC 300
 AGTTGATAGT TATATTCCAA CTCCAACCTCG TGATACTGAA AAAGACTTCT 350
 TGATGCCAAT TGAAGACGTT TTCTCAATTT CAGGTCGTGG TACTGTTGTT 400
 ACAGGTAGAA TTGAAAAGG TGTTGTAAAA GTAGGTGATA CTATCGAAAT 450
 15 CGTTGGTATT AAAGACACTC AAACAACAAC TGTAACAGGT GTTGAAATGT 500
 TCAGAAAAGA AATGGATCAA GGCGAGGCAG GAGATAACGT AGGTGTTCTT 550
 CTTCGTGGTA CTAAGAAAAGA AGAAGTTATT CGCGGTATGG TTCTTGCTAA 600
 ACCAAAATCA ATTACTCCAC ACACTGACTT CGAAGCTGAA GTTTATATCT 650
 TAAATAAAGA TGAAGGTGGT AGACATACTC CATTCTTTAA CAACTATAGA 700
 20 CCACAGTTTT ATGTAAGAAC AACTGATGTT ACAGGTTCTGA TTAAATTAGC 750
 TGATGGTGTT GAAATGGTTA TGCCAGGTGA AAATGTGAGA ATTACTGTAA 800
 GCTTGATCGC TCCAGTAGCA CTTGAAGAAG GAACT 835

25

2) INFORMATION FOR SEQ ID NO: 1676

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676

TTCTGCAGCA GACGGCCCTA TGCCACAAAC TAGAGAGCAT ATCTTACTTT 50
 CTCGTCAAGT AGGTGTACCA TATATTGTTG TTTTCATGAA CAAAGCTGAT 100
 ATGGTTGATG ATGCAGAATT ATTAGAATTA GTTGAAATGG AAATTAGAGA 150
 45 ATTACTAAGC TCTTATGATT TCCCAGGAGA TGATACTCCA ATTATTTTCAG 200
 GTTCAGCATT ACAAGCTCTT GAAGAAGCAA AAGCTGGTCA AGATGGTGAA 250
 TGGTCTAAAA AAATCTTAGA TCTTATGGCT GCAGTTGATG ATTATATTCC 300
 AACTCCGGCT CGTGATACAG ATAAAGATTT CTTGATGCCA ATCGAAGATG 350
 TTTTCTCAAT CTCAGGTCGT GGAAGTGTG TTAGCGGTAG AATTGAAAAA 400
 50 GGTGTTGTAA AAGTTGGTGA TACTATAGAA ATCGTTGGTA TTAGAGACAC 450
 TCAAACAACC ACAGTTACTG GTGTTGAAAT GTTTAGAAAA GAAATGGATC 500
 AAGGTGAAGC TGGTGATAAT GTTGGTGTAT TACTTCGTGG AACTAAAAAA 550
 GAAGATGTTG AACGTGGTAT GGTTCCTGCT AAACCAAAAT CAATCACTCC 600

	ACATACTGAT	TTTGAAGCAG	AAGTTTATAT	CTTAAATAAA	GATGAAGGTG	650
	GTCGTCATAC	TCCATTCTTT	AATAATTATA	GACCGCAATT	TTATGTAAGA	700
	ACAACTGATG	TTACAGGTGC	TATTAACTT	GCAGAAGGCG	TTGAGATGGT	750
	TATGCCAGGC	GATAATGATA	GAATTACTGT	AAGTCTTATT	GCTCCAGTTG	800
5	CACTTGAGGA	AG				812

2) INFORMATION FOR SEQ ID NO: 1677

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
 (B) STRAIN: ATCC 35980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677

25	GCTATTCTTG	TATGTTTCAGC	TGCAGATGGT	CCAATGCCAC	AGACTAGAGA	50
	GCATATTCTA	CTATCAAGAC	AAGTTGGTGT	TCCATACATA	GTTGTTTTCT	100
	TAAATAAAGA	AGATATGGTT	GATGATGCTG	AGCTTATAGA	GTTGGTTGAA	150
	GTTGAGGTTA	GAGATTTATT	AAATGAATAT	GATTTCCCTG	GAGATGATAC	200
	TCCAATCGTA	ATAGGTTCTG	CTCTTAAAGC	TTTAGAAGAA	GCAAAAGCTG	250
30	GAACAGAGGG	TGAATGGTCT	GCTAAAATTA	TGAAACTTAT	GGATGCTGTT	300
	GATAGCTATA	TCCCAACTCC	AACAAGAGAT	ACAGATAAAG	ATTTCCCTTAT	350
	GCCAATCGAA	GATATCTTCT	CAATTTCTGG	TCGTGGTACA	GTTGTAACAG	400
	GTAGAATTGA	AAAAGGTGTA	GTAAAAGTTG	GCGAGACTAT	TGAGATAGTT	450
	GGTATTAGAC	CTACTCAAAC	AACAACAGTT	ACTGGTGTTG	AAATGTTTAG	500
35	AAAAGAGCTA	GATCAAGGTG	AAGCTGGAGA	TAATGTTGGT	ATCTTGTTAA	550
	GAGGTACAAA	AAAAGAAGAT	GTTGAAAGAG	GTATGGTTTT	ATGTAAACCA	600
	AAATCAATCA	CTCCTCACAA	GAAATTTGAA	GGCGAAGTTT	ATATTCTTAC	650
	AAAAGATGAA	GGTGGTAGAC	ATACTCCTTT	CTTTAGTAAC	TATAGACCAC	700
	AATTTTATGT	TAGAACAACA	GATGTAACAG	GTTCTATATC	TCTTCCTGAG	750
40	GGAACAGAGA	TGGATATGCC	TGGTGATAAT	GTAAAACTTA	CAGTTGAACT	800
	TATAAACCCA	ATTGCTCTTG	AGCAAGGA			828

45 2) INFORMATION FOR SEQ ID NO: 1678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter upsaliensis*

(B) STRAIN: ATCC 49815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678

5
 10
 15
 20
 25

CGATTTTGGT	TGTTTCTGCT	GCTGATGGTC	CTATGCCACA	AACTAGAGAG	50
CACATTTTGC	TTTCTCGTCA	AGTGGGTGTT	CCTTATATCG	TAGTTTTTAT	100
GAATAAGGCT	GATATGGTTG	ATGATGCAGA	GCTTTTAGAA	TTGGTTGAAA	150
TGGAAATTAG	AGAACTTTTA	AGCTCTTATG	ATTTCCCGGG	CGATGACACT	200
CCTATCATTT	CAGGCTCTGC	TCTTCAAGCC	TTAGAAGAGG	CTAAGGCGGG	250
ACAAGATGGC	GAGTGGTCAG	CTAAGATTTT	AGAGCTTATG	AAGGCAGTTG	300
ATGAGTATAT	CCCAACTCCT	GTTCGCGATA	CTGAAAAAGA	TTTCTTGATG	350
CCTATTGAAG	ATGTTTTTTC	AATTTCTGGT	CGTGGAAGTG	TTGTAACAGG	400
TAGAATTGAA	AAAGGTGTGG	TTAAAGTCGG	CGATACTATT	GAGATAGTAG	450
GTATCAAAGA	TACTCAAAC	ACAACAGTTA	CAGGCGTTGA	GATGTTTAGA	500
AAAGAAATGG	ATCAAGGTGA	GGCTGGCGAT	AATGTCGGTG	TGCTTTTAAG	550
AGGAACAAAA	AAAGAAGATG	TTCTTCGTGG	TATGGTTCTT	GCAAAGCCTA	600
AATCTATCAC	TCCTCATACT	GATTTTGAAG	CAGAAGTTTA	TATTCTAAAT	650
AAAGATGAGG	GCGGTCGCCA	TACTCCTTTC	TTTAACAATT	ATCGTCCGCA	700
GTTTTATGTA	AGAACGACTG	ATGTAACTGG	TTCTATTAAA	TTAGCTGATG	750
GTGTTGAGAT	GGTTATGCCG	GGTGAAAATG	TAAGAATTAC	AGTTAGCCTT	800
ATCGCTCCAG	TTGCACTTGA				820

2) INFORMATION FOR SEQ ID NO: 1679

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Globicatella sanguis*

(B) STRAIN: ATCC 51173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679

45
 50

CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	GTGAACATAT	CTTATTATCA	50
CGTCAAGTAG	GTGTTCTTA	CATGGTTGTC	TTCTTAAACA	AAGTTGACAT	100
GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	TGAAATGGAA	GTTCGTGATT	150
TATTATCTGA	ATACGAATTC	CCTGGAGACG	ACGTTCCAGT	AATCGCTGGT	200
TCAGCTTTAA	AAGCTTTAGA	AGGCGAAGAA	CAATATGAAG	CAAAAGTATT	250
AGAATTAATG	GAAGCTGTAG	ATACATACAT	TCCAGAACCA	GTTCGTGATA	300
CTGAAAAACC	ATTCATGATG	CCAGTTGAAG	ATGTGTTCTC	AATCACAGGT	350
CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	CGTGGACAAG	TTAAAGTTGG	400
TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	AGAAATTAGC	AAAACAAC	450
TAAGTGGTGT	TGAAATGTTC	CGTAAATTAT	TAGATTACGC	TGAAGCTGGA	500

	GATAACATTG	GTGCGTTATT	ACGTGGTGT	ACACGTGAAC	AAATCCAACG	550
	TGGTCAAGTA	TTAGCAAAAC	CAGGAACAAT	TACACCTCAT	ACTAAATTTCG	600
	AGGCGGAAGT	TTACGTATTA	TCAAAAGAAG	AAGGTGGACG	TCATACTCCA	650
	TTCTTCGCTA	ACTACCGTCC	TCAATTCTAC	TTCCGTACAA	CTGACGTTAC	700
5	AGGTGTTGTA	GAATTACCAG	AAGGTACAGA	AATGGTAATG	CCTGGAGATA	750
	ACGTATCAAT	GACAGTTGAA	TTAATTCACC	CAA		783

10 2) INFORMATION FOR SEQ ID NO: 1680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus acidophilus*
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680

25	GCTATCTTAG	TTGTTGCTGC	AACTGATGGT	CCTATGCCAC	AAACTCGTGA	50
	ACACATTTTG	CTTGCTCGTC	AAGTTGGTGT	TAACATACATC	GTAATATTCT	100
	TGAACAAGTG	CGATTTAGTT	GACGACCCAG	AATTGATCGA	CTTGGTTGAA	150
	ATGGAAGTTC	GTGACTTGTT	GACTGAATAC	GATTACCCTG	GTGATGATAT	200
30	TCCAGTTGTT	CGTGGTTCAG	CATTAAAGGC	TTTACAAGGT	GACAAGGAAG	250
	CTCAAGACCA	AATCATGAAG	TTGATGGACA	TTGTTGATGA	ATACATCCCA	300
	ACTCCAGAAC	GTCAAACCTGA	CAAGCCATTC	TTGATGCCAG	TTGAAGACGT	350
	ATTCATATC	ACTGGTCGTG	GTACTGTTGC	TTGAGGTCGT	ATCGACCGTG	400
	GTACTGTTAA	GGTCGGTGAC	GAAGTTGAAA	TCGTTGGTTT	GGTAGATAAA	450
35	GTTCTTAAGT	CAGTTGTTAC	TGGTTTGGA	ATGTTCCACA	AGACTTTGGA	500
	CTTAGGTGAA	GCCGGCGATA	ACGTTGGTGT	ATTGCTTCGT	GGTGTGACC	550
	GTGATCAAGT	TGTTTCGTGGT	CAAGTATTGG	CTGCACCCGG	CTCAATCCAA	600
	ACTCATAAGA	AGTTTAAGGC	ACAAGTTTAT	GTTTTGAAGA	AGGACGAAGG	650
	TGGTCGTAC	ACTCCATTCT	TCTCAGACTA	CCGTCCACAA	TTCTACTTCC	700
40	ACACCACTGA	TATTACTGGT	GAAATTGAAT	TGCCAGAAGG	TACTGAAATG	750
	GTTATGCCTG	GTGATAACAC	TGAATTCAC	GTTACTTTGA	TCAAGCCAGC	800
	TGCCATCGAA	AAGGGTACTA	AGT			823

45

2) INFORMATION FOR SEQ ID NO: 1681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leuconostoc mesenteroides* subsp.
dextranicum
 (B) STRAIN: ATCC 19255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681

10	GCTGCAACTG	ATGGTCCTAT	GCCACAAACA	CGTGAACACA	TCTTGTTGGC	50
	ACGTCAAGTT	GGTGTGACT	ACTTGGTTGT	CTTCTTGAAC	AAGACTGATT	100
	TGGTTGATGA	TGAAGAATTA	GTTGAATTGG	TTGAAATGGA	AGTTCGTGAA	150
	TTGTTGTCAG	AATATGACTT	CCCAGGTGAC	GATATTCCTG	TACTTAAGGG	200
	TTCAGCTTTG	AAGGCTTTGG	AAGGTGATCC	TGAACAAGTT	AAGGTTATCG	250
15	AAGAATTGAT	GGATACTGTT	GATTTCATACA	TTCCAGAACC	AGCACGTGAA	300
	ACAGACAAGC	CATTCTTGAT	GCCTGTCGAA	GACGCTTCA	CAATCACTGG	350
	TCGTGGTACA	GTTGCTTCTG	GTCGTGTTGA	CCGTGGTGTA	TTGACTACAG	400
	GAACTGAAAT	TGAAATCGTT	GGTTTGAAGG	ACGAAGTTCA	AAAGACTACT	450
	GTTACAGGTA	TCGAAATGTT	CCGTAAGACT	TTGGAAGAAG	CTCAAGCGGG	500
20	TGATAACATT	GGTGCATTGT	TGCGTGGTGT	TGATCGTAGC	AACATTGAAC	550
	GTGGTCAAGT	TTTGCAAAG	CCAGGTTCAA	TTAAGACACA	CAAGAAGTTC	600
	AAGGCTGAAG	TTTATGTCTT	GACAAAGGAA	GAAGGTGGTC	GTCATACACC	650
	ATTCTTCACT	AACTACCGTC	CACAATTCTA	CTTCCACACA	ACTGATGTTA	700
	CAGGTGTTGT	TGAATTGCCA	GCCGGTGTTG	AAATGGTTAT	GCCTGGTGAC	750
25	CAAGTGACAT	TCGAAATCGA	ATTGATCTCA	CCAGTTGCCA	TCG	793

2) INFORMATION FOR SEQ ID NO: 1682

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682

45	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTT	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAACCTTCTTG	AGCAATACGA	ATTGCAAGAG	GATACTCCAA	200
	TCGTTTCGTGG	TTCTGCACTG	GGTGCAATTGA	ATGGTGTTGA	CAAGTGGGTT	250
50	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAACAG	GACGTATTGA	GACTGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450

	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACTTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
5	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GCGGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	GTAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

10

2) INFORMATION FOR SEQ ID NO: 1683

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 800 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ruminococcus bromii*
- (B) STRAIN: ATCC 27255

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683

	GGTTGCTGCT	ACTGACGGCC	CGATGCCTCA	GACTCGTGAG	CACGTTCTGC	50
	TCGCTCGTCA	GGTGGGTGTG	CCCGCCATCG	TCGTCGCCCT	CAACAAGTGC	100
	GACATGGTTG	ACGATGAGGA	GCTCATTGAG	CTTGTCGAGA	TGGAGGTCGG	150
30	CGAGCTGCTG	ACCTCGCAGG	AGTTCGACGG	CGACAACATGC	CCTGTCGTTT	200
	GCATCTCCGC	CTTCCAGGCC	CTCCAGGGTG	ACGAGAAGTG	GACCCAGTCG	250
	ATCCTCGACC	TCATGGACGC	CGTGGACGAG	TACATCCCGC	AGCCTGAGCG	300
	CGATCTCGAC	AAGCCCTTCC	TTATGCCGAT	CGAGGACGTC	TTCACCATCA	350
	CCGGCCCGTG	CACCGTTGTC	ACCGGTCGTG	TCGAGCGTGG	TGTCGTCAAG	400
35	ACTGGCGAAG	AGGTCGAGAT	CGTCGGTATC	CACGAGAAGA	CCCAGAAGAC	450
	CACCGTTACC	GGTGTCGAGA	TGTTCCGTAA	GATCCTCGAC	GAGGGCCGCG	500
	CTGGTGAGAA	CGTCGGCGTT	CTGCTCCGTG	GCACCAAGAA	GGAGGACGTC	550
	GTTCGCGGCA	TGGTCCTCTC	CAAGCCTGGT	TCCACCACCC	CCCACACCGA	600
	CTTCGAGGGC	CAGGTCTACG	TCCTCAAGAA	GGATGAGGGT	GGCCGCCACA	650
40	AGCCGTTCTT	CTCCCATTAC	AGCCCCCAGT	TCTACTTCCG	TACCACGGAC	700
	GTGACTGGCA	CTGTTGAGCT	CCCCGAGGGC	ACCGAGATGG	TCATGCCTGG	750
	CGACAACACC	GACATGACTG	TGCACCTGAT	TCACCCGGTT	GCCATGGAGG	800

45

2) INFORMATION FOR SEQ ID NO: 1684

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 545 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 5 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684

	TGTCTTTTATT	CAGGAACTGA	TTGTATGTTT	CTTCTCGTTT	ATATATAACA	50
10	TACCTTCTAT	ATTTTCATGTG	TTTCTAACGA	ACTCATAGAA	CAACATTGCC	100
	AAGGCTCACG	GTGGTTACTC	CGTGTTTACC	GGTGTCGGTG	AGCGTACCCG	150
	TGAAGGAAAC	GATCTGTACC	ACGAAATGCA	GGAAACCCGC	GTCATCCAGC	200
	TGGACGGCGA	GTCCAAAGTC	GCCCTCGTCT	TCGGCCAGAT	GAACGAGCCC	250
	CCCGGAGCCC	GTGCCCCTGT	TGCCCTGACC	GGTCTGACCA	TCGCTGAATA	300
15	CTTCCGTGAC	GAAGAAGGCC	AAGATGGTAC	GTTCCCCCAT	TCCATATATG	350
	TTTCTTGTGC	GCTTTGCCAA	CTAAACACCA	CCTAGTGCTC	CTCTTCATCG	400
	ACAATATCTT	CCGCTTCACC	CAAGCCGGTT	CCGAAGTGTC	CGCCCTGCTA	450
	GGCCGCATCC	CCTCCGCCGT	CGGCTATCAA	CCCACCCTCG	CCGTCGACAT	500
20	GGGTGGTATG	CAGGAGCGCA	TCACAACCTAC	AACAAAAGGC	TCCAT	545

2) INFORMATION FOR SEQ ID NO: 1685

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
 35 (B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685

	GATATCGCTT	TATGGAAATT	CGAAACTCCA	AAATTCCACG	TTACYGTTAT	50
40	CGATGCTCCA	GGTCACAGAG	ATTTTCATCAA	GAATATGATT	ACYGGTACCT	100
	CCCAAGCTGA	TTGTGCTATT	TTAATCATTG	CTGGTGGTGT	TGGTGAATTC	150
	GAAGCTGGTA	TCTCCAAAGA	TGGTCAAACC	AGAGAACACG	CTTTGTTAGC	200
	TTTCACCTTA	GGTGTYAAAC	AATTGATTGT	TGCCGTTAAC	AAAATGGACT	250
	CTGTCAAATG	GGATCAATCC	CGTTTCGAAG	AAATCGTCAA	GGAAGCTTCC	300
45	GGTTTCATCA	AGAAAGTTGG	TTACAACCCA	AAGACTGTTC	CATTCGTTCC	350
	AATCTCTGGT	TGGAATGGTG	ACAACATGAT	TGAAGTYTCW	GCTAACGCYC	400
	CATGGTACAA	AGGTTGGGAA	AAGGAAACCA	AAGCYGGTGT	CGTTAAAGGT	450
	AAAACCTTTAT	TAGAAGCCAT	TGATGCTATT	GAACCACCTT	CAAGACCAAC	500
	TGAAAAACCA	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATTGGTGGTA	550
50	TCGGAACCGT	ACCAGTCGGT	ARAGTTGAAA	CCGGTGTCAT	TAAACCAGGT	600
	ATGATTGTTA	CTTTCGCCCC	AGCCGGTGTT	ACTACTGAAG	TCAAATCTGT	650
	TGAAATGCAT	CACGAACAAT	TAGAAGCTGG	TTACCCAGGT	GACAATGTTG	700
	GTTTCAACGT	CAAGAATGTT	TCAGTTAAAG	AAATCAGAAG	AGGTAAHGTT	750

	GCTGGTGA	CT	CA	AC	GC	800
	TCAAGTTA	TT	GT	CT	TA	850
	CAGTTTTG	GA	TT	GT	CA	900
	TTGGAAA	GA	TT	GA	CA	950
5	ATTCATCA	AA	TCTGGT	GACG	CTGCTA	1000
	CATTRTGT	GT	TGAAGCT	TTTC		1020

10 2) INFORMATION FOR SEQ ID NO: 1686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686

25	TGCTGCTTCC	GATGGTCAAA	TGTACGATTG	ATATTCCTTC	CAGCCAGTCA	50
	GGATAACAGC	TGATACCAGT	TGCAAATAGG	CCCCAGACTC	GTGAGCACTT	100
	GTTGCTTGCC	CGTCAGGTTG	GTGTCCAGAA	GATCGTTGTC	TTCGTCAACA	150
	AGGTTGACGC	TGTCGATGAC	CCTGAGATGT	TGGAGCTTGT	TGAGCTCGAG	200
30	ATGCGTGAGC	TCCTCAACAC	TTACGGTTTC	GAGGGAGAGG	AGACCCCTAT	250
	CATCTTCGGT	TCCGCCCTGT	GCGCTCTCGA	AGGCCGCCGC	GAGGACATTG	300
	GTACTCAGCG	TATTGACTCC	CTCCTCGAGG	CCGTTGACAC	TTGGATCCCT	350
	ACCCCCCAGC	GTGACTTGGA	CAAGCCCTTC	CTGATGTCCA	TTGAGGAAGT	400
	TTTCTCCATT	GGTGGTCGTG	GTACCGTCGC	CTCTGGTCGT	GTCGAGCGTG	450
35	GTCTCCTCAA	GAAGGATACC	GAAGTTGAAA	TTCACGGTGC	TGATGGTATT	500
	CTGAAGACCA	AGGTCACCGA	CATTGAGACC	TTCAAGAAGA	GCTGCGATGA	550
	GTCTCGTGCT	GGTGACAAC	CCGGTCTTCT	CCTCCGTGGT	ATCCGTCGTG	600
	AGGATGTTTC	TCGTGGTATG	GTCATCGCTG	CCCCTGGCTC	CATCAAGGCC	650
	TCCAAGAAGT	TCATGGTCTC	CATGTACGTC	TTGACTGAGG	CTGAAGGTGG	700
40	CCGCAAGAAC	GGCTTCGGTG	CCAATAACCG	CCCCCAGGCT	TTCATCCGCA	750
	CTGCTGGTAA	GTTTCGAACT	ATTTGATTCA	TTGATCACGT	CCCTAACTGT	800
	TACTTTAGAC	GAGGCTTGCG	ACCTTCATTT	CCCTGATGAG	GCCGACAAGG	850
	ACCGCCACGT	CATGCCCGGT	GACAACGTCG	AAATGGTCCT	CAACCTCAAC	900
45	AACCCCGTTG	CTGCTGAGGC	TGGACAGCG			929

2) INFORMATION FOR SEQ ID NO: 1687

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus terreus*

(B) STRAIN: WSA-174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687

```

10  TGCCGCTTCC GATGGTCAGA TGTACGCTCA AGCCCCAGTT TCCATATAAA      50
    CATAAACGAT CTATCATCAG CACAACGCTG ACTTCTTCGC TTCCAGGCCC      100
    CAGACCCGTG AGCACTTGCT GTTGGCCCGT CAGGTCGGTG TCCAGAAGAT      150
    CGTGGTCTTC GTCAACAAGG TCGATGCCGT TGATGACCCG GAGATGTTGG      200
15  AGCTCGTTGA GCTGGAAATG CGCGAGCTCC TGACCAGCTA CGGATTCGAG      250
    GGTGAAGAGA CCCCCATCAT CTTCGGTTCT GCTCTCTGCG CTCTTGAGGG      300
    CCGCCGTCCT GAGATTGGTA CTGAGAAGAT TGACGAGCTG ATGCACGCCG      350
    TCGACACCTG GATCCCCACC CCCCAGCGTG ACCTCGACAA GCCCTTCCTG      400
    ATGTCCGTCG AGGAAGTCTT CTCCATTGCT GGTCGTGGTA CCGTCGCTTC      450
20  CGGCCGTGTC GAGCGTGGTA TTCTGAAGAA GGATAGCGAA GTCGAGATCA      500
    TCGGTGGTGC TTTCGACGCC ACGAAGACCA AGGTCACTGA CATCGAGACC      550
    TTCAAGAAGT CTTGCGACGA GTCTCGCGCT GGTGACAACT CTGGTCTCCT      600
    CCTCCGTGGT ATCCGTCGTG AGGATGTTCG GCGTGGTATG GTCATTGCTG      650
    CTCCTGGCAG CACCAAGGCC CACGACAAGT TCCTTGTCTC TATGTACGTC      700
25  CTCACTGAGG CTGAGGGTGG CCGTCGTACC GGATTCGGTA CCAACTACCG      750
    CCCCCAGGTC TTCATCCGTA CTGCCGGTAA GTGTTCCTGG AAGAGGCTTT      800
    GAGCCTATAT AGGATCTCGG ATAATTTACT AATCCACCAT ATAGATGAGG      850
    CCGCTGACCT CAGCTTCCCC GACAACGATG ACTCCCGCCG TGTCATGCCC      900
    GGTGACAACG TTGAGATGGT CCTGAAGACC CACCGCCCCG TGGCTGCTGA      950
30  G                                                                951

```

2) INFORMATION FOR SEQ ID NO: 1688

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Candida norvegica*

(B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688

```

50  CGTTGCCGCT ACCGATGGTC AAATGCCTCA AACTAGAGAA CATTGCTAT      50
    TGGCTAGACA GGTGTTGTT CAACACATTG TCGTGTGTTGT TAACAAGGTT      100
    GACACTATTG ATGATCCAGA AATGTTGGAA TTGGTTGAAA TGGAAATGAG      150
    AGAGTTGATT GCCACTTATG GTTTCGATGG TGATAACACC CCAGTTATCA      200

```


	TGGGTTCTGC	TCTATGTGCT	TTGGAAGGTC	GTGAACCTGA	AATCGGTGCT	250
	CAATCAATCG	ACAGATTGTT	GGAAGCCGTT	GATGAATACA	TTCCAACCTCC	300
	AACTAGAGAT	TTGGAAAAAC	CATTCTTGAT	GGGTGTTGAA	GATGTCTTCT	350
	CCATTTCTGG	TAGAGGTACC	GTCTGTACCG	GTCGTGTTGA	AAGAGGTAAC	400
5	TTGAAGAAAG	GTGATGAAAT	CGAAATTGTC	GGCTACAACA	AGACTCCAAT	450
	CAAAACCACC	GTCACCGGTA	TTGAGATGTT	CAAAAAGGAA	TTAGACCAAG	500
	CTATGGCTGG	TGATAACTGT	GGTATCTTAT	TACGTGGTGT	TAAGAGAGAT	550
	GATATCAAGA	GAGGTATGGT	TATCTCTAAA	GTCAACACCG	TTTCCGCACA	600
	CACCAAATTC	TTGGCCTCTT	TATACGTCTT	GAATAAGAA	GAAGGTGGTC	650
10	GTCATTCAGG	TTTTGCTGAA	AACTACAGAC	CTCAATTGTT	CATCAGAACC	700
	GGTGATGTCA	CTGTTACTTT	AACCTTCCCA	GAAGATGCTG	ATCACTCTCA	750
	GCAAGTCTTA	CCAGGTGACA	ACGTTGAAAT	GGAATGTACC	TTGGTTCATC	800
	CAACTGCTCT	TGAAACCGGT	CAA			823

15

2) INFORMATION FOR SEQ ID NO: 1689

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 201076

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689

	GCTGCTACTG	ACGGTCAAAT	GCCTCAAAC	AGGGAACATA	TGTTGTTGGC	50
	GAGACAAGTT	GGTATCCAAA	ACTTGTTGT	TTTTGTAAAC	AAAGTTGATA	100
35	CCATTGATGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGGGAA	150
	TTATTGAGCT	CTTATGGGTT	TGATGGTGAA	AACACTCCAG	TTATCATGGG	200
	ATCAGCCTTG	TGTGCTTTAG	AAGGTAAACA	ACCAGAAATC	GGTGTTC AAG	250
	CCATTCAAAA	ATTATTGGAT	GCTGTTGATG	AATATATTCC	AACTCCAGAA	300
	AGAGATGCTG	ACCAACCATT	TTTGATGCCA	GTGGAAGATG	TGTTTTCTAT	350
40	TTCAGGTAGA	GGAACCGTTG	TCACCGGAAG	AGTTGAAAGA	GGTATGTTGA	400
	AGAAAGGTGA	AGAAGTAKAA	GTCATTGGTG	AAAACCTCATT	TAAGGCTACT	450
	TCCACGGGTA	TTGAGATGTT	CAAAAAGGAA	TTGGATGCCG	CTATGGCCGG	500
	TGACAACTGT	GGTATTTTGT	TGAGAGGTGT	CAAGAGAGAC	GAAGTCAAGA	550
	GGGGTATGGT	TTTGGCCAAA	CCAGGTACCA	CCACCCACCA	CCAAAAGTTT	600
45	TTGGCTTCCA	TTTATATCTT	GACTGCTGAA	GAAGGTGGAC	G TAGTACCCC	650
	TTTCAGTGAA	GGATACAAAC	CACAATGTTT	CTTTAGAACT	AGTGATGTTA	700
	CCACGACATT	TACTTTCCCA	GAAGGTGAAG	GTGTTGACCA	CTCACAAATG	750
	GTTATGCCAG	GAGRCAATGT	TGAAATGGTG	GGAACCTTAA	TCAAGAAAGC	800
	TCC					803

50

2) INFORMATION FOR SEQ ID NO: 1690

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690

CAGGTCCTGT TGCGACTGAA GAA

23

15

2) INFORMATION FOR SEQ ID NO: 1691

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691

CACAGATAAA CCTGAGTGTG CTTTC

25

30

2) INFORMATION FOR SEQ ID NO: 1692

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692

GGTGAGAACT GTGGTATCTT ACTT

24

45

2) INFORMATION FOR SEQ ID NO: 1693

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693

CATTTCAACG CCTTCTTTCA ACTG

24

10

2) INFORMATION FOR SEQ ID NO: 1694

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694

AAGGCAAGGA TGACAACGGC

20

25

2) INFORMATION FOR SEQ ID NO: 1695

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695

ACGATTTCCTTCTTCCTG G

21

40

2) INFORMATION FOR SEQ ID NO: 1696

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696

ATGTTCTGT AGTTGCTGGA

20

5

2) INFORMATION FOR SEQ ID NO: 1697

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697

TTTCTTCAGC AATACCAACA AC

22

20

2) INFORMATION FOR SEQ ID NO: 1698

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698

35 GGAATCAACA GATGGTTTAC AAA

23

2) INFORMATION FOR SEQ ID NO: 1699

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699

50

GCATCTTCTG GGAAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1700

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700

AAGATGCGGA AAGAAGCGAA

20

2) INFORMATION FOR SEQ ID NO: 1701

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701

ATTATGGATC AGTTCTTGGA TCA

23

2) INFORMATION FOR SEQ ID NO: 1702

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: Challis V288
 (C) ACCESSION NUMBER: L20574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702

TTCATAGACG	CTGAGCACGC	TTTGGATCCA	TCTTACGCGG	CTGCTCTAGG	50
TGTAAATATT	GATGAGCTGT	TGCTATCTCA	ACCAGATTCT	GGTGAGCAAG	100
GTTTAGAAAT	TGCAGGAAAA	TTGATTGACT	CTGGGGCAGT	TGATTTAGTT	150

GTCATCGACT	CTGTTGCAGC	TCTTGTACCA	CGTGCGGAAA	TCGATGGAGA	200
TATCGGTGAT	AGC				213

5

2) INFORMATION FOR SEQ ID NO: 1703

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 692 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
- (B) STRAIN: strain GS-5
- (C) ACCESSION NUMBER: M61897

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703

GGGCCGGAAT	CTTCTGGTAA	GACAACTGTC	GCTCTTCATG	CTGCTGCTCA	50
GGCGCAAAAA	GATGGCGGTA	TTGCCGCTTT	CATTGATGCA	GAACATGCCC	100
25 TTGATCCAGC	CTATGCTGCT	GCTCTTGCG	TTAATATTGA	TGAGCTTTTG	150
CTTTCACAAC	CAGATTCAGG	AGAACAGGGT	CTTGAAATTG	CAGGGAAATT	200
GATTGATTCT	GGCGCTGTTG	ATTTAGTTGT	TGTTGACTCA	GTGGCAGCTT	250
TAGTACCACG	TGCGGAGATT	GACGGAGATA	TTGGTAATAG	TCATGTTGGC	300
TTACAAGCAC	GCATGATGAG	TCAAGCGATG	CGTAAATTAT	CAGCTTCAAT	350
30 CAATAAAACA	AAAACCATTG	CTATTTTTTAT	TAATCAATTG	CGGGAAAAAG	400
TTGGTATTAT	GTTTGGTAAAT	CCAGAAACAA	CCCCTGGCGG	GCGTGCCTTG	450
AAGTTTTTATT	CTTCTGTGCG	TCTTGATGTC	CGCGGCAATA	CTCAAATTAA	500
AGGAACCGGG	GAACAAAAAG	ACAGCAATAT	TGGTAAAGAG	ACCAAAATTA	550
AAGTTGTAA	AAATAAAGTT	GCTCCACCAT	TTAAGGAAGC	TTTTGTAGAA	600
35 ATTATATATG	GTGAAGGCAT	TTCTCGTACA	GGTGAATTAG	TTAAGATTGC	650
CAGTGATTTG	GGAATTATCC	AAAAAGCTGG	AGCTTGGTAC	TC	692

40 2) INFORMATION FOR SEQ ID NO: 1704

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: Z17307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704

	ATGGCGAAAA	AACCAAAAAA	ATTAGAAGAA	ATTTCAAAAA	AATTTGGGGC	50
	AGAACGTGAA	AAGGCCTTGA	ATGACGCTCT	TAAATTGATT	GAGAAAGACT	100
5	TTGGTAAAGG	ATCAATCATG	CGTTTGGGTG	AACGTGCGGA	GCAAAAGGTG	150
	CAAGTGATGA	GCTCAGGTTT	TTTAGCTCTT	GACATTGCCC	TTGGCTCAGG	200
	TGGTTATCCT	AAGGGACGTA	TCATCGAAAT	CTATGGCCCA	GAGTCATCTG	250
	GTAAGACAAC	GGTTGCCCTT	CATGCAGTTG	CACAAGCGCA	AAAAGAAGGT	300
	GGGATTGCTG	CCTTTATCGA	TGCGGAACAT	GCCCTTGATC	CAGCTTATGC	350
10	TGCGGCCCTT	GGTGTCAATA	TTGACGAATT	GCTCTTGTCT	CAACCAGACT	400
	CAGGAGAGCA	AGGTCTTGAG	ATTGCGGGAA	AATTGATTGA	CTCAGGTGCA	450
	GTTGATCTTG	TCGTAGTCGA	CTCAGTTGCT	GCCCTTGTTT	CTCGTGCGGA	500
	AATTGATGGA	GATATCGGAG	ATAGCCATGT	TGGTTTGCAG	GCTCGTATGA	550
	TGAGCCAGGC	CATGCGTAAA	CTTGGCGCCT	CTATCAATAA	AACCAAAACA	600
15	ATTGCCATTT	TTATCAACCA	ATTGCGTGAA	AAAGTTGGAG	TGATGTTTGG	650
	AAATCCAGAA	ACAACACCGG	GCGGACGTGC	TTTGAAATTC	TATGCTTCAG	700
	TCCGCTTGGA	TGTTTCGTGGT	AATACACAAA	TTAAGGGAAC	TGGTGATCAA	750
	AAAGAAACCA	ATGTCGGTAA	AGAACTAAG	ATTAAGGTTG	TAAAAAATAA	800
	GGTAGCTCCA	CCGTTTAAGG	AAGCCGTAGT	TGAAATTATG	TACGGAGAAG	850
20	GAATTTCTAA	GACTGGTGAG	CTTTTGAAGA	TTGCAAGCGA	TTTGATATT	900
	ATCAAAAAAG	CAGGGGCTTG	GTATTCTTAC	AAAGATGAAA	AAATTGGGCA	950
	AGGTTCTGAG	AATGCTAAGA	AATACTTGGC	AGAGCACCCA	GAAATCTTTG	1000
	ATGAAATTGA	TAAGCAAGTC	CGTTCTAAAT	TTGGCTTGAT	TGATGGAGAA	1050
	GAAGTTTCAG	AACAAGATAC	TGAAAACAAA	AAAGATGAGC	CAAAGAAAGA	1100
25	AGAAGCAGTG	AATGAAGAAG	TTCCGCTTGA	CTTAGGCGAT	GAACCTGAAA	1150
	TCGAAATTGA	AGAATAAGCT	GTAAAGCAG	TGGAGAAATC	CGCTACTTTT	1200
	TCGA					1204

30.

2) INFORMATION FOR SEQ ID NO: 1705

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 981 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: NZ131
- (C) ACCESSION NUMBER: U21934

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705

	ATGCGTTCAG	GAAGTCTAGC	TCTTGATATT	GCTTGGATAG	CTGGTGGTTA	50
	TCCTAAAGGA	CGTATCATCG	AAATCTATGG	TCCAGAGTCT	TCCGGTAAAA	100
50	CGACTGTGGC	TTTACATGCT	GTAGCACAAG	CTCAAAAAGA	AGGTGGAATC	150
	GCAGCCTTTA	TCGATGCCGA	GCATGCGCTT	GATCCAGCTT	ATGCTGCTGC	200
	GCTTGGGGTT	AATATTGATG	AACTTCTCTT	GTCTCAACCA	GATTCTGGAG	250
	AACAAGGACT	TGAAATTGCA	GGTAAATTGA	TTGATTCTGG	TGCGGTTGAC	300

	CTGGTTGTTG	TCGATTCAGT	AGCAGCTTTA	GTGCCACGTG	CTGAAATTGA	350
	TGGTGATATT	GGCGATAGCC	ATGTCGGATT	GCAAGCACGT	ATGATGAGTC	400
	AGGCCATGCG	TAAATTATCA	GCTTCTATTA	ATAAAACAAA	AACTATCGCA	450
	ATCTTTATCA	ACCAATTGCG	TGAAAAAGTT	GGTGTGATGT	TTGGAAATCC	500
5	TGAAACAACA	CCAGGTGGTC	GAGCTTTGAA	ATTCTATGCT	TCTGTTCCGC	550
	TGGATGTGCG	TGGAAACAAC	CAAATTAAAG	GAAGTGGTGA	CCAAAAGATA	600
	GCCAGCATTG	GTAAGGAGAC	CAAATCAAG	GTTGTTAAAA	ACAAGGTCGC	650
	TCCGCCATTT	AAGGTAGCAG	AAGTTGAAAT	CATGTATGGG	GAAGGTATTT	700
	CTCGTACAGG	GGAGCTTGTC	AAAATTGCTT	CTGATTGGA	CATTATCCAA	750
10	AAAGCAGGTG	CTTGTTCTC	TTATAATGGT	GAGAAGATTG	GCCAAGGTTT	800
	TGAAAATGCT	AAGCGTTATT	TGGCCGATCA	TCCACAATTG	TTTGATGAAA	850
	TCGACCGTAA	AGTACGTGTT	AAATTTGGTT	TGCTTGAAGA	AAGCGAAGAA	900
	GAATCTGCTA	TGGCAGTAGC	ATCAGAAGAA	ACCGATGATC	TTGCTTTAGA	950
15	TTTAGATAAT	GGTATTGAAA	TTGAAGATTA	A		981

2) INFORMATION FOR SEQ ID NO: 1706

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius* subsp. *thermophilus*
- (C) ACCESSION NUMBER: M94062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706

35	GCGTATGCAC	GAGCTCTAGG	TGTTAATATC	GATGAGCTTC	TTTTGTCGCA	50
	GCCTGATTCT	GGTGAGCAAG	GTCTCGAAAT	TGCAGGTAAG	CTGATTGACT	100
	CTGGTGCAGT	GGATTTAGTT	GTTGTTGACT	CAGTTGCGGC	CTTCGTACCA	150
	CGTGACAGAA	TTGATGGAGA	TAGTGGTGAC	AGTCATGTAG	GACTTCAAGC	200
	GCGTATGATG	AGTCAAGCCA	TGCGTAAACT	TTCTGCATCT	ATTAATAAAA	250
40	CAAAAACGAT	TGCTATCTTT	ATTAACCAGT	TGCGTGAAAA	AGTTGGTATC	300
	ATGTTTGGTA	AC				312

45 2) INFORMATION FOR SEQ ID NO: 1707

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: J02967

5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707

	ATGAAAAACA	CAATACATAT	CAACTTCGCT	ATTTTTTTTAA	TAATTGCAAA	50
	TATTATCTAC	AGCAGCGCCA	GTGCATCAAC	AGATATCTCT	ACTGTTGCAT	100
10	CTCCATTATT	TGAAGGAAC	GAAGGTTGTT	TTTTACTTTA	CGATGCATCC	150
	ACAAACGCTG	AAATTGCTCA	ATTCAATAAA	GCAAAGTGTG	CAACGCAAAT	200
	GGCACCAGAT	TCAACTTTCA	AGATCGCATT	ATCACTTATG	GCATTTGATG	250
	CGGAAATAAT	AGATCAGAAA	ACCATATTCA	AATGGGATAA	AACCCCCAAA	300
	GGAATGGAGA	TCTGGAACAG	CAATCATACA	CCAAAGACGT	GGATGCAATT	350
15	TTCTGTTGTT	TGGGTTTCGC	AAGAAATAAC	CCAAAAAATT	AGATTAAATA	400
	AAATCAAGAA	TTATCTCAAA	GATTTTGATT	ATGGAAATCA	AGACTTCTCT	450
	GGAGATAAAG	AAAGAAACAA	CGGATTAACA	GAAGCATGGC	TCGAAAAGTAG	500
	CTTAAAAAATT	TCACCAGAAG	AACAAATTCA	ATTCCTGCGT	AAAATTATTA	550
	ATCACAATCT	CCCAGTTAAA	AACTCAGCCA	TAGAAAACAC	CATAGAGAAC	600
20	ATGTATCTAC	AAGATCTGGA	TAATAGTACA	AAACTGTATG	GGAAAAGTGG	650
	TGCAGGATTC	ACAGCAAATA	GAACCTTACA	AAACGGATGG	TTTGAAGGGT	700
	TTATTATAAG	CAAATCAGGA	CATAAATATG	TTTTTGTGTC	CGCACTTACA	750
	GGAAACTTGG	GGTCGAATTT	AACATCAAGC	ATAAAAGCCA	AGAAAAATGC	800
	GATCACCATT	CTAAACACAC	TAAATTTATA	A		831

25.

2) INFORMATION FOR SEQ ID NO: 1708

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: HH22
 (C) ACCESSION NUMBER: M60253

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708

45	TTGAAAAAGT	TAATATTTTT	AATTGTAATT	GCTTTAGTTT	TAAGTGCATG	50
	TAATTCAAAC	AGTTCACATG	CCAAAGAGTT	AAATGATTTA	GAAAAAAAT	100
	ATAATGCTCA	TATTGGTGTT	TATGCTTTAG	ATACTAAAAG	TGGTAAGGAA	150
	GTAATAATTTA	ATTCAGATAA	GAGATTTGCC	TATGCTTCAA	CTTCAAAAGC	200
	GATAAATAGT	GCTATTTTGT	TAGAACAAGT	ACCTTATAAT	AAGTTAAATA	250
50	AAAAAGTACA	TATTAACAAA	GATGATATAG	TTGCTTATTC	TCCTATTTTA	300
	GAAAAATATG	TAGGAAAAGA	TATCACTTTA	AAAGCACTTA	TTGAGGCTTC	350
	AATGACATAT	AGTGATAATA	CAGCAAACAA	TAAAATTATA	AAAGAAATCG	400
	GTGGAATCAA	AAAAGTTAAA	CAACGTCTAA	AAGAACTAGG	AGATAAAGTA	450

	ACAAATCCAG	TTAGATATGA	GATAGAATTA	AATTACTATT	CACCAAAGAG	500
	CAAAAAAGAT	ACTTCAACAC	CTGCTGCTTT	CGGTAAGACT	TTAAATAAAC	550
	TTATCGCAA	TGGAATAA	AGCAAAGAAA	ACAAAAAATT	CTTACTTGAT	600
	TTAATGTTAA	ATAATAAAAG	CGGAGATACT	TTAATTAAAG	ACGGTGTTCC	650
5	AAAAGACTAT	AAGGTTGCTG	ATAAAAGTGG	TCAAGCAATA	ACATATGCTT	700
	CTAGAAATGA	TGTTGCTTTT	GTTTATCCTA	AGGGCCAATC	TGAACCTATT	750
	GTTTTAGTCA	TTTTTACGAA	TAAAGACAAT	AAAAGTGATA	AGCCAAATGA	800
	TAAGTTGATA	AGTGAAACCG	CCAAGAGTGT	AATGAAGGAA	TTTTAA	846

10

2) INFORMATION FOR SEQ ID NO: 1709

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 555 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: M29695

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709

	ATGTCCGCGA	GCACCCCCCC	CATAACTCTT	CGCCTCATGA	CCGAGCGCGA	50
	CCTGCCGATG	CTCCATGACT	GGCTCAACCG	GCCGCACATC	GTTGAGTGGT	100
30	GGGGTGCGA	CGAAGAGCGA	CCGACTCTTG	ATGAAGTGCT	GGAACACTAC	150
	CTGCCCAGAG	CGATGGCGGA	AGAGTCCGTA	ACACCGTACA	TCGCAATGCT	200
	GGGCGAGGAA	CCGATCGGCT	ATGCTCAGTC	GTACGTCGCG	CTCGGAAGCG	250
	GTGATGGCTG	GTGGGAAGAT	GAAACTGATC	CAGGAGTGCG	AGGAATAGAC	300
	CAGTCTCTGG	CTGACCCGAC	ACAGTTGAAC	AAAGGCCTAG	GAACAAGGCT	350
35	TGTCCGCGCT	CTCGTTGAAC	TACTGTTCTC	GGACCCCACC	GTGACGAAGA	400
	TTCAGACCGA	CCCGACTCCG	AACAACCATC	GAGCCATACG	CTGCTATGAG	450
	AAGGCAGGAT	TCGTGCGGGA	GAAGATCATC	ACCACGCCTG	ACGGGCCGGC	500
	GGTTTACATG	GTTCAAACAC	GACAAGCCTT	CGAGAGAAAG	CGCGGTGTTG	550
	CCTAA					555

40

2) INFORMATION FOR SEQ ID NO: 1710

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: K02987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710

5	ATGAACCAGA	AAAACCCTAA	AGACACGCAA	AATTTTATTA	CTTCTAAAAA	50
	GCATGTAAAA	GAAATATTGA	ATCACACGAA	TATCAGTAAA	CAAGACAACG	100
	TAATAGAAAT	CGGATCAGGA	AAAGGACATT	TTACCAAAGA	GCTAGTCAAA	150
	ATGAGTCGAT	CAGTTACTGC	TATAGAAATT	GATGGAGGCT	TATGTCAAGT	200
10	GACTAAAGAA	GCGGTAAACC	CCTCTGAGAA	TATAAAAGTG	ATTCAAACGG	250
	ATATTCTAAA	ATTTTCCTTC	CCAAAACATA	TAAACTATAA	GATATATGGT	300
	AATATTCCTT	ATAACATCAG	TACGGATATT	GTCAAAGAG	TTACCTTTGA	350
	AAGTCAGGCT	AAATATAGCT	ATCTTATCGT	TGAGAAGGGA	TTTGCGAAAA	400
	GATTGCAAAA	TCTGCAACGA	GCTTTGGGTT	TACTATTAAT	GGTGGAGATG	450
15	GATATAAAAA	TGCTCAAAAA	AGTACCACCA	CTATATTTTC	ATCCTAAGCC	500
	AAGTGTAGAC	TCTGTATTGA	TTGTTCTTGA	ACGACATCAA	CCATTGATTT	550
	CAAAGAAGGA	CTACAAAAAG	TATCGATCTT	TTGTTTATAA	GTGGGTAAAC	600
	CGTGAATATC	GTGTTCTTTT	CACTAAAAAC	CAATTCCGAC	AGGCTTTGAA	650
	GCATGCAAAT	GTCACTAATA	TTAATAAACT	ATCGAAGGAA	CAATTTCTTT	700
20	CTATTTTCAA	TAGTTACAAA	TTGTTTCACT	AA		732

2) INFORMATION FOR SEQ ID NO: 1711

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: BM2570
 (C) ACCESSION NUMBER: M19270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711

40	ATGAACAAAA	ATATAAAATA	TTCTCAAAAC	TTTTTAACGA	GTGAAAAAGT	50
	ACTCAACCAA	ATAATAAAAC	AATTGAATTT	AAAAGAAACC	GATACCGTTT	100
	ACGAAATTGG	AACAGGTAAA	GGGCATTTAA	CGACGAAACT	GGCTAAAATA	150
	AGTAAACAGG	TAACGTCTAT	TGAATTAGAC	AGTCATCTAT	TCAACTTATC	200
45	GTCAGAAAAA	TTAAAATCGA	ATACTCGTGT	CACTTTAATT	CACCAAGATA	250
	TTCTACAGTT	TCAATTCCCT	AACAAACAGA	GGTATAAAAT	TGTTGGGAAT	300
	ATTCCTTACC	ATTTAAGCAC	ACAAATTATT	AAAAAAGTGG	TTTTTGAAAG	350
	CCATGCGTCT	GACATCTATC	TGATTGTTGA	AGAAGGATTC	TACAAGCGTA	400
	CCTTGGATAT	TCACCGAACA	CTAGGGTTGC	TCTTGCACAC	TCAAGTCTCG	450
50	ATTCAGCAAT	TGCTTAAGCT	GCCAGCGGAA	TGCTTTTCATC	CTAAACCAAG	500
	AGTAAACAGT	GTCTTAATAA	AACTTACCCG	CCATACCACA	GATGTTCCAG	550
	ATAAATATTG	GAAGCTATAT	ACGTACTTTG	TTTCAAAATG	GGTCAATCGA	600
	GAATATCGTC	AACTGTTTAC	TAAAAATCAG	TTTCATCAAG	CAATGAAACA	650

CGCCAAAGTA	AACAATTTAA	GTACCGTTAC	TTATGAGCAA	GTATTGTCTA	700
TTTTTAATAG	TTATCTATTA	TTTAACGGGA	GGAAATAA		738

5

2) INFORMATION FOR SEQ ID NO: 1712

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 735 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: RN451
- (C) ACCESSION NUMBER: M17990

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712

ATGAACGAGA	AAAATATAAA	ACACAGTCAA	AACTTTATTA	CTTCAAAACA	50
TAATATAGAT	AAAATAATGA	CAAATATAAG	ATTAAATGAA	CATGATAATA	100
25 TCTTTGAAAT	CGGCTCAGGA	AAAGGGCATT	TTACCCTTGA	ATTAGTACAG	150
AGGTGTAATT	TCGTAAGTGC	CATTGAAATA	GACCATAAAT	TATGCAAAAC	200
TACAGAAAAT	AAACTTGTTG	ATCACGATAA	TTTCCAAGTT	TTAAACAAGG	250
ATATATTGCA	GTTTAAATTT	CCTAAAAACC	AATCCTATAA	AATATTTGGT	300
AATATACCTT	ATAACATAAG	TACGGATATA	ATACGCAAAA	TTGTTTTTGA	350
30 TAGTATAGCT	GATGAGATTT	ATTTAATCGT	GGAATACGGG	TTTGCTAAAA	400
GATTATTAAA	TACAAAACGC	TCATTGGCAT	TATTTTTAAT	GGCAGAAGTT	450
GATATTTCTA	TATTAAGTAT	GGTTCCAAGA	GAATATTTTC	ATCCTAAACC	500
TAGAGTGAAT	AGCTCACTTA	TCAGATTAAA	TAGAAAAAAA	TCAAGAATAT	550
CACACAAAGA	TAAACAGAAG	TATAATTATT	TCGTTATGAA	ATGGGTTAAC	600
35 AAAGAATACA	AGAAAATATT	TACAAAAAAT	CAATTTAACA	ATTCCTTAAA	650
ACATGCAGGA	ATTGACGATT	TAAACAATAT	TAGCTTTGAA	CAATTCTTAT	700
CTCTTTTCAA	TAGCTATAAA	TTATTTAATA	AGTAA		735

40

2) INFORMATION FOR SEQ ID NO: 1713

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(C) ACCESSION NUMBER: U00456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713

5	ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
	TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
	AAAAATTCGA	TCCGCACTAC	ATCGGAATTA	CAAAAACGG	CGTATGGAAG	150
	CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
	ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
10	AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
	TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
	CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGCAATG	GACAAATCAC	400
	TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
	ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
15	CTTTGTGAAG	CCGGCACGGT	CAGGTTTCGTC	CTTTGGCGTA	ACCAAAGTAA	550
	ACAGTACGGA	AGAATAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
	GGAAAAATCT	TAATTGAGCA	AGCGATTTTCG	GGCTGTGAGG	TCGGCTGCGC	650
	GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
	GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
20	GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
	ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
	GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
	GTTCTAAACG	AGGTCAATAC	CCTGCCCCGT	TTTACATCGT	ACAGCCGCTA	950
	TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
25	GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 1714

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

35

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*

(B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714

45	GCACAGGTTC	AGTTGGGCTT	GATCTTGCTT	TAGGTATAGG	CGGTGTTCCA	50
	AAAGGAAGAA	TTATAGAAAT	TTATGGRCTT	GAAAGTTCAG	GTAAAACCAC	100
	TCTAACTCTA	CACATTATCG	CAGAATGCCA	AAAAGCAGGT	GGRGTTTGTG	150
	CTTTTATCGA	TGCAGAACAT	GCRCTTGATG	TRAAATATGC	TAAAAATTTG	200
	GGTGTAATA	CAGATGATTT	GTATGTTTCT	CAGCCTGATT	TTGGAGARCA	250
50	AGCCTTAGAA	ATTGTAGAAA	CTATAGCAAG	AAGTGGCGCA	GTAGATCTTA	300
	TCGTAGTAGA	TAGCGTTGCA	GCGCTTACCC	CAAAAGCAGA	AATTGAAGGC	350
	GATATGGGTG	ATCAACATGT	AGGACTTCAA	GCAAGACTTA	TGTCTCAAGC	400
	TCTAAGAAAA	CTTACAGGTA	TAGTTCATAA	AATGAATACC	ACAGTAATTT	450

	TYATCAACCA	AATTCGTATG	AAAATCGGTG	CTATGGGTTA	TGGTACTCCT	500
	GAAACCACAA	CAGGTGGAAA	TGCATTAAAA	TTTTATGCTT	CTGTGCGTTT	550
	AGATGTTAGA	AAAGTAGCAA	CCTTAAACA	AAACGAAGAA	CCTATAGGAA	600
	ACCGCGTTAA	AGTAAAAGTA	GTTAAAAATA	AAGTTGCTCC	TCCATTTCAGA	650
5	CAAGCTGAAT	TTGATGTGAT	GTTTGGAGAG	GGTTTAAGCC	GTGAAGGTGA	700
	ATTGATCGAT	TATGGTGTAA	AACTTGATAT	CGTAGATAAA	AGTGGTGCGT	750
	GGTTTTCTTA	TAAAGATAAA	AAACTTGGAC	AAGGTAGAGA	AAATTCAAAA	800
	GCTTCTTAA	AAGAAAAC				818

10

2) INFORMATION FOR SEQ ID NO: 1715

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175
 25 (C) ACCESSION NUMBER: AF124224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715

	TGGTGCTATC	TTAGTAGTAT	CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	50
30	GTGAACACAT	CTTATTATCA	CGTCAAGTAG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
	ACACTCCAGT	TGTTGCAGGT	TCTGCTTTAC	GCGCTTTAGA	AGGCGACGCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ACGAATACAT	300
35	TCCAACCTCCA	GAACGYGACG	TTGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATCACAGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGTGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTTTCAGA	450
	AGAAACTTCA	AAAACAACCTG	TAAGTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGG	GATAACATTG	GTACATTATT	ACGTGGTGTT	550
40	ACACGTGACA	ACATCGAACG	TGGACAAAGT	CTTGCTAAAC	CAGGAACAAT	600
	CACTCCACAT	ACTAAATTCA	AAGCTGAAGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACATCAC	TGGTGTGTTG	GTGTTACCAG	AAGGCGTTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATTCACC	800
45	CAGTAGCGA					809

2) INFORMATION FOR SEQ ID NO: 1716

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia defectiva*
(B) STRAIN: ATCC 49176
(C) ACCESSION NUMBER: AF124225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716

	CGGCGCGATC	CTCGTTGTAT	CTGCTGCTGA	CGGCCCAATG	CCACAAACTC	50
	GTGAACACAT	CCTCTTGTCT	CGTCAAGTTG	GTGTTCCCTTA	CATCGTAGTA	100
15	TTCTTGAACA	AAGTTGACAT	GGTTGACGAC	GAAGAATTGC	TCGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACC	TCTTGTCTGA	ATACGACTTC	CCAGGCGACG	200
	AACTCCAGT	TATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	AACTACGAAG	CTAAAGTTTT	AGAATTGATG	GAACAAGTTG	ATGCTTACAT	300
	TCCAGAACCA	GAACGTGACA	CTGACAAGCC	ATTCATGATG	CCAGTCGAAG	350
20	ACGTATTCTC	TATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGTCAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCGAAGA	450
	AGAAACTTCT	AAGACTACCG	TTACCGGTGT	TGAAATGTTC	CGTAAGTTAT	500
	TGGATTACGC	TGAAGCTGGG	GACAACGTTG	GTACCTTGTT	ACGTGGTGTA	550
	ACTCGTGACC	AAATCCAACG	TGGTCAAGTA	TTATCTAAAC	CAGGTTCAAT	600
25	CACTCCGYAC	ACTAAGTTCG	AAGCTGAAGT	GTACGTATTG	TCTAAAGAAG	650
	AAGGTGGTCG	TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCAGGCGACA	ACGTACAAAT	GGTTGTTGAA	TTGATCCACC	800
30	CAATCGCGAT	CGAAGAA				817

2) INFORMATION FOR SEQ ID NO: 1717

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*
(B) STRAIN: ATCC 49725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717

	CGGCGCTATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
50	GCGAGCACGT	TCTGCTTGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTCGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	GGAGATGGAG	ATCTCCGAGC	TGCTCGCAGA	GCAGGACTAC	GATGAGGAAG	200
	CTCCTATCGT	TCACATCTCC	GCTCTGAAGG	CACTCGAGGG	TGACGAGAAG	250

	TGGGTACAGT	CCATCGTTGA	CCTGATGGAT	GCCTGCGACA	ACTCCATCCC	300
	TGATCCGGAG	CGCGCTACCG	ATCAGCCGTT	CTTGATGCCT	ATCGAGGACA	350
	TCTTCACCAT	TACCGGCCCG	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGTCGTCTGA	ACGTCAACGA	GGACGTTGAG	ATCATCGGTA	TCCAGGAGAA	450
5	GTCCCAGAAC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGC	AAGATGATGG	500
	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTGCG	TGGTACCAAG	550
	CGTGAGGACG	TTGAGCGTGG	CCAGGTTGTT	ATCAAGCCGG	GCGCTTACAC	600
	CCCTCACACC	AAGTTCGAGG	GTTCCGTCTA	CGTCCTGAAG	AAGGAAGAGG	650
	GCGGCCGCCA	CACCCCGYTC	ATGAACAAC	ACCGTCCTCA	GTTCTACTTC	700
10	CGCACCACCG	ACGTTACCGG	TGTTGTGAAC	CTGCCTGAGG	GCACCGAGAT	750
	GGTTATGCCT	GGCGACAACG	TTGAGATGTC	TGTTGAGCTC	ATCCAGCCTG	800
	TTGCTATGGA	CGAG				814

15

2) INFORMATION FOR SEQ ID NO: 1718

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 814 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*
- (B) STRAIN: ATCC 33031

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718

	CGGCGCCATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GTGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTAGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAGCTGC	TGGAGCTCGT	150
35	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CACCTGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
	TGGGCTAAGC	AGATCCTGGA	GCTCATGGAG	GCTTGCGACA	ACTCCATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGRGGACA	350
	TCTTCACCAT	TACCGGCCCG	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
40	GGCGTCCTGA	ACCTGAACGA	CGAGGTCGAG	ATCCTGGGCA	TCCGCGAGAA	450
	GTCCACCAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
	ACACCGCAGA	GGCTGGCGAC	AACGCCGCAC	TGCTGCTGCG	TGGCCTGAAG	550
	CGCGAAGATG	TTGAGCGTGG	TCAGATCGTT	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
45	GTGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTATTTT	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCGGAGG	GCACCGAGAT	750
	GGTTATGCCG	GGCGACAACG	TTGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

50

2) INFORMATION FOR SEQ ID NO: 1719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*
 (B) STRAIN: ATCC 43216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719

15	CGGCGCCATC	CTGGTTGTTG	CCGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GCGAGCACGT	TCTGCTGGCY	CGCCAGGTTG	GCGTTCGTA	CATCCTGGTT	100
	GCACTGAACA	AGTGTGACAT	GGTTGACGAT	GAGGAGCTGC	TGGAGCTCGT	150
	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CTCCGGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
20	TGGGCTAACC	AGATTCTCGA	GCTGATGCAG	GCTTGCGACG	AGTCTATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGWGGACA	350
	TCTTCACCAT	TACCGGTCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCATCCTGA	ACCTGAACGA	CGAGGTTGAG	ATCCTGGGTA	TCCGCGAGAA	450
	GTCCCAGAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
25	ACACCGCAGA	GGCTGGCRAC	AACGCTGCAC	TGCTGCTGCG	TGGTCTGAAG	550
	CGCGAGGACG	TTGAGCGTGG	CCAGATCATC	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCTGAGG	GCACCGAGAT	750
30	GGTTATGCCG	GGCGACAACG	TYGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

35 2) INFORMATION FOR SEQ ID NO: 1720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720

50	CGGCGCTATC	TTGGTTGTTG	CAGCTACCGA	CGGCCCAATG	CCACAGACTC	50
	GCGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTGGTT	100
	GCACTAAACA	AGTGCGACAT	GGTTGACGAC	GAGGAAATCC	TCGAGCTCGT	150

	CGAGATGGAG	ATCCGCGAAT	TGCTGGCTGA	CCAGGAATTC	GACGAAGAAG	200
	CTCCAATCGT	TCACATCTCC	GCAGTCGGCG	CCTTGGAAGG	CGAAGAGAGG	250
	TGGGTAAACG	CCATCGTTGA	ACTGATGGAT	GCTTGTGACG	AGTCGATCCC	300
	TGATCCAGAC	CGTGCTACCG	ACAAGCCATT	CCTGATGCCT	ATCGAGGACA	350
5	TCTTCACCAT	TACCGGTCGT	GGCACC GTTG	TTACGGGTCG	TGTTGAGCGT	400
	GGTTCCTGA	AGGTCAACGA	AGAAGTCGAG	ATCATCGGCA	TCAAGGAAAA	450
	GTCCCAGAAG	ACCACCATCA	CCGGTATCGA	AATGTTCCGC	AAGATGCTGG	500
	ACTACACCGA	GGCCGGCGAC	AACGCTGGTC	TGCTGCTTCG	CGGTACCAAG	550
	CGTGAAGACG	TTGAGCGTGG	ACAGGTATATC	GTTGCTCCAG	GTGCTTACAG	600
10	CACCCACAAG	AAGTTCGAAG	GTTCCGTCTA	CGTTCTTTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAACT	ACCGTCCTCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTTACC	CTGCCTGAGG	GCACCGAG	748

15

2) INFORMATION FOR SEQ ID NO: 1721

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 813 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium striatum*
- (B) STRAIN: ATCC 6940

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721

	GGCGCTATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCGRTGC	CGCAGACCCG	50
	CGAGCACGTT	CTTCTGGCTC	GCCAGGTTGG	CGTTCCTTAC	ATCCTCGTTG	100
	CACTGAACAA	GTGCGACATG	GTTGACGACG	AGGAAATTAT	CGAGCTCGTC	150
35	GAGATGGAGA	TCCGCGAACT	GCTCGCAGAG	CAGGACTACG	ATGAGGAAGC	200
	TCCGATCGTT	CACATCTCTG	CTCTGAAGGC	TCTTGAGGGC	GRCGAGAAGT	250
	GGGTACAGGC	TATCGTTGAC	CTGATGCAGG	CTTGCGATGA	CTCCATCCCG	300
	GATCCGGAGC	GCGAGCTGGA	CAAGCCGTTC	CTGATGCCAA	TCGAGGACAT	350
	CTTCACCATC	ACCGGCCGCG	GTACCGTTGT	TACTGGCCGT	GTTGAGCGTG	400
40	GCTCCCTGAA	CGTCAACGAG	GACGTTGAGA	TCATCGGTAT	CCAGGACARG	450
	TCCATCTCCA	CCACCGTTAC	CGGTATCGAG	ATGYTCCGCA	AGATGATGGA	500
	CTACACCGAG	GCTGGCGACA	ACTGTGGTCT	GCTTCTGCGT	GGTACCAAGC	550
	GTGAAGAGGT	TGAGCGCGGC	CAGGTTGTTA	TTAAGCCGGG	CGCTTACACC	600
	CCTCACACCC	AGTTCGAGGG	TTCCGTCTAC	GTCCTGAAGA	AGGAAGAGGG	650
45	CGGCCGCCAC	ACCCCGTTCA	TGGACAACCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTTACCGGC	GTCATCAAGC	TGCCTGAGGG	CACCGAGATG	750
	GTTATGCCTG	GCGACAACGT	CGAGATGTCY	GTCGAGCTGA	TCCAGCCGGT	800
	CGCTATGGAC	GAG				813

50

2) INFORMATION FOR SEQ ID NO: 1722

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025
 (C) ACCESSION NUMBER: AF124220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCCCTTA	CATCGTTGTA	100
TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TTGAATTAGT	150
TGAAATGGAA	GTTCGTGACT	TATTAACCTGA	ATACGACTTC	CCAGGCGACG	200
ACACTCCAGT	TATCGCAGGT	TCAGCGTTGA	AAGCTTTAGA	AGGCGACGCT	250
TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ACGAATATAT	300
CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
CGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
TAGACTACGC	TGAAGCAGGT	GACAACATCG	GTGCTTTGTT	ACGTGGTGTT	550
GCACGTGAAG	ATATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTATGTTCTA	ACTAAAGAAG	650
AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
TTCCGTACAA	CTGACGTAAC	TGGTGTAGTT	GATCTACCAG	AAGGTACTGA	750
AATGGTWATG	CCTGGGGATA	ACGTAACCTAT	GGAAGTTGAA	TTGATYCACC	800
CAATYGCGGT	AGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
 (B) STRAIN: ATCC 14018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723

TGGCGCAATC	CTCGTGGTTG	CTGCTACCGA	CGGTCCAATG	GCTCAGACCC	50
GTGAACACGT	CTTGCTTGCT	AAGCAGGTGC	GCGTTCCAAA	AATTCTTGTT	100

	GCTTTGAACA	AGTGCGATAT	GGTTGACGAC	GAAGAGCTTA	TCGATCTCGT	150
	TGAAGAAGAG	GTCCGTGACC	TCCTCGAAGA	AAACGGCTTC	GATCGCGATT	200
	GCCCAGTCYT	CCGTACTTCC	GCTTACGGCG	CTTTGCATGA	TGACGCTCCA	250
	GACCACGACA	AGTGGGTAGA	GACCGTCAAG	GAAGTCATGA	AGGCTGTTGA	300
5	CGAGTACATC	CCAACCCCAA	CTCACGATCT	TGACAAGCCA	TTCTTGATGC	350
	CAATCGAAGA	TGTGTTTACC	ATCTCCGGTC	GTGGTYCCGT	TGTCACCGGT	400
	CGTGTTGAGC	GTGGTAAGCT	CCCAATCAAC	ACCCAGTTG	AGATCGTTGG	450
	TTTGCGCGAT	ACCCAGACCA	CCACCGTCAC	CTCTATCGAG	ACCTTCCACA	500
	AGCAGATGGA	TGAGGCAGAG	GCTGGCGATA	ACACTGGTCT	TCTTCTCCGC	550
10	GGTATCAACC	GTACCGACGT	TGAGCGTGGT	CAGGTTGTGG	CTGCTCCAGG	600
	TTCTGTGACT	CCACACACCA	AGTTCGAAGG	CGAAGTTTAC	GTCTTGACCA	650
	AGGACGAAGG	TGGCCGTCAC	TCGCCATTCT	TCTCCAACTA	CCGTCCACAG	700
	TTCTACTTCC	GTACCACCGA	TGTTACTGGC	GTTATCACCT	TGCCAGACGG	750
	CATCGAAATG	GTTTCAGCCAG	GCGATCACGC	AACCTTCACT	GTTGAGTTGA	800
15	TCCAGGCTAT	CGCAATGGAA	GAG			823

2) INFORMATION FOR SEQ ID NO: 1724

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Listeria innocua*
- (B) STRAIN: ATCC 33090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
40	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
45	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTT	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
50	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1725

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACATAT	TCTTACTTTC	ACGTCAAGTT	GGTGTTCAT	ACATCGTTGT	100
	ATTCATGAAC	AAATGTGACA	TGGTTGACGA	TGAAGAATTA	CTTGAATTAG	150
20	TTGAAATGGA	AATTCGTGAT	CTATTAAGT	AATATGAATT	CCCTGGCGAC	200
	GACATTCCTG	TAATCAAAGG	TTCAGCTCTT	AAAGCACTTC	AAGGTGAAGC	250
	TGATTGGGAA	GCTAAAATTG	ACGAGTTAAT	GGAAGCTGTA	GATTCTTACA	300
	TTCCAACCTC	AGAACGTGAT	ACTGACAAAC	CATTCATGAT	GCCAGTTGAG	350
	GATGTATTCT	CAATCACTGG	TCGTGGAACA	GTTGCAACTG	GACGTGTTGA	400
25	ACGTGGACAA	GTTAAAGTTG	GTGACGAAGT	AGAAGTTATC	GGTATTGAAG	450
	AAGAAAGCAA	AAAAGTAGTA	GTAAGTGGAG	TAGAAATGTT	CCGTAAATTA	500
	CTAGACTACG	CTGAAGCTGG	CGACAACATT	GGCGCACTTC	TACGTGGTGT	550
	TGCTCGTGAA	GATATCCAAC	GTGGTCAAGT	ATTAGCTAAA	CCAGGTTCGA	600
	TTACTCCACA	TACTAACTTC	AAAGCTGAAA	CTTATGTTTT	AACTAAAGAA	650
30	GAAGGTGGAC	GTCATACTCC	ATTCTTCAAC	AACTACCGCC	CACAATTCTA	700
	TTTCCGTACT	ACTGACGTAA	CTGGTATTGT	TACACTTCCA	GAAGGTACTG	750
	AAATGGTAAT	GCCTGGTGAT	AACATTGAGC	TTGCAGTTGA	ACTAATTGCA	800
	CCAATCGCTA	TCGAAGAC				818

2) INFORMATION FOR SEQ ID NO: 1726

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: LSPQ 5093202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
--	------------	------------	------------	------------	------------	----

	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
5	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCW	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATCGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
10	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGT	550
	GCTCGTGAAG	ATATCCAACR	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
15	AATGGTAAYG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*
 (B) STRAIN: ATCC 35967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGTGATG	200
40	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
45	AGAAAGCAAA	AAAGTAATAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGT	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAT	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
50	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1728

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728

CGGTGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
AGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
ATGTACCTGT	AATCGCTGGT	TCAGCATTAR	AAGCTTTAGA	AGGCGATGCT	250
CAATACGAAG	AAAAAATCTT	AGAATTARTG	GAAGCTGTAG	ATACTTACAT	300
TCCAAC TCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
CACATCTAAA	ACAAC TGTTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	500
ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTTGCT	550
CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	650
GTGGACGTCA	CACTCCATT C	TTCTCAAAC T	ATCGTCCACA	ATTCTATTT C	700
CGTACTACTG	ACGTAAC TGG	TGTTGTTT CAC	TTACCAGAAG	GTACTGAAAT	750
GGTAATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCAA	800
TCGCGATTGA	AGAC				814

2) INFORMATION FOR SEQ ID NO: 1729

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
------------	------------	------------	------------	------------	----

	GTGAACACAT	TCTTTTATCA	CGTRACGTTG	GTGYTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAY	GAAGAATTAT	TAGAATTRGT	150
	AGAAATGGAA	GTTTCGTGRCT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACGCT	250
5	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTYCAT	300
	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAATC	GARATCATCG	GTATGCAAGA	450
	AGAATCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
10	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCATTATT	ACGTGGTGT	550
	TCACGTGATG	ATGTACAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTACTAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGATGT	TTACGTTTTA	TCTAAAGATG	650
	AAGGTGGTCG	TCATACGCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTTACTA	CTGACGTAAC	TGGTGTGTGTT	AACTTACCAG	AAGGTACTGA	750
15	AATGGTTATG	CCTGGCGATA	ACGTTGAAAT	GGATGTTGAA	TTAATTTCTC	800
	CAATCGCTAT	TGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1730

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*
 (B) STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730

35	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
40	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
45	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGT	550
	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
50	TTCCGTTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTGATCGCTC	800
	CAATCGCGAT	TGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1731

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731

	CGGAGCTATC	CTTGTAGTTG	CTTCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTAAACA	CCTTATCGTA	100
20	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	ATACGACTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCACTTGA	AGGCGACGAA	250
	AAATACGAAG	ACATCATCAT	GGAATTGATG	AGCACTGTTG	ATGAGTACAT	300
	TCCAGAACCA	GAACGTGATA	CTGACAAACC	TTTACTTCTT	CCAGTTGAAG	350
25	ATGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTCGTGTCAA	CGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
	AGATATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCAAGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTT	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
30	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAAGTTCCAG	CAGGAACAGA	750
	AATGGTTATG	CCTGGTGATA	ACGTTACTAT	CGAAGTTGAA	TTGATTCAAC	800
35	CAATCGCCGT	AGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1732

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732

	CGGAGCTATC	CTTGTAAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TATTGTCAGA	ATACGACTTC	CCAGGTGACG	200
5	ATCTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATACGAAG	ACATCGTTAT	GGAATTGATG	AACACAGTTG	ATGAGTATAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTATCG	TTAAAGTCAA	CGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
10	AGAAACTCRA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTAG	GTGTCCTTCT	TCGTGGTGTT	550
	CAACGTGATG	AAATCGAACG	TGGACAAAGT	ATCGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	CTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
15	TTCCGTACTA	CTGACGTTAC	AGGTTCAATC	GAACTTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTGACAAT	CGACGTTGAG	TTGATTCACC	800
	CAATCGCCGT	AGAACAA				817

20

2) INFORMATION FOR SEQ ID NO: 1733

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
(B) STRAIN: ATCC 7073

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733

	CGGTGCGATC	CTTGTAAGTAG	CATCTACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTT	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGATTCT	250
	AAATACGAAG	ACATCATCAT	GGACTTGATG	AACACTGTTG	ACGAATACAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGTTGCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTGTTG	TTCGTGTCAA	TGACGAAGTT	GAAATCGTTG	GTCTTAAAGA	450
	AGACATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGRAGG	TATTGCCGGA	GATAACGTCG	GTGTTCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTGCAC	CTGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAACTTCCTG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1734

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Agrobacterium tumefaciens*
 (C) ACCESSION NUMBER: x99673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734

AACATGATCA	CCGGTGCTGC	CGAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
GGCTGCCGAC	GGCCCGATGC	CACAGACCCG	CGAGCACATC	CTGCTTGCCC	100
GTCAGGTGGG	CGTTCCGGCC	ATCGTCGTGT	TCCTCAACAA	GGTCGACCAG	150
GTTGACGACG	CCGAGCTTCT	CGAGCTCGTC	GAGCTTGAAG	TTCGCGAACT	200
TCTGTCGTCC	TACGACTTCC	CGGGCGACGA	TATCCCGATC	ATCAAGGGTT	250
CGGCACTTGC	TGCTCTTGAA	GATTCTGACA	AGAAGATCGG	TGAAGACGCG	300
ATCCGCGAGC	TGATGGCTGC	TGTCGACGCC	TACATCCCGA	CGCCTGAGCG	350
TCCGATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACGGTTGTG	ACGGGTCGCG	TTGAGCGCGG	TATCGTCAAG	450
GTTGGTGAAG	AAGTCGAAAT	CGTCGGCATC	CGTCCGACCT	CGAAGACGAC	500
TGTTACCGGC	GTTGAAATGT	TCCGCAAGCT	GCTCGACCAG	GGCCAGGCCG	550
GCGACAACAT	CGGTGCACTC	GTTGCGGGCG	TTACCCGTGA	CGGCGTCGAG	600
CGTGGTCAGA	TCCTGTGCAA	GCCGGGTTTCG	GTCAAGCCGC	ACAAGAAGTT	650
CATGGCAGAA	GCCTACATCC	TGACGAAGGA	AGAAGGCGGC	CGTCATACGC	700
CGTTCTTCAC	GAATAACCGT	CCGCAGTTCT	ACTTCCGTAC	GACTGACGTT	750
ACCGGTATCG	TTTCGCTTCC	TGAAGGCACG	GAAATGGTTA	TGCCTGGCGA	800
CAACGTCACT	GTTGAAGTCG	AGCTGATCGT	TCCGATCGCG	ATGGAAGAAA	850
AGCTGCGCTT	CGCTATCCGC	GAAGGCGGCC	GTACCGTCGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1735

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*
 (B) STRAIN: 168
 (C) ACCESSION NUMBER: Z99104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735

	ATGATCACTG	GTGCTGCGCA	AATGGACGGA	GCTATCCTTG	TAGTATCTGC	50
	TGCTGATGGC	CCAATGCCAC	AAACTCGTGA	GCACATCCTT	CTTTCTAAAA	100
	ACGTTGGTGT	ACCATACATC	GTTGTATTCT	TAAACAAATG	CGACATGGTA	150
5	GACGACGAAG	AGCTTCTTGA	ACTAGTTGAA	ATGGAAGTTC	GCGATCTTCT	200
	TAGCGAATAC	GACTTCCCTG	GTGATGATGT	ACCAGTTGTT	AAAGGTTCTG	250
	CTCTTAAAGC	TCTTGAAGGA	GACGCTGAGT	GGGAAGCTAA	AATCTTCGAA	300
	CTTATGGATG	CGGTTGATGA	GTACATCCCA	ACTCCAGAAC	GCGACACTGA	350
	AAAACCATTC	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	400
10	GTACAGTTGC	TACTGGCCGT	GTAGAACGCG	GACAAGTTAA	AGTCGGTGAC	450
	GAAGTTGAAA	TCATCGGTCT	TCAAGAAGAG	AACAAGAAAA	CAACTGTTAC	500
	AGGTGTTGAA	ATGTTCCGTA	AGCTTCTTGA	TTACGCTGAA	GCTGGTGACA	550
	ACATTGGTGC	CCTTCTTCGC	GGTGTATCTC	GTGAAGAAAT	CCAACGTGGT	600
	CAAGTACTTG	CTAAACCAGG	TACAATCACT	CCACACAGCA	AATTCAAAGC	650
15	TGAAGTTTAC	GTTCTTTCTA	AAGAAGAGGG	TGGACGTCAT	ACTCCATTCT	700
	TCTCTAACTA	CCGTCCCTCAG	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	750
	ATCATCCATC	TTCCAGAAGG	CGTAGAAATG	GTTATGCCTG	GAGATAACAC	800
	TGAAATGAAC	GTTGAACTTA	TTTCTACAAT	CGCTATCGAA	GAAGGAACCT	850
	GTTTCTCTAT	TCGTGAAGGC	GGACGTACTG	TTGGT		885
20						

2) INFORMATION FOR SEQ ID NO: 1736

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*
 (B) STRAIN: DSM 2151
 (C) ACCESSION NUMBER: P33165

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736

40	ATGGTTACTG	GTGCTGCTCA	GATGGACGGT	GCTATCATTG	TAGTTGCTGC	50
	TACTGATGGT	CCGATGCCTC	AGACTCGTGA	GCACATCCTT	TTGGCTCGTC	100
	AGGTAAACGT	TCCGAAGCTG	GTTGTATTCA	TGAACAAGTG	CGATATGGTT	150
	GAAGATGCTG	AGATGTTGGA	ACTTGTGTA	ATGGAAATGA	GAGAATTGCT	200
	TTCATTCTAT	GATTTCGACG	GTGACAATAC	TCCGATCATT	CAGGGTTCTG	250
45	CTCTTGGTGC	ATTGAACGGC	GTAGAAAAAT	GGGAAGACAA	AGTAATGGAA	300
	CTGATGGAAG	CTGTTGATAC	TTGGATTCCA	CTGCCTCCGC	GCGATGTTGA	350
	TAAACCTTTC	TTGATGCCGG	TAGAAGACGT	GTTCTCTATC	ACAGGTCGTG	400
	GTAAGTAGC	TACAGGTCGT	ATCGAAACTG	GTGTTATCCA	TGTAGGTGAT	450
	GAAATCGAAA	TCCTCGGTTT	GGGTGAAGAT	AAGAAATCAG	TTGTAACAGG	500
50	TGTTGAAATG	TTCCGCAAAC	TTCTGGATCA	GGGTGAAGCT	GGTGACAACG	550
	TAGGTCTGTT	GCTTCGTGGT	GTTGACAAGA	ACGAAATCAA	ACGTGGTATG	600
	GTTCTTTGTA	AACCGGGTCA	GATTAAACCT	CACTCTAAAT	TCAAAGCAGA	650
	GGTTTATATC	CTGAAGAAAG	AAGAAGGTGG	TCGTCACACT	CCATTCCATA	700

ACAAATATCG	TCCTCAGTTC	TACCTGCGTA	CTATGGACTG	TACAGGTGAA	750
ATCACTCTTC	CGGAAGGAAC	TGAAATGGTA	ATGCCGGGTG	ATAACGTAAC	800
TATCACTGTA	GAGTTGATCT	ATCCGGTTGC	ACTGAACATC	GGTCTTCGTT	850
TCGCTATCCG	CGAAGGTGGA	CGTACAGTAG	GT		882

5

2) INFORMATION FOR SEQ ID NO: 1737

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 (B) STRAIN: U78183
 (C) ACCESSION NUMBER: U78183

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737

25	AATATGATTA	CAGGAGCAGC	TCAAATGGAT	GCAGCGATAC	TTTTAGTTGC	50
	TGCTGATAGT	GGTGCTGAGC	CTCAAACAAA	AGAGCATTTG	CTTCTTGCTC	100
	AAAGAATGGG	AATAAAGAAA	ATAATAGTTT	TTTTAAATAA	ATTGGACTTA	150
	GCAGATCCTG	AACTTGTTGA	GCTTGTTGAA	GTTGAAGTTT	TAGAACTTGT	200
	TGAAAAATAT	GGCTTTTCAG	CTGATACTCC	AATAATCAAA	GGTTCAGCTT	250
30	TTGGGGCTAT	GTCAAATCCA	GAAGATCCTG	AATCTACAAA	ATGCGTTAAA	300
	GAAGTTCTTG	AATCTATGGA	TAATTATTTT	GATCTTCCAG	AAAGAGATAT	350
	TGACAAGCCA	TTTTTGCTTG	CTGTTGAAGA	TGTATTTTCT	ATTTTCAGGAA	400
	GAGGCACTGT	TGCTACTGGG	CGTATTGAAA	GAGGTATTAT	TAAAGTTGGT	450
	CAAGAAGTTG	AAATAGTTGG	AATTAAAGAA	ACCAGAAAAA	CTACTGTTAC	500
35	TGGTGTGAA	ATGTTCCAGA	AAATTCCTGA	GCAAGGTCAA	GCAGGGGATA	550
	ATGTTGGTCT	TCTTTTGAGA	GGCGTTGATA	AAAAAGACAT	TGAGAGGGGG	600
	CAAGTTTGT	CAGCTCCAGG	TACAATTACT	CCACACAAGA	AATTTAAAGC	650
	TTCAATTTAT	TGTTTGACTA	AAGAAGAAGG	CGGTAGGCAC	AAGCCATTTT	700
	TCCCAGGGTA	TAGACCACAG	TTCTTTTTTA	GAACAACCGA	TGTTACTGGA	750
40	GTTGTTGCTT	TAGAGGGCAA	AGAAATGGTT	ATGCCTGGTG	ATAATGTTGA	800
	TATTATTGTT	GAGCTGATCT	CTTCAATAGC	TATGGATAAG	AATGTAGAAT	850
	TTGCTGTTTCG	AGAAGGTGGA	AGAACCGTTG	CTTCAGGA		888

45

2) INFORMATION FOR SEQ ID NO: 1738

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevibacterium linens*
 5 (B) STRAIN: DSM 20425
 (C) ACCESSION NUMBER: X76863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738

10	AACATGATCA	CCGGTGCCGC	TCAGATGGAC	GGTGCGATCC	TCGTCGTCGC	50
	CGCTACCGAC	GGACCGATGC	CCCAGACCCG	TGAGCACGTG	CTGCTCGCGC	100
	GTCAGGTCGG	CGTTCCCTAC	ATCGTCGTGG	CTCTGAACAA	GTCCGACATG	150
	GTCGATGACG	AGGAGCTCCT	CGAGCTCGTC	GAATTCGAGG	TCCGCGACCT	200
	GCTCTCGAGC	CAGGACTTCG	ACGGAGACAA	CGCTCCGGTC	ATTCCGGTGT	250
15	CCGCTCTCAA	GGCGCTGGAA	GGCGACGAGA	AGTGGGTCAA	GAGCGTTCAG	300
	GATCTCATGG	CTGCCGTCGA	TGACAACGTT	CCGGAGCCGG	AGCGCGATGT	350
	CGACAAGCCG	TTCCTCATGC	CCGTGCGAGG	CGTCTTCACG	ATCACCGGTC	400
	GTGGAACCGT	CGTCACCGGT	CGTGTCGAGC	GCGGCGTGCT	CCTGCCTAAC	450
	GACGAAATCG	AAATCGTCGG	CATCAAGGAG	AAGTCGTCCA	AGACGACTGT	500
20	CACCGCTATC	GAGATGTTCC	GCAAGACCCT	GCCGGATGCC	CGTGCAGGTG	550
	AGAACGTCGG	TCTGCTCCTC	CGCGGCACCA	AGCGCGAGGA	TGTTGAGCGC	600
	GGTCAGGTCA	TCGTGAAGCC	GGGTTCGATC	ACCCCGCACA	CCAAGTTCGA	650
	GGCTCAGGTC	TACATCCTGA	GCAAGGACGA	GGGCGGACGT	CACAACCCGT	700
	TCTACTCGAA	CTACCGTCCG	CAGTTCTACT	TCCGGACCAC	GGACGTCACC	750
25	GGTGTTCATCA	CGCTGCCCCGA	GGGCACCGAG	ATGGTCATGC	CCGGCGACAA	800
	CACCGATATG	TCGGTCGAGC	TCATCCAGCC	GATCGCTATG	GAGGACCGCC	850
	TCCGCTTCGC	AATCCGCGAA	GGTGGCCGCA	CCGTCGGCGC	CGGT	894

30

2) INFORMATION FOR SEQ ID NO: 1739

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: F/IC-Cal-13
 45 (C) ACCESSION NUMBER: L22216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739

	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
50	AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300

	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	AGCGCGGCAT	CGTGAAGGTC	450
	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
5	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
10	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTCTGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCGGC		888

15

2) INFORMATION FOR SEQ ID NO: 1740

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*
 (B) STRAIN: S85
 (C) ACCESSION NUMBER: X76866

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740

	AACATGGTGA	CTGGTGCTGC	TCAGATGGAC	GGCGCTATCC	TCGTTGTTGC	50
	CGCTACTGAC	GGTCCGATGC	CGCAGACTCG	CGAACACATC	CTTCTCGCTC	100
35	ACCAGGTTGG	CGTGCCGAAG	ATCGTCGTGT	TCATGAACAA	GTGCGACATG	150
	GTTGACGATG	CTGAAATTCT	CGACCTCGTC	GAAATGGAAG	TTCGCGAACT	200
	CCTCTCCAAG	TATGACTTCG	ACGGTGACAA	CACCCCGATC	ATCCGTGGTT	250
	CCGCTCTCAA	GGCCCTCGAA	GGCGATCCGG	AATACCAGGA	CAAGGTCATG	300
	GAATCATGA	ACGCTTGCGA	CGAATACATC	CCGCTCCCGC	AGCGCGATAC	350
40	CGACAAGCCG	TTCCTCATGC	CGATCGAAGA	CGTGTTACAG	ATTACTGGCC	400
	GCGGCACTGT	CGCTACTGGC	CGTATCGAAC	GCGGTGTCGT	TCGCTTGAAC	450
	GACAAGGTTG	AACGTATCGG	TCTCGGTGAA	ACCACCGAAT	ACGTCATCAC	500
	CGGTGTTGAA	ATGTTCCGTA	AGCTCCTCGA	CGACGCTCAG	GCAGGTGACA	550
	ACGTTGGTCT	CCTCCTCCGT	GGTGCTGAAA	AGAAGGACAT	CGTCCGTGGC	600
45	ATGGTTCTCG	CAGCTCCGAA	GTCTGTCACT	CCGCACACCG	AATTTAAGGC	650
	TGAAATCTAC	GTTCTCACGA	AGGACGAAGG	TGGCCGTCAC	ACGCCGTTCA	700
	TGAATGGCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTTACTGGT	750
	ACGATCCAGC	TCCCGGAAGG	TGTCGAAATG	GTTACTCCGG	GTGACACGGT	800
	CACGATCCAC	GTGAACCTCA	TCGCTCCGAT	CGCTATGGAA	AAGCAGCTCC	850
50	GCTTCGCTAT	CCGTGAAGGT	GGACGTACTG	TTGGTGCTGG	C	891

2) INFORMATION FOR SEQ ID NO: 1741

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*
 (B) STRAIN: DSM 13524
 (C) ACCESSION NUMBER: X76867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741

	AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGTGCTATCT	TAGTTGTGGC	50
	TGCATCAGAC	GGTCCTATGC	CTCAAACAAA	AGAACACATC	CTGCTTGCTG	100
20	CCCAGGTAGG	TGTACCTAAA	ATGGTTGTGT	TTCTGAATAA	AGTTGACCTC	150
	GTTGACGACG	AAGAGCTCCT	GGAGCTGGTT	GAGATCGAGG	TTCGCGAAGA	200
	ACTGACTAAA	CGCGGTTTCG	ACGGCGACAA	CACTCCAATC	ATCAAAGGTT	250
	CCGCTACAGG	CGCCCTCGCT	GGTGAAGAAA	AGTGGGTAA	AGAAATTGAA	300
	AACCTGATGG	ACGCTGTTGA	CAGCTACATC	CCACTGCCTC	CTCGTCCGGT	350
25	TGATCTGCCG	TTCCTGATGA	GCGTAGAGGA	CGTATTCTCT	ATCACTGGTC	400
	GTGGTACTGT	TGCTACCGGT	CGTATCGAGC	GTGGCCGTAT	CAAAGTTGGT	450
	GAGCCTGTTG	AGATCGTAGG	TCTGCAGGAG	TCTCCCCTGA	ACTCTACCGT	500
	TACAGGTGTT	GAGATGTTCC	GCAAACCTCCT	CGACGAAGGT	GAAGCTGGTG	550
	ATAACGCCGG	TCTCCTCCTC	CGTGGTGTG	AAAAAACACA	GATCCGTCGC	600
30	GGTATGGTAA	TCGTAAACC	CGGTTCCATC	ACTCCGCACA	CGGACTTCAA	650
	AGGCGAAGTT	TACGTACTGA	GCAAAGACGA	AGGTGGCCGT	CACACTCCAT	700
	TCTTCAACAA	ATACCGTCCT	CAATTCTACT	TCCGTACAAC	TGACGTTACA	750
	GGTGAAGTAG	AACTGAACGC	AGGAACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CACCAACCTG	ACCGTTAAAC	TGATCCAACC	GATCGCTATG	GAAAAAGGTC	850
35	TGAAATTTCG	GATCCGCGAA	GGTGGCCGTA	CCGTAGGTGC	AGGA	894

2) INFORMATION FOR SEQ ID NO: 1742

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: 26695
 (C) ACCESSION NUMBER: AE000626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742

	AACATGATCA	CCGGTGCGGC	GCAAATGGAC	GGAGCGATTT	TGGTTGTTTC	50
	TGCAGCTGAT	GGCCCTATGC	CTCAAACCTAG	GGAGCATATC	TTATTGTCTC	100
5	GTCAAGTAGG	CGTGCCTCAC	ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	150
	GTAGATGACC	AAGAATTGTT	AGAACTTGTA	GAAATGGAAG	TGCGCGAATT	200
	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC	GTAGCGGGTT	250
	CAGCTTTAAG	AGCTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG	300
	GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	350
10	TCCAGAAAGA	GACACTGAAA	AAACTTTCTT	GATGCCGGTT	GAAGATGTGT	400
	TCTCTATTGC	GGGTAGAGGG	ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	450
	GTGGTGAAAG	TAGGCGATGA	AGTGGAAATC	GTTGGTATCA	GACCTACACA	500
	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG	TTGGAAAAAG	550
	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAAGAA	600
15	GAAGTGGAAC	GCGGTATGGT	TCTATGCAAA	CCAGGTTCTA	TCACTCCGCA	650
	CAAGAAATTT	GAGGGAGAAA	TTTATGTCCT	TTCTAAAGAA	GAAGGCGGGA	700
	GACACACTCC	ATTCTTCACC	AATTACCGCC	CGCAATTCTA	TGTGCGCACA	750
	ACTGATGTGA	CTGGCTCTAT	CACCCTTCCT	GAAGGCGTAG	AAATGGTTAT	800
	GCCTGGCGAT	AATGTGAAAA	TCACTGTAGA	GTTGATTAGC	CCTGTTGCGT	850
20	TAGAGTTGGG	AACTAAATTT	GCGATTCTGT	AAGGCGGTAG	GACCGTTGGT	900
	GCTGGT					906

25 2) INFORMATION FOR SEQ ID NO: 1743

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*
 (B) STRAIN: IFO 3333
 (C) ACCESSION NUMBER: M17788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743

	AACATGATCA	CCGGCGCCGC	TCAGATGGAC	GGCGCGATCC	TCGTGGTCGC	50
	CGCTACCGAC	GGCCCGATGG	CCCAGACCCG	TGAGCACGTG	CTCCTGGCCC	100
	GCCAGGTCGG	CGTGCCGGCC	CTGCTCGTGG	CCCTGAACAA	GTCGGACATG	150
45	GTGGAGGACG	AGGAGCTCCT	CGAGCGTGTC	GAGATGGAGG	TCCGGCAGCT	200
	GCTGTCCTCC	AGGAGCTTCG	ACGTCGACGA	GGCCCCGGTC	ATCCGCACCT	250
	CCGCTCTGAA	GGCCCTCGAG	GGCGACCCCC	AGTGGGTCAA	GTCCGTCGAG	300
	GACCTCATGG	ATGCCGTGGA	CGAGTACATC	CCGGACCCGG	TGCGCGACAA	350
	GGACAAGCCG	TTCCTGATGC	CGATCGAGGA	CGTCTTCACG	ATCACCGGCC	400
50	GTGGCACCGT	GGTGACCGGT	CGCGCCGAGC	GCGGCACCCT	GAAGATCAAC	450
	TCCGAGGTCG	AGATCGTCGG	CATCCGCGAC	GTGCAGAAGA	CCACTGTCAC	500
	CGGCATCGAG	ATGTTCCACA	AGCAGCTCGA	CGAGGCCTGG	GCCGGCGAGA	550
	ACTGCGGTCT	GCTCGTGCGC	GGTCTGAAGC	GCGACGACGT	CGAGCGCGGC	600

	CAGGTGCTGG	TGGAGCCGGG	CTCCATCACC	CCGCACACCA	ACTTCGAGGC	650
	GAACGTCTAC	ATCCTGTCCA	AGGACGAGGG	TGGGCGTCAC	ACCCCGTTCT	700
	ACTCGAACTA	CCGCGCGCAG	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	750
	GTCATCACGC	TGCCCCGAGGG	CACCGAGATG	GTCATGCCCCG	GCGACACCAC	800
5	CGAGATGTCG	GTCGAGCTCA	TCCAGCCGAT	CGCCATGGAG	GAGGGCCTCG	850
	GCTTCGCCAT	CCGCGAGGGT	GGCCGCACCG	TGGGCTCCGG	C	891

10 2) INFORMATION FOR SEQ ID NO: 1744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: Erdmann.
 (C) ACCESSION NUMBER: X63539

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744

	AACATGATCA	CCGGCGCCGC	GCAGATGGAC	GGTGCGATCC	TGGTGGTTCG	50
	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	CGAGCACGTT	CTGCTGGCGC	100
	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	CGCTGAACAA	GGCCGACGCA	150
30	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	GAGATGGAGG	TCCGCGAGCT	200
	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	CCCGGTTGTG	CGGGTCTCGG	250
	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	GGGTTGCCTC	TGTCGAGGAA	300
	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	GACCCGGTCC	GCGAGACCGA	350
	CAAGCCGTTT	CTGATGCCGG	TCGAGGACGT	CTTACCATT	ACCGGCCGCG	400
35	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	GCGTGATCAA	CGTGAACGAG	450
	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	ACCACCAAGA	CCACCGTCAC	500
	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	CCAGGGCCAG	GCGGGCGACA	550
	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	GCGAGGACGT	CGAGCGTGGC	600
	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	CCGCACACCG	AGTTCGAAGG	650
40	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	CGGCCGGCAC	ACGCCGTTCT	700
	TCAACAACCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTGACCGGT	750
	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	GTGATGCCCCG	GTGACAACAC	800
	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	CGCCATGGAC	GAAGGTCTGC	850
45	GTTTCGCGAT	CCGCGAGGGT	GGCCGCACCG	TGGGCGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1745

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(B) STRAIN: G37

(C) ACCESSION NUMBER: U39732

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745

	AATATGATCA	CAGGTGCTGC	ACAAATGGAT	GGAGCTATTC	TAGTTGTTTC	50
	AGCAACTGAT	AGTGTGATGC	CCCAAACCCG	CGAGCACATC	TTACTTGCCC	100
	GCCAAGTAGG	GGTTCCTAAA	ATGGTAGTTT	TTCTAAACAA	GTGTGATATT	150
15	GCTAGTGATG	AAGAGGTACA	AGAACTTGTT	GCTGAAGAAG	TACGTGATCT	200
	GTTAACTTCC	TATGGTTTTG	ATGGTAAGAA	CACTCCTATT	ATTTATGGCT	250
	CAGCTTTAAA	AGCATTGGAA	GGTGATCCAA	AGTGGGAGGC	TAAGATCCAT	300
	GATTTGATTA	AAGCAGTTGA	TGAATGGATT	CCAACTCCTA	CACGTGAAGT	350
	AGATAAACCT	TTCTTATTAG	CAATTGAAGA	TACGATGACC	ATTACTGGTA	400
20	GAGGTACAGT	TGTTACAGGA	AGAGTTGAAA	GAGGTGAACT	CAAAGTAGGT	450
	CAAGAAGTTG	AAATTGTTGG	TTTAAACCA	ATTAGAAAAG	CAGTTGTTAC	500
	TGGAATTGAA	ATGTTCAAAA	AGGAACTTGA	TTCAGCAATG	GCTGGTGACA	550
	ATGCTGGGGT	ATTATTACGT	GGTGTGAAC	GTAAAGAAGT	TGAAAGAGGT	600
	CAAGTTTTAG	CAAACCAGG	CTCTATTAAA	CCGCACAAGA	AATTTAAAGC	650
25	TGAGATCTAT	GCTTTAAAGA	AAGAAGAAGG	TGGTAGACAC	ACTGGTTTTT	700
	TAAACGGTTA	CCGTCCTCAA	TTCTATTTC	GTACCACTGA	TGTAAGTGGT	750
	TCTATTGCTT	TAGCTGAAAA	TACTGAAATG	GTTCTACCTG	GTGATAATGC	800
	TTCTATTACT	GTTGAGTTAA	TTGCTCCTAT	CGCTTGTGAA	AAAGGTAGTA	850
30	AGTTCTCAAT	TCGTGAAGGT	GGTAGAACTG	TAGGGGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 1746

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

45 (B) STRAIN: MS11

(C) ACCESSION NUMBER: L36380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746

50	AACATGATTA	CCGGCGCCGC	ACAAATGGAC	GGTGCAATCC	TGGTATGTTC	50
	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	CGAACACATC	CTGCTGGCCC	100
	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	TCATGAACAA	ATGCGACATG	150
	GTCGACGATG	CCGAGCTGTT	CCAAGTGGTT	GAAATGGAAA	TCCGCGACCT	200

	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	CTGCCCCGATC	GTACAAGGTT	250
	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	CTTACGAAGA	AAAAATCTTC	300
	GAAGTGGCTA	CCGCATTGGA	CAGATACATC	CCGACTCCCG	AGCGTGCCGT	350
	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	CGTGTTCTCC	ATTTCCGGCC	400
5	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	GAGGTATCAT	CCACGTTGGT	450
	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	ACCCAAAAAA	CCACCTGTAC	500
	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAG	GCGGGCGACA	550
	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	GTGAAGACGT	AGAACGCGGT	600
	CAGGTATTGG	CCAAACGGGG	TACTATCACT	CCTCACACCA	AGTTCAAAGC	650
10	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	CGGCCCCCAT	ACCCCGTTTT	700
	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	GTACCACTGA	CGTAACCGGC	750
	ACGATTACTT	TGGAAAAAGG	TGTGGAAATG	GTAATGCCGG	GTGAGAACGT	800
	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	CGCTATGGAA	GAAGGTCTGC	850
15	GCTTTGCGAT	TCGCGAAGGC	GGCCGTACCG	TGGGTGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1747

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 891 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Rickettsia prowazekii*
 - 30 (B) STRAIN: Madrid E
 - (C) ACCESSION NUMBER: Z54170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747

35	AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	50
	TGCTGCTGAT	GGTCCTATGC	CTCAAACCTAG	AGAACATATA	TTACTGGCAA	100
	AACAGGTAGG	TGTACCTGCT	ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	150
	GTAGATGATC	CTGACCTATT	AGAATTAGTT	GAGATGGAAG	TAAGAGAATT	200
	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	ATTAAAGGTT	250
40	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAT	300
	GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	350
	AGATAAACCT	TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTTCAGGCA	400
	GAGGTACCGT	TGTAACCTGGT	AGAGTGAGGT	CAGGCATAAT	TAAGGTGGGT	450
	GAAGAAATTG	AAATAGTAGG	TCTAAAAAAT	ACGCAAAAAA	CGACTTGTAC	500
45	AGGTGTAGAA	ATGTTTCAGAA	AATTACTTGA	TGAAGGACAA	TCTGGAGATA	550
	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAGAGGA	600
	CAAGTACTTG	CAAACCTGG	GAGCATAAAA	CCGCATGATA	AATTTGAAGC	650
	TGAAGTGTAT	GTGCTTAGTA	AAGAGGAAGG	TGGACGTCAT	ACCCCATTTA	700
	CTAATGATTA	TCGCCCACAG	TTCTATTTTA	GAACAACAGA	TGTTACCGGC	750
50	ACAATAAAAT	TGCCTTCTGA	TAAGCAGATG	GTTATGCCTG	GAGATAATGC	800
	TACTTTTTCA	GTAGAATTAA	TTAAGCCGAT	TGCTATGCAA	GAAGGGTTAA	850
	AATTCTCTAT	ACGTGAAGGT	GGTAGAACAG	TAGGAGCCGG	T	891

2) INFORMATION FOR SEQ ID NO: 1748

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: LT2 trpE91
 (C) ACCESSION NUMBER: X55116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748

	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	GGCGCGATCC	TGGTTGTTGC	50
20	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	TGAGCACATC	CTGCTGGGTC	100
	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	ATGCGACATG	150
	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	TTCGCGAACT	200
	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	GTTCGTGGTT	250
	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAATCATC	300
25	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	CCGGAACCAG	AGCGTGCGAT	350
	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	400
	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	CAAAGTGGGC	450
	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	CTACCTGTAC	500
	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	GCCGGTGAGA	550
30	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	650
	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	700
	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	CGTGACTGGT	750
	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	800
35	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	GACGGTCTGC	850
	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

40 2) INFORMATION FOR SEQ ID NO: 1749

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
 (B) STRAIN: DSM 50426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749

	ATGATCACTG	GTGCTGCACA	GATGGACGGC	GCGATTCTGG	TAGTCGCTTC	50
	AACAGACGGT	CCAATGCCAC	AGACTCGTGA	GCACATCCTG	CTTTCTCGTC	100
5	AGGTTGGCGT	ACCATTCATC	ATCGTATTCA	TGAACAAATG	TGACATGGTA	150
	GATGACGAAG	AGCTGTTAGA	GCTAGTTGAG	ATGGAAGTGC	GTGAACTGTT	200
	ATCAGAATAC	GATTTCCCAG	GTGATGACTT	ACCGGTAATC	CAAGGTTTCA	250
	CTCTGAAAGC	GCTAGAAGGC	GAGCCAGAGT	GGGAAGCAAA	AATCCTTGAA	300
	TTAGCAGCGG	CGCTGGATTTC	TTACATTCCA	GAACCACAAC	GTGACATCGA	350
10	TAAGCCGTTT	CTACTGCCAA	TCTGAAGACGT	ATTCTCAATT	TCAGGCCCGTG	400
	GTACAGTAGT	AACAGGTCGT	GTGAGCGTG	GTATTGTACG	CGTAGGCGAC	450
	GAAGTTGAAA	TCGTTGGTGT	ACGTGCGACA	ACTAAGACAA	CGTGTACTGG	500
	TGTAGAAATG	TTCCGTAAAC	TGCTTGACGA	AGGTCGTGCA	GGTGAGAACT	550
	GTGGTATTTT	GTTACGTGGT	ACTAAGCGTG	ATGACGTAGA	ACGTGGTCAA	600
15	GTATTAGCGA	AGCCAGGTTT	AATCAACCCA	CACACTACTT	TTGAATCAGA	650
	AGTTTACGTA	CTGTCAAAAG	AAGAAGGTGG	TCGTACACAG	CCATTCTTCA	700
	AAGGCTACCG	TCCACAGTTC	TACTTCCGTA	CAACTGACGT	AACCGGTACT	750
	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	ATGCCAGGCG	ATAACATCAA	800
	GATGGTAGTG	ACACTGATTT	GCCCAATCGC	GATGGACGAA	GGTTTACGCT	850
20	TCGCAATCCG	TGAAGGCGGT	CGTACAGTGG	T		881

2) INFORMATION FOR SEQ ID NO: 1750

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 897 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*
- (B) STRAIN: DW4
- (C) ACCESSION NUMBER: X82820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750

40

	AACATGATCA	CGGGCGCGGC	GCAGATGGAC	GGAGCGATTTC	TGGTGGTGTC	50
	CGCGGCCGAC	GGCCCGATGC	CCCAGACGCG	TGAGCACATC	CTGCTGGCCA	100
	GGCAGGTGGG	CGTGCCCTAC	ATCGTCGTCT	TCCTGAACAA	GGTGGACATG	150
	CTGGACGATC	CGGAGCTGCG	CGAGCTGGTG	GAGATGGAGG	TGCGCGACCT	200
45	GCTCAAGAAG	TACGAGTTCC	CGGGCGACAG	CATCCCCATC	ATCCCTGGCA	250
	GCGCGCTCAA	GGCGCTGGAG	GGAGACACCA	GCGACATCGG	CGAGGGAGCG	300
	ATCCTGAAGC	TGATGGCGGC	GGTGGACGAG	TACATCCCGA	CGCCGCAGCG	350
	TGCGACGGAC	AAGCCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCCATCG	400
	CAGGCCGAGG	AACGGTGGCG	ACGGGCCGAG	TGGAGCGCGG	CAAGATCAAG	450
50	GTGGGCGAGG	AAGTGGAGAT	CGTGGGGATC	CGTCCGACGC	AGAAGACGGT	500
	CATCACGGGG	GTGGAGATGT	TCCGCAAGCT	GCTGGACGAG	GGCATGGCGG	550
	GAGACAACAT	CGGAGCGCTG	CTGCGAGGCC	TGAAGCGCGA	GGACCTGGAG	600
	CGTGGGCAGG	TGCTGGCGAA	CTGGGGGAGC	ATCAACCCGC	ACACGAAGTT	650

	CAAGGCGCAG	GTGTACGTGC	TGTCGAAGGA	AGAGGGAGGG	CGGCACACGC	700
	CGTTCTTCAA	GGGATACCGG	CCGCAGTTCT	ACTTCCGGAC	GACGGACGTG	750
	ACCGGAACGG	TGAAGCTGCC	GGACAACGTG	GAGATGGTGA	TGCCGGGAGA	800
	CAACATCGCC	ATCGAGGTGG	AGCTCATTAC	TCCGGTCGCC	ATGGAGAAGG	850
5	AGCTGCCGTT	CGCCATCCGT	GAGGGTGGCC	GCACGGTGGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1751

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiomonas cuprina*
 (B) STRAIN: Hoe5
 (C) ACCESSION NUMBER: x76871

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1751

25

	AACATGATCA	CCGGTGCGGC	CCAGATGGAC	GGCGCCATCC	TGGTCGTGTC	50
	CGCCGCCGAC	GGCCCCATGC	CCCAAACCCG	CGAGCACATC	CTGCTGGCGC	100
	GTCAGGTGGG	CGTGCCCTAC	ATCATCGTGT	TCCTCAACAA	GTGCGACATG	150
	GTCGACGACG	CCGAGCTGCT	CGAACTCGTC	GAGATGGAAG	TGCGCGAGCT	200
30	GCTGTCCAAG	TACGACTTCC	CCGGTGACGA	CACCCCCATC	ATCAAGGGCT	250
	CGGCCAAGCT	GGCCCTCGAA	GGCGACAAGG	GCGAACTGGG	CGAAGGCGCC	300
	ATTCTCAAGC	TGGCCGAGGC	CCTGGACACC	TACATCCCCA	CGCCCGAGCG	350
	GGCCGTCGAC	GGCGCGTTCC	TCATGCCCGT	GGAAGACGTG	TTCTCCATCT	400
	CCGGGCGCGG	CACGGTGGTC	ACCGGGCGTG	TGGAGCGCGG	CATCATCAAG	450
35	GTCGGCGAGG	AAATCGAGAT	TGTCGGCCTC	AAGCCCACCC	TCAAGACCAC	500
	CTGCACCGGC	GTGGAAATGT	TCAGGAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACGT	CGGCATCTTG	CTGCGCGGCA	CCAAGCGCGA	GGAAGTCGAG	600
	CGCGGCCAGG	TGCTGTGCAA	ACCCGGCTCG	ATCAAGCCCC	ACACCCACTT	650
	CACCGCCGAG	GTGTACGTGC	TGAGCAAGGA	CGAGGGCGGC	CGCCACACCC	700
40	CCTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGCAC	CACCGACGTC	750
	ACCGGCGCCA	TCGAACTGCC	CAAGGACAAG	GAAATGGTCA	TGCCCGGCCA	800
	TAATGTGAGC	ATCACCGTCA	AGCTCATCGC	CCCCATCGCC	ATGGAAGAAG	850
	GCCTGCGCTT	CGCCATCCGC	GAAGGCGGCC	GCACCGTCGG	CGCCGGC	897

45

2) INFORMATION FOR SEQ ID NO: 1752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: AE001202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752

```

10 AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC 50
    TGCGCCTGAC GGC GTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC 100
    GTCAGGTTGG TGTTCCCTCC ATCATTGTTT TTTTGAACAA GGTTGATTTG 150
    GTTGATGATC CTGAGTTGCT AGAGCTGGTG GAAGAAGAGG TGC GTGATGC 200
15 GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC AAGGGGTCTG 250
    CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGTATT 300
    GAGGAACTGC TTGCGGCCAT GGATTCCCTAC TTTGAAGACC CAGTGC GTGA 350
    CGACGCAAGA CCTTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG 400
    GGCGTGGTAC CGTTGTCACG GGGCGCATCG AATGTGGGGT AATTAGTCTG 450
20 AATGAAGAGG TCGAGATCGT CGGGATTAAG CCCACTAAGA AAACAGTGGT 500
    TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA ATTGCAGGTG 550
    ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAAGA GGTTGAGCGC 600
    GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA 650
    GGCGCAGATC TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT 700
25 TTTTTC AAGG TTATCGTCCG CAGTTTTATT TTAGAACTAC TGACATTACC 750
    GGTACGATTT CTCTTCCTGA AGGGGTAGAC ATGGTGAAGC CGGGGGATAA 800
    CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG GACAAGGGTC 850
    TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT 894
  
```

30

2) INFORMATION FOR SEQ ID NO: 1753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Ureaplasma urealyticum*
 (B) STRAIN: ATCC 33697
 (C) ACCESSION NUMBER: Z34275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753

```

50 AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC 50
    TGCATCTGAT GGGGTTATGG CTCAAACATA AGAACATATT TTATTAGCAC 100
    GTCAAGTTGG TGTTCCAAAA ATCGTTGTTT TCTTAAACAA ATGTGATTTT 150
    ATGACAGATC CAGATATGCA AGATCTTGTT GAAATGGAAG TTCGTGAATT 200
    ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT ATTCGTGGTT 250
  
```


	CAGGTCTTAA	GGCTTTAGAA	GGAGATCCAG	TTTGAGAAGC	AAAAATTGAT	300
	GAATTAATGG	ACGCAGTTGA	TTCATGAATT	CCATTACCAG	AACGTAGTAC	350
	TGACAAACCA	TTCTTATTAG	CAATTGAAGA	TGTATTACACA	ATTTACAGGAC	400
	GTGGTACAGT	AGTAACTGGA	CGTGTGTAAC	GTGGTGTATT	AAAAGTTAAT	450
5	GATGAGGTTG	AAATTGTTGG	TCTAAAAGAC	ACTCAAAAAA	CTGTTGTTAC	500
	AGGAATTGAA	ATGTTTAGAA	AATCATTAGA	TCAAGCTGAA	GCTGGTGATA	550
	ATGCTGGTAT	TTTATTACGT	GGTATTAAAA	AAGAAGATGT	TGAACGTGGT	600
	CAAGTACTTG	TAAAACCAGG	ATCAATTAAA	CCTCACCGTA	CTTTTACTGC	650
	TAAAGTTTAT	ATTCTTAAAA	AAGAAGAAGG	TGGACGTCAT	ACACCTATTG	700
10	TTTCAGGATA	CCGTCCACAA	TTCTATTTTA	GAACAACAGA	TGTAACAGGT	750
	GCTATTTTCAT	TACCTGCTGG	TGTTGATTTG	GTTATGCCAG	GTGATGACGT	800
	TGAAATGACT	GTAGAATTAA	TTGCTCCAGT	TGCGATTGAA	GATGGATCTA	850
	AATTCTCAAT	CCGTGAAGGT	GGTAAACTG	TAGGTCATGG	T	891

15

2) INFORMATION FOR SEQ ID NO: 1754

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 909 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Wolinella succinogenes*
- (B) STRAIN: DSM 1740
- 30 (C) ACCESSION NUMBER: X76862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754

	AACATGATTA	CAGGTGCTGC	TCAAATGGAT	GGCGCGATTC	TTGTTGTTTC	50
35	TGCGGCGGAT	GGCCCCATGC	CCCAAAC TAG	GGAGCACATT	CTTCTTTCTC	100
	GACAAGTAGG	CGTTCCTTAC	ATCGTG GTTT	TCTTGAACAA	AGAAGATATG	150
	GTTGATGACG	CTGAGCTTCT	TGAGCTTGTT	GAAATGGAAG	TTAGAGAACT	200
	TCTTAGCAAC	TACGACTTCC	CTGGAGATGA	CACTCCTATC	GTTGCAGGTT	250
	CCGCTCTTAA	AGCTCTTGAA	GAGGCTAACG	ACCAGGAAAA	TGTTGGCGAG	300
40	TGGGGCGAGA	AAGTATTGAA	GCTTATGGCT	GAGGTTGACC	GATATATTCC	350
	TACGCCTGAG	CGAGATGTGG	ATAAGCCTTT	CCTTATGCCT	GTTGAAGACG	400
	TATTCTCCAT	CGCGGGTCGT	GGAACCGTTG	TGACAGGAAG	AATTGAAAGA	450
	GGCGTGTTA	AAGTCGGTGA	CGAAGTAGAA	ATCGTTGGTA	TCCGAAACAC	500
	ACAAAAACA	ACCGTAACTG	GCGTTGAGAT	GTTCCGAAAA	GAGCTCGACA	550
45	AGGGTGAGGC	GGGTGACAAC	GTTGGTGTTT	TTTTGAGAGG	CACCAAGAAA	600
	GAAGATGTTG	AGAGAGGTAT	GGTTCTTTGT	AAAATAGGTT	CTATCACTCC	650
	TCACACTAAC	TTTGAAGGTG	AAGTTTACGT	TCTTTCCAAA	GAGGAAGGCG	700
	GACGACACAC	TCCATTCTTC	AATGGATACC	GACCTCAGTT	CTATGTTAGA	750
	ACTACAGACG	TTACCGGTTT	TATCTCTCTT	CCTGAGGGCG	TAGAGATGGT	800
50	TATGCCTGGT	GACAACGTTA	AGATCAATGT	TGAGCTTATC	GCTCCTGTAG	850
	CCCTCGAAGA	GGGAACACGA	TTGCGGATCC	GTGAAGGTGG	TCGAACCGTT	900
	GGTGCGGGT					909

2) INFORMATION FOR SEQ ID NO: 1755

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755

15	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
	AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
20	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300
	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	AGCGCGGCAT	CGTGAAGGTC	450
25	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
30	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTCGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCCGC		888

2) INFORMATION FOR SEQ ID NO: 1756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756

TGAAAGTTCA	GGTAAACAA	CAGTTTCATT	ACACGCAATT	GCAGAAGTAC	50
------------	-----------	------------	------------	------------	----

AGCGTCAAGG	TGGACAAGCA	GCGTTCATTG	ATGCTGAGCA	TGCAATGGAT	100
CCTGTATATG	CACAAAAACT	AGGTGTTAAC	ATCGATGAAT	TACTATTATC	150
ACAACCTGAT	ACAGGGGAGC	AAGGTTTAGA	AATCGCAGAA	GCACTTGTAC	200
GAAGTGGTGC	GGTTGATATT	ATCGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
5 CCGAAAGCTG	AAATTGAAGG	AGACATGGGT	GACTCACACG	TAGGTTTACA	300
AGCTCGTCTA	ATGTCTCAAG	CACTTCGTAA	ACTTTCAGGT	GCAATCAATA	350
AATCAAAAAC	AATCGCAATC	TTTATTAACC	AAATTCGT		388

10

2) INFORMATION FOR SEQ ID NO: 1757

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 388 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: ATCC 4229

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757

TGAAAGTTCA	GGTAAAACAA	CAGTTTCATT	ACACGCAATT	GCAGAAGTAC	50
AGCGTCAAGG	TGGACAAGCA	GCGTTCATTG	ATGCTGAGCA	TGCAATGGAT	100
CCTGTATATG	CACAAAAACT	AGGTGTTAAC	ATCGATGAAT	TACTATTATC	150
30 ACAACCTGAT	ACAGGGGAGC	AAGGTTTAGA	AATCGCAGAA	GCACTTGTAC	200
GAAGTGGTGC	GGTTGATATT	ATCGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
CCGAAAGCTG	AAATTGAAGG	AGACATGGGT	GACTCACACG	TAGGTTTACA	300
AGCTCGTCTA	ATGTCTCAAG	CACTTCGTAA	ACTTTCAGGT	GCAATCAATA	350
35 AATCAAAAAC	AATCGCAATC	TTTATTAACC	AAATTCGT		388

2) INFORMATION FOR SEQ ID NO: 1758

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 7064
- (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758

```

    TGAAAGTTCA GGTAAAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC      50
    AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT      100
    CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC      150
5   ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC      200
    GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
    CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA      300
    AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA      350
    AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT      388
10

```

2) INFORMATION FOR SEQ ID NO: 1759

```

15   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 388 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Bacillus cereus
25   (B) STRAIN: ATCC 13472
          (C) ACCESSION NUMBER:

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759

```

30   TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
    AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT      100
    CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
    ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC      200
    GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
35   CCGAAAGCAG AGATTGAAGG TGACATGGGT GACTCACACG TAGGTTTACA      300
    AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
    AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

40

2) INFORMATION FOR SEQ ID NO: 1760

```

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 374 bases
45   (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA
50
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Bacillus mycoides
          (B) STRAIN: ATCC 6462

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760

```

5  AAACGACAGT TTCATTACAT GCAATTGCAG AAGTACAACG TCAAGGTGGA      50
   CAAGCAGCAT TCATCGATGC GGAGCACGCA ATGGATCCTG TATATGCACA      100
   AAAATTAGGC GTTAACATAG ATGAATTACT ATTATCACAG CCTGATACAG      150
   GGGAGCAAGG ATTAGAAATC GCAGAAGCAC TTGTACGAAG TGGTGCGGTT      200
   GACATTATCG TAATTGACTC TGTAGCAGCT CTTGTACCGA AAGCAGAGAT      250
   TGAAGGAGAC ATGGGTGACT CACACGTAGG TTTACAAGCA CGTTTAATGT      300
10 CACAAGCACT TCGTAAGCTT TCAGGAGCAA TCAACAAATC AAAACAATT      350
   GCAATCTTTA TTAACCAAAT TCGT                                374

```

15 2) INFORMATION FOR SEQ ID NO: 1761

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 381 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Bacillus pseudomycoides
    (B) STRAIN: NRRL BD-10

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761

```

30  GGAAAGTTCA GGTAAAACAA CGGTTTCCTT ACATGCGATT GCAGAAAGTGC      50
   AACGTCAAGG TGGACAAGCG GCATTTATTG ATGCGGAGCA TGCGATGGAT      100
   CCTGTATATG CACAAAAGTT AGGTGTTAAT ATTGATGAGT TACTATTATC      150
   GCAGCCTGAT ACAGGAGAAC AAGGTTTAGA AATCGCAGAA GCATTAGTAC      200
35  GAAGCGGTGC GATTGATATC ATTGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CAAAAGCAG AAATCGAAGG GGAAATGGGT GACTCCCACG TTGGTTTACA      300
   AGCGCGTTTA ATGTCACAAG CACTTCGTAA GCTTCTGGT GCGATTAACA      350
   AATCAAAAAC AATTGCAATC TTCATTAACC A                                381

```

40

2) INFORMATION FOR SEQ ID NO: 1762

(i) SEQUENCE CHARACTERISTICS:

```

45  (A) LENGTH: 388 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Bacillus thuringiensis

```

(B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762

```

5  TGAAAGTTCA GGTAACACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
   ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
10  CCGAAAGCAG AGATTGAAGG CGACATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

15

2) INFORMATION FOR SEQ ID NO: 1763

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 388 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

     (A) ORGANISM: Bacillus thuringiensis
     (B) STRAIN: HER 1418

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763

```

   TGAAAGTTCA GGTAACACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATTG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
35  ACAGCCTGAT ACAGGGGAGC AAGGATTGGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCGAAAGCAG AGATTGAAGG CGATATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

40

2) INFORMATION FOR SEQ ID NO: 1764

(i) SEQUENCE CHARACTERISTICS:

```

45  (A) LENGTH: 358 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764

5 CTCCTATCTG GATTATGCGA TGTCGGTTCAT TGTTGGCCGT GCGCTGCCGG 50
 ATGTCCGAGA TGGCCTGAAG CCGGTACACC GTCGCGTACT ATACGCCATG 100
 AACGTATTGG GCAATGACTG GAACAAAGCC TATAAAAAAT CTGCCCGTGT 150
 CGTGGGTGAC GTCATCGGTA AATACCACCC TCATGGTGAT ACTGCCGTAT 200
 10 ACGACACCAT TGTACGTATG GCGCAGCCCT TCTCCCTGCG TTACATGCTG 250
 GTAGATGGCC AGGGTAACTT TGGTTCGGTC GACGGCGACT CCGCCGCAGC 300
 GATGCGTTAT ACGGAAATCC GTATGTGCGAA GATCGCCCAT GAACTGATGG 350
 CCGACCTC 358

15

2) INFORMATION FOR SEQ ID NO: 1765

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 365 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765

TTAAGAACTC TTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG 50
 CTGCCGGATG TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTTTA 100
 35 CGCCATGAAC GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCAG 150
 CCCGTGTTCGT TGGTGACGTA ATCGGTAAAT ACCACCCGCA CGGCGACTCC 200
 GCGGTATACG ACACCATCGT GCGTATGGCG CAGCCGTTCT CGCTGCGTTA 250
 CATGCTGGTG GACGGCCAGG GTAACTTTGG TTCCATCGAC GGCGACTCCG 300
 CCGCGGCGAT GCGTTATACC GAAATTCGTC TGGCGAAAAT CGCTCATGAG 350
 40 CTGATGGCCG ATCTT 365

2) INFORMATION FOR SEQ ID NO: 1766

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766

```

AAGAGCTCGT ATCTGGATTA TGCGATGTCG GTCATTGTTG GCCGTGCGCT      50
GCCGGATGTC CGAGATGGCC TGAAACCGGT ACACCGTCGC GTACTTTACG      100
CCATGAACGT ATTGGGCAAT GACTGGAACA AAGCCTATAA AAAATCCGCC      150
10 CGTGTTCGTTG GTGACGTAAT CGGTAAATAC CACCCTCATG GTGATACCGC      200
CGTTTATGAC ACCATTGTAC GTATGGCACA GCCATTCTCC TTGCGTTATA      250
TGCTGGTCTGA TGGCCAGGGT AACTTCGGTT CTGTCGATGG CGACTCCGCC      300
GCAGCGATGC GTTATACGGA AATCCGTATG TCGAAAATCG CCCA          344

```

15

2) INFORMATION FOR SEQ ID NO: 1767

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 345 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767

```

AACTCTTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
GGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
35 TGAACGTATT GGGCAATGAC TGGAACAAAG CCTATAAAAA ATCAGCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAC CCGCACGGCG ACTCCGCGGT      200
ATACGACACC ATCGTGCGTA TGGCGCAGCC GTTCTCGCTG CGTTACATGC      250
TGGTGGACGG CCAGGGTAAC TTTGGTTCCA TCGACGGCGA CTCCGCCGCG      300
CGGATGCGTT ATACCGAAAT TCGTCTGGCG AAAATCGCTC ATGAG          345

```

40

2) INFORMATION FOR SEQ ID NO: 1768

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 356 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768

```

5   CTTATCTGGA TTATGCGATG TCGGTCATTG TTGGCCGTGC GCTGCCGGAT      50
    GTCCGAGATG GCCTGAAGCC GGTACACCGT CGCGTACTTT ACGCCATGAA      100
    CGTATTGGGC AATGACTGGA ACAAAGCCTA TAAAAAATCA GCCCGTGTCTG      150
    TTGGTGACGT AATCGGTAAA TACCACCCGC ACGGCGACTC CGCGGTATAC      200
10  GACACCATCG TGC GTATGGC GCAGCCGTTT TCGCTGCGTT ACATGCTGGT      250
    GGACGGCCAG GGTAACCTTG GTTCCATCGA CGGCGACTCC GCCGCGGCCGA      300
    TGC GTTATAC CGAAATTCGT CTGGCGAAAA TCGCTCATGA GCTGATGGCC      350
    GATCTT                                     356
  
```

15

2) INFORMATION FOR SEQ ID NO: 1769

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 361 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
```

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Klebsiella pneumoniae subsp. pneumoniae
    (B) STRAIN: ATCC 29011
  
```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769

```

    TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC      50
    TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC      100
35  GCCATGAACG TATTGGGCAA TGA CTGGAAC AAAGCCTATA AAAAATCAGC      150
    CCGTGTCGTT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG      200
    CGGTATACGA CACCATCGTG CGTATGGCGC AGCCGTTCTC GCTGCGTTAC      250
    ATGCTGGTGG ACGGCCAGGG TAACTTTGGT TCCATCGACG GCGACTCCGC      300
    CGCGGCGATG CGTTATACCG AAATTCGTCT GCGGAAAATC GCTCATGAGC      350
40  TGATGGCCGA T                                     361
  
```

2) INFORMATION FOR SEQ ID NO: 1770

45

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 365 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
50  (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *rhinoscleromatis*

(B) STRAIN: ATCC 13824

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770

	TAAGAACTCT	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	50
	TGCCGGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	100
10	GCCATGAACG	TATTGGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCAGC	150
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCACCCGCAC	GGCGACTCCG	200
	CGGTATACGA	CACCATCGTG	CGTATGGCGC	AGCCGTTCTC	GCTGCGTTAC	250
	ATGCTGGTGG	ACGGCCAGGG	TAACCTTGGT	TCCATCGACG	GCGATTCCGC	300
	CGCGGCGATG	CGTTATACCG	AAATTCGTCT	GGCGAAAATC	GCTCATGAGC	350
15	TGATGGCCGA	TCTTG				365

2) INFORMATION FOR SEQ ID NO: 1771

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Klebsiella terrigena*

(B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771

35	TCGTATCTGG	ATTATGCGAT	GTCGGTCATT	GTTGGCCGTG	CGCTGCCGGA	50
	TGTCCGAGAT	GGGTGAAAC	CGGTACACCG	TCGCGTACTT	TACGCCATGA	100
	ACGTATTGGG	CAATGACTGG	AACAAAGCCT	ATAAAAAATC	CGCCCGTGTC	150
	GTTGGTGACG	TAATCGGTAA	ATATCACCT	CACGGTGATA	CCGCCGTTTA	200
	TGACACCATT	GTACGTATGG	CGCAGCCATT	CTCCTTGCGT	TATATGCTGG	250
40	TCGATGGCCA	GGGTAACTTC	GGTTCTGTCT	ATGGCGACTC	CGCCGCAGCG	300
	ATGCGTTATA	CGGAAATCCG	TATGTCGAAA	ATCGCCACG	AGCTGATGGC	350
	CGACCTC					357

45

2) INFORMATION FOR SEQ ID NO: 1772

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 968 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772

```

10 CAGTACACAG GCGAGTTCTT TTTGCGATGA GTGAGTTAAG TAATGATTGG      50
   AATAAGCCGT ATAAAAAATC TGCTCGTGTA GTAGGGGATG TCATTGGTAA      100
   ATATCATCCT CATGGGGATA CAGCTGTTTA TGACACTATT GTTCGTATGG      150
   CTCAGCCCTT TTCCATGCGT TATATGCTGA TTGATGGGCA GGGTAATTTT      200
   GGCTCTGTAG ATGGAGATGC TCCAGCTGCC ATGCGTTACA CTGAAGTAAG      250
   AATGTCCAAA GTGGCGCATG CTTTACTGGC TGATTTGGAT AAGGAAACCG      300
15 TTGATTTTAG TCCTAACTAT GATGAAACAG AATTTGCTCC AGTGGTATTG      350
   CCATCGAGAA TTCCCAATTT ACTAGTTAAT GGCTCTTCCG GTATTGCGGT      400
   AGGGATGGCT ACTAATATTC CACCACATAA TCTTACCGAA GTAATCAATG      450
   CATGTATTGC TTTAGTGGAT GAACCTGACA CGAGTCTTGA AGATTTAATG      500
   GAAATTATTC CTGGCCCTGA TTTTCCTACA GCCGCAATTA TTAATGGTCG      550
20 TGCTGGAATT ATTGAAGGTT ATCGTACTGG AAAAGGGCGG GTTGTTATCA      600
   GGGCACGCAC AGAAATTGAA ACGGATGAAA GTTCAGGCCG TCAGTCAATT      650
   ATTATTCAGG AATTACCCTA TCAGGTGAAT AAAGCGCGTT TGATCGAGCG      700
   TATTGCTGAA TTGGTAAGGG ACAAGAAAAT CGAAGGAATT TCCGGCTTGA      750
   GAGATGAGTC AGACAAGCAA GGAATGAGAG TAGTCATTGA ATTAAAACGC      800
25 AATGAAGTAG CAGATGTGGT ATTGAATAAC CTGTTGCTC ATACTCAAAT      850
   GCAAAATGTA TTCGGAATTA ATATGGTTGC TCTGGTGGAT GGCCAACCGC      900
   GTACTTTGAA TTTGAAGCAA ATACTGGAAT ATTTTATAAA ACATCGAAGA      950
   GAGGTTGTTA CCAGACGC                                     968

```

30

2) INFORMATION FOR SEQ ID NO: 1773

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 25933

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773

```

50 CACCGCCGAG TGCTATTTGC GATGAATGTA CTGGGAAACG ATTGGAATAA      50
   ACCTTATAAA AAATCAGCCC GTGTTGTTGG GGATGTAATC GGTAATATC      100
   ACCCGCACGG TGACAGTGCT GTCTATGAAA CGATTGTTTCG TTTAGCACAG      150
   CCTTTTTCTA TGCGCTACAT GTTGGTTGAC GGTCAGGGTA ACTTCGGGTC      200
   AGTTGATGGT GACTCCGCGG CGGCTATGCG TTATACCGAA GTTCGTATGG      250
   CGAAGATCGC CCATGAACTG CTGGCGGATT TGGAAAAAGA GACGGTCGAC      300

```

	TTTGTTTCCTA	ACTATGATGG	AACAGAAAAT	ATACCGGCTG	TTATGCCAAC	350
	CCGTATTCCA	AACTTGTTAG	TTAATGGCTC	TTCAGGTATT	GCCGTTGGGA	400
	TGGCAACGAA	TATCCCTCCG	CATAACCTCG	GTGAAGTTAT	CGACGGTTGT	450
	CTTGCCATATG	TTGATAATGA	AGACATCACC	ATAGAAGAAT	TAATGGAATA	500
5	TATTACCGGG	CCTGATTTTC	CGACTGCTGC	GATTATTAAT	GGTCGCAGAG	550
	GAATATTAGA	TGCTTATCGT	ACAGGGCGTG	GAAAGATTTA	TATCCGTGCT	600
	CAGGCTGATA	TTGAAACTGA	TGAGAAAACA	GGTCGCGAAA	CCATTATCGT	650
	GACAGAAATT	CCTTATCAGG	TGAATAAAGC	CCGTTTAATT	GAAAAAATTG	700
	CGGAGCTTGT	AAAAGATAAA	CGTATTGAAG	GTATCAGCGG	ATTACGTGAC	750
10	GAGTCTGATA	AAGACGGTAT	GCGTATTGTT	GTTGAGATCA	AACGTGATGC	800
	AGTCGGTGAA	GTAAGTATTAA	ATCACCTCTT	TTCACAAACT	CAAATGCAAG	850
	TCTCTTTTGG	TATTAATATG	GTTGCGCTTC	ATCAAGGCCA	ACCAAATTA	900
	TTGAACCTAA	AAGAAATTAT	CGCAGCCTTT	ATTGCGCATC	GTCGTGAAGT	950
	GGTGACTCGC	CGTACCA				967

2) INFORMATION FOR SEQ ID NO: 1774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 30 (B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774

	CCAGTACACC	GCAGAGTATT	GTATGCGATG	AATGTATTGG	GAAATGATTG	50
35	GAATAAACCC	TATAAAAAAT	CTGCCCCGAT	TGTTGGGGAC	GTCATCGGTA	100
	AATACCATCC	ACATGGTGAT	AGCGCTGTTT	ACGAGACAA	CGTTCGTCTT	150
	GCTCAGCCTT	TCTCAATGCG	TTACATGCTG	GTTGATGGTC	AGGGAAACTT	200
	CGGTTCTGTT	GACGGAGACT	CCGCAGCGGC	AATGCGTTAT	ACGGAAATCC	250
	GTATGGCGAA	AATTGCCCAT	GAACACTTGT	CTGACCTTGA	AAAAGAAACC	300
40	GTTGATTTCG	TTCCTAACTA	TGACGGAACA	GAGCACATTC	CTGAAGTTAT	350
	GCCAACGAAA	ATCCCAAACC	TTTTGGTTAA	TGGGTCGTCA	GGTATTGCTG	400
	TTGGGATGGC	AACCAATATC	CCACCTCACA	ATTTAGGGGA	GGTGATTAAT	450
	GGTTGTCTTG	CCTATATAGA	AGACGAAGAC	ATCAGCATTG	ATGGTTTAAT	500
	GGAACACATT	CCAGGGCCTG	ATTTCCCAAC	CGCAGCTATT	ATTAATGGCC	550
45	GTCGTGGGAT	TATTGATGCG	TATCGCACAG	GGCGTGGCAA	GGTCTATATC	600
	CGTGCAAGCG	CTGAAGTGGA	AGTCGATGAG	AAAAATGGTC	GCGAAACCAT	650
	TATTGTCAGC	GAAATTCCTT	ATCAAGTGAA	TAAAGCTCGC	TTGATTGAAA	700
	AAATTGCTGA	GTTAGTTAAA	GACAAGCGTG	TTGAAGGTAT	CAGTGCACTG	750
	CGTGACGAGT	CTGATAAAGA	CGGTATGCGT	ATTGTTATTG	AAATCAAACG	800
50	CGATGCGGGT	GGTGAAGTTG	TACTGAACAA	CTTATATTCC	CTGACCCAAT	850
	TGCAAGTTTC	TTTTGGTATC	AATATGGTAG	CTCTACACCA	AGGGCAGCCG	900
	AAAATACTGA	ATTTAAAAGA	TATCATTGCT	GCTTTTGTGC	GTCACCGCCG	950
	TGAAGTCGTC	ACTCGTCGTA	CGATTTTC			978

2) INFORMATION FOR SEQ ID NO: 1775

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775

15 CCAGTACACC GTCGCGTTCT TTTCGCGATG AATGTATTAG GAAACGATTG 50
 GAATAAACCT TATAAAAAAT CAGCCCGTGT TGTTGGGGAT GTTATCGGTA 100
 AATATCACCC GCACGGTGAC AGTGCTGTTT ATGAAACGAT AGTTCGTTTA 150
 20 GCACAGCCTT TTTCTATGCG TTACATGTTG GTTGACGGGC AGGGTAACTT 200
 CGGGTCAGTT GATGGTGACT CGGCGGCTGC AATGCGTTAT ACCGAAGTTC 250
 GTATGGCGAA AATCGCCCAT GAACTGCTGG CGGATTTGGA AAAAGAAACG 300
 GTTGATTTTG TTCCTAACTA TGATGGAACA GAGCATATCC CGGCAGTCAT 350
 GCCAACCCGT ATTCCAACT TATTAGTCAA TGGTTCTTCA GGTATCGCAG 400
 25 TCGGGATGGC AACAAACATT CCTCCGCATA ACCTAGGTGA AGTTATCGAC 450
 GGCTGTCTTG CTTATGTTGA TAACGAAGAC ATCACTATTG AAGAGTTGAT 500
 GGAGCATATC ACGGGGCCTG ATTTCCCAAC TGCCGCTATT ATTAATGGCC 550
 GCAGAGGAAT TTTAGATGCT TACCGTACTG GCGCGGAAA AATTTATATT 600
 CGTGACACAAG CTGATGTAGA AACCGATGAG AAAACTGGTC GCGAAACAAT 650
 30 TATCGTGACG GAAATTCCTT ATCAGGTGAA CAAAGCTCGC TTAATTGAAA 700
 AAATTGCAGA GCTTGTTAAA GATAAACGTA TTGAAGGCAT TAGCGGATTA 750
 CGTGATGAGT CAGATAAAGA TGGTATGCGC ATTGTTGTTG AAATTAAGCG 800
 TGATGCTGTT GGTGAAGTTG TACTAAATCA CTTATTTTCT CAGACTCAGA 850
 TGCAGGTTTC TTTTGGTATT AACATGGTTG CACTGCATCA AGGTCAACCG 900
 35 AAAGTGTTAA ACCTGAAAGA AATTATTTCA GCCTTTATTC GTCACCGTCG 950
 TGAAGTGGTG ACTCGTCGTA CTATTTTTT 978

40 2) INFORMATION FOR SEQ ID NO: 1776

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 940 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776

	TGGGTAATGA	CTGGAATAAG	CCATACAAAA	AATCGGCCCG	TGTAGTCGGG	50
	GACGTTATCG	GTAAATATCA	CCCGCATGGT	GACAGCGCGG	TCTACGACAC	100
5	AATTGTGCGT	ATGGCCCAGC	CGTTCTCACT	GCGCTATATG	CTGGTGGATG	150
	GGCAGGGCAA	CTTCGGTTCC	GTTGATGGCG	ACTCCGCCGC	AGCGATGCGT	200
	TATACCGAAA	TCCGTATGTC	TAAAATTGCT	CACGAATTGT	TGGCGGACTT	250
	AGAAAAAGAT	ACCGTCGACT	TCGTGCCGAA	CTATGACGGT	ACGGAGCAAA	300
	TTCCTGCCGT	AATGCCAACC	CGAATCCCTA	ACTTGCTGGT	TAACGGCTCG	350
10	TCAGGTATTG	CTGTCGGTAT	GGCAACCAAT	ATTCCGCCGC	ATAACCTTTC	400
	TGAGGTTATT	GATGGCTGTC	TGGCCTATAT	CGAAGATGAA	AACATCACCA	450
	TTGAAGGGTT	GATGGAGTAC	ATCCCGGGGC	CAGATTTCCT	AACTGCTGCG	500
	ATTATCAATG	GTCGCCGTGG	TATTGAAGAA	GCTTATCGTA	CTGGCCGTGG	550
	CAAGGTGTAT	ATCCGTGCCC	GTGCTGAAGT	TGAGGCTGAC	GCTTAAACCG	600
15	GTCGCGAAAC	CATTATTGTT	CACGAGATCC	CGTATCAGGT	GAACAAGGCG	650
	CGGTTGATTG	AAAAAATCGC	CGAGCTGGTT	AAAGAAAAAC	GCGTAGAAGG	700
	CATCAGTGCG	TTGCGTGATG	AGTCTGATAA	AGACGGCATG	CGTATCGTGA	750
	TTGAAATCAA	ACGTGATGCT	GTCGGGGAAG	TGGTTCTGAA	CAACCTCTAT	800
	TCTCTGACGC	AATTGCAGGT	GACTTTCGGT	ATCAATATGG	TGGCTCTGTC	850
20	TCAAGGGCAG	CCTAAGTTGC	TTAACCTGAA	AGACATTTTG	GTTGCTTTTCG	900
	TGCGCCACCG	CCGTGAAGTG	GTGACTCGCC	GTACCATTTT		940

25 2) INFORMATION FOR SEQ ID NO: 1777

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777

40	CCGTTTATTG	GCGATGGCCT	GAAGCCGGTC	CAGCGTCGCA	TCGTCTATGC	50
	GATGTCTGAA	CTGGGTCTGA	ACGCCAGCGC	GAAGTTCAAA	AAGTCCGCCC	100
	GCACCGTCGG	TGACGTGCTG	GGTAAATACC	ATCCCCACGG	CGACAGCGCG	150
	TGCTATGAAG	CCATGGTGCT	GATGGCTCAG	CCCTTCTCCT	ACCGCTATCC	200
45	GCTGGTTGAC	GGTCAGGGAA	ACTGGGGGGC	GCCGGACGAT	CCTAAATCCT	250
	TCGCCGCAAT	GCGTTATACC	GAATCCCGTT	TGTCGAAGTA	TGCTGAACTG	300
	CTGCTGAGCG	AACTGGGGCA	AGGCACCGTT	GACTGGGTAC	CAAACCTCGA	350
	CGGCACTTTG	CAGGAGCCGA	AGATGCTGCC	TGCGCGCCTG	CCCAATATTC	400
	TGCTAAACGG	TACTACCGGC	ATTGCCGTTG	GGATGGCGAC	GGACATTCCG	450
50	CCGCACAACC	TGCGTGAAGT	GGCCCGGGCG	GCCATTACCC	TGATTGAAAA	500
	GCCGCAAAC	TCGCTGGATG	ACCTGCTGGA	TATCGTGCAG	GGGCCGGATT	550
	ATCCTACCGA	AGCGGAAATC	ATTACCCCCC	GTGCCGAAAT	CCGCAAAATC	600
	TACCAGAATG	GCCGCGGTTT	GGTGCGGATG	CGCGCGGTAT	GGGCCAAAGA	650

AGACGGCGCG GTGGTGAT

668

5 2) INFORMATION FOR SEQ ID NO: 1778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778

20
GTTTATTGGC GATGGCCTGA AGCCGGTCCA GCGTCGCATC GTCTATGCGA 50
TGTCTGAACT GGGTCTGAAC GCCAGCGCGA AGTTCAAAAA GTCCGCCCCG 100
ACCGTCGGTG ACGTGCTGGG TAAATACCAT CCCCACGGCG ACAGCGCGTG 150
CTATGAAGCC ATGGTGCTGA TGGCTCAGCC CTTCTCCTAC CGCTATCCGC 200
25 TGGTTGACGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC TAAATCCTTC 250
GCCGCAATGC GTTATACCGA ATCCCGTTTG TCGAAGTATG CTGAACTGCT 300
GCTGAGCGAA CTGGGGCAAG GCACCGTTGA CTGGGTACCA AACTTCGACG 350
GCACTTTGCA GGAGCCGAAG ATGCTGCCTG CGCGCCTGCC CAATATTCTG 400
CTAAACGGTA CTACCGGCAT TGCCGTTGGG ATGGCGACGG ACATTCCGCC 450
30 GCACAACCTG CGTGAAGTGG CCCGGGCGGC CATTACCCTG ATTGAAAAGC 500
CGCAAACCTC GCTGGATGAC CTGCTGGATA TCGTGCAGGG GCCGGATTAT 550
CCTACCGAAG CGGAAATCAT TACCCCCCGT GCCGAAATCC GCAAATCTA 600
CCAGAATGGC CGCGGTTCCG TCGGATGCG CGCGGTATGG GCCAAAGAAG 650
ACGGCGCGGT GGTGATTAGC GCGCTGCCGC ATCAGGTTTC CGGCGCCCCG 700
35 GTGCTTGAGC AGAT 714

2) INFORMATION FOR SEQ ID NO: 1779

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
(B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779

	TTGGCGATGG	CTTAAAACCG	GTCCAGCGTC	GCATCGTCTA	TGCGATGTCC	50
	GAGCTGGGGC	TGAACGCCAG	CGCGAAATTC	AAAAAGTCCG	CCCGCACCGT	100
	CGGCGACGTG	TTGGGTAAAT	ATCACCCGCA	CGGCGACAGC	GCCTGCTATG	150
5	AAGCGATGGT	GCTGATGGCG	CAGCCGTTCT	CTTACCGCTA	TCCGCTGGTG	200
	GATGGTCAGG	GAAACTGGGG	GGCGCCGGAC	GATCCCAAAT	CTTTCGCCGC	250
	CATGCGTTAC	ACCGAATCCC	GCCTGTCGAA	GTATGCCGAG	CTGCTGCTCA	300
	GCGAGCTGGG	GCAGGGGACG	GTCGACTGGG	TGCCAAACTT	TGACGGTACG	350
	CTGCAGGAGC	CGAAAATGCT	GCCAGCGCGT	TTGCCGAACA	TCCTGCTGAA	400
10	CGGCACCACC	GGCATCGCGG	TAGGTATGGC	GACCGATATT	CCTCCGCACA	450
	ACCTGCGGGA	AGTGGCCAAA	GCGGCGATTA	CGCTGATTGA	GCAGCCGAAA	500
	ACCACCCTCG	ACGAACTGCT	GGATATCGTA	CAGGGGCCGG	ATTTCCCGAC	550
	CGAGGCGGAG	ATCATCACCT	CGCGGGCGGA	AATTCGAAAA	ATCTACCAGA	600
	ACGGGCGCGG	CTCAGTGCGC	ATGCGCGCGG	TGTGGAGTAA	AGAGGACGGC	650
15	GCGGTGGTGA	TCAGCGCGCT	GCCGCATCAG	GTCTCCGGCG	CCAAAGTGCT	700
	GGAGCAGATT	GCGGCGCAGA	TG			722

20 2) INFORMATION FOR SEQ ID NO: 1780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780

35	GTCCAGCGTC	GCATCGTTTA	TGCGATGTCT	GAGCTGGGGC	TGAACGCCAG	50
	CGCGAAGTTC	AAAAAGTCCG	CCCGCACCGT	GGGTGATGTG	CTGGGTAAAT	100
	ATCACCCGCA	CGGCGATAGC	GCATGCTATG	AAGCTATGGT	GCTGATGGCG	150
	CAGCCATTCT	CCTACCGCTA	CCCGCTGGTG	GATGGGCAGG	GGAAGTGGGG	200
40	GGCACCGGAC	GATCCTAAAT	CCTTCGCCGC	GATGCGTTAT	ACCGAATCCC	250
	GTTTGTGCGAA	GTATGCGGAA	CTGCTGCTGG	GCGAACTGGG	GCAGGGAACC	300
	GTCGACTGGG	TGCCGAACTT	CGACGGGACG	ATGCAGGAGC	CGAAAAATGCT	350
	GCCTGCGCGT	CTGCCGAATA	TTCTGCTGAA	CGGCACTACC	GGCATCGCCG	400
	TCGGTATGGC	AACCGATATT	CCTCCGCACA	ACCTGCGTGA	AGTGGCGCAG	450
45	GCGGCGATTA	CCCTGATCGA	AAAACCGCAG	ACCTCGCTCG	ACGAACTGCT	500
	GGATATCGTT	CACGGACCCG	ACTACCCGAC	CGAAGCCGAA	ATCATTACTC	550
	CACGCGCGGA	GATCCGCAAA	ATCTACCAGA	ACGGCCGCGG	TTCGGTGC GG	600
	ATGCGCGCGG	TATGGAAAAA	AGAGGACGGC	GCGGTCGTGA	TTACGGCGTT	650
	GCCGCATCAG	GTTTCCGGCG	CCCGCGTGCT	GGAGCAAATT	GC	692
50						

2) INFORMATION FOR SEQ ID NO: 1781

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 700 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781

15 GTTTATTGGC GATGGCTTAA AACCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCCGAGCT GGGGCTGAAC GCCAGCGCGA AATTCAAAAA GTCCGCCCCG 100
 ACCGTCGGCG ACGTGTTGGG TAAATATCAC CCGCACGGCG ACAGCGCCTG 150
 CTATGAAGCG ATGGTGCTGA TGGCGCAGCC GTTCTCTTAC CGCTATCCGC 200
 20 TGGTGGATGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC CAAATCTTTC 250
 GCCGCCATGC GTTACACCGA ATCCCGCCTG TCGAAGTATG CCGAGCTGCT 300
 GCTCAGCGAG CTGGGGCAGG GGACGGTCGA CTGGGTGCCA AACTTTGACG 350
 GCACGCTGCA GGAGCCGAAA ATGCTGCCAG CGCGTTTGCC GAACATCCTG 400
 CTGAACGGCA CCACCGGCAT CGCGGTAGGC ATGGCGACCG ATATTCCTCC 450
 25 GCACAACCTG CGGGAAGTGG CCAAAGCGGC GATTACGCTG ATTGAGCAGC 500
 CGAAAACAC CCTCGACGAA CTGCTGGATA TCGTACAGGG GCCGGATTTC 550
 CCGACCGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA 600
 CCAAAACGGG CGCGGCTCAG TCGCATGCG CGCGGTGTGG AGTAAAGAGG 650
 ACGGCGCGGT GGTGATCAGC GCGCTGCCGC ATCAGGTCTC CGGCGCCAAA 700
 30

2) INFORMATION FOR SEQ ID NO: 1782

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782

50 ATTGGCGATG GCTTAAACCC GGTCCAGCGT CGCATCGTCT ATGCGATGTC 50
 CGAGCTGGGG CTGAACGCCA GCGCGAAATT CAAAAAGTCC GCCCGCACCG 100
 TCGGCGACGT GTTGGGTAAA TATCACCCGC ACGGCGACAG CGCCTGCTAT 150
 GAAGCGATGG TGCTGATGGC GCAGCCGTTC TCTTACCGCT ATCCGCTGGT 200
 GGATGGTCAG GGAAACTGGG GGGCGCCGGA CGATCCCAA TCTTTCGCCG 250

	CCATGCGTTA	CACCGAATCC	CGCCTGTCTGA	AGTATGCCGA	GCTGCTGCTC	300
	AGCGAGCTGG	GGCAGGGGAC	GGTCGACTGG	GTGCCAAACT	TTGACGGCAC	350
	GCTGCAGGAG	CCGAAAATGC	TGCCAGCGCG	TCTGCCGAAC	ATCCTGCTGA	400
	ACGGCACCAC	CGGCATCGCG	GTAGGCATGG	CGACCGATAT	TCCTCCGCAC	450
5	AACCTGCGGG	AAGTGGCCAA	AGCGGCGATT	ACGCTGATTG	AGCAGCCGAA	500
	AACCACCCTC	GACGAACTGC	TGGATATCGT	ACAGGGGCCG	GATTTCCCGA	550
	CCGAGGCGGA	GATCATCACC	TCGCGGGCGG	AAATTCGCAA	AATCTACCAG	600
	AACGGGCGCG	GCTCAGTGCG	CATGCGCGCG	GTGTGGAGTA	AAGAGGACGG	650
	CGCGGTGGTG	ATCAGTGCGC	TGCCGCATCA	GGTCTCTGGC	GCCAAAGTGC	700
10	TGGAGCAGAT	TGCGGCGCAG	ATGCGC			726

2) INFORMATION FOR SEQ ID NO: 1783

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 29011

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783

30	GGCTTAAAAC	CGGTCCAGCG	TCGCATCGTC	TATGCGATGT	CCGAGCTGGG	50
	GCTGAACGCC	AGCGCGAAAT	TCAAAAAGTC	CGCCCGCACC	GTCGGCGACG	100
	TGTTGGGTAA	ATATCACCCG	CACGGCGACA	GCGCCTGCTA	TGAAGCGATG	150
	GTGCTGATGG	CGCAGCCGTT	CTCTTACCGC	TATCCGCTGG	TGGATGGTCA	200
	GGGAAACTGG	GGGGCGCCGG	ACGATCCCAA	ATCTTTTGCC	GCCATGCGTT	250
35	ACACCGAATC	CCGCCTGTCT	AAGTATGCCG	AGCTGCTGCT	CAGCGAGCTG	300
	GGGCAGGGGA	CGGTCGACTG	GGTGCCAAAC	TTTGACGGCA	CGCTGCAGGA	350
	GCCGAAAATG	CTGCCAGCGC	GTCTGCCGAA	CATCCTGCTG	AACGGCACCA	400
	CCGGCATCGC	GGTAGGCATG	GCGACCGATA	TTCTCCGCA	CAACCTGCGG	450
	GAAGTGGCCA	AAGCGGCGAT	TACGCTGATT	GAGCAGCCGA	AAACCACCCT	500
40	CGACGAACTG	CTGGATATCG	TACAGGGGCC	GGATTTCCCG	ACCGAGGCGG	550
	AGATCATCAC	CTCGCGGGCG	GAAATTCGCA	AAATCTACCA	GAACGGGCGC	600
	GGCTCAGTGC	GATGCGCGC	GGTGTGGAGT	AAAGAGGACG	GCGCGGTGGT	650
	GATCAGTGCG	CTGCCGCATC	AGGTCTCCGG	CGCCAAAGTG	CTGGAGCAGA	700
	TTGCGG					706

45

2) INFORMATION FOR SEQ ID NO: 1784

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784

	TTGGCGATGG	CTTAAAACCG	GTCCAGCGTC	GCATCGTCTA	TGCGATGTCC	50
	GAGCTGGGGC	TGAACGCCAG	CGCGAAATTC	AAAAAGTCCG	CCCGCACCGT	100
	CGGCGACGTG	TTGGGTAAAT	ATCACCCGCA	CGGCGACAGC	GCCTGCTATG	150
15	AAGCGATGGT	GCTGATGGCG	CAGCCGTTCT	CTTACCGCTA	TCCGCTGGTG	200
	GATGGTCAGG	GAAACTGGGG	GGCGCCGGAC	GATCCCAAAT	CTTTCGCCGC	250
	CATGCGTTAC	ACCGAATCCC	GCCTGTGCGA	GTATGCCGAG	CTGCTGCTCA	300
	GCGAGCTGGG	GCAGGGGACG	GTCGACTGGG	TGCCAAACTT	TGACGGGCACG	350
	CTGCAGGAGC	CGAAAATGCT	GCCAGCGCGT	CTGCCGAACA	TCCTGCTGAA	400
20	CGGCACCACC	GGCATCGCGG	TAGGCATGGC	GACCGATATT	CCTCCGCACA	450
	ACCTGCGGGA	AGTGGCCAAA	GCGGCGATTA	CGCTGATTGA	GCAGCCGAAA	500
	ACCACCCTCG	ACGAACTGCT	GGATATCGTA	CAGGGGCCGG	ATTTCCCGAC	550
	CGAGGCGGAG	ATCATCACCT	CGCGGGCGGA	AATTCGCAAA	ATCTACCAGA	600
	ACGGGCGCGG	CTCA				614

25

2) INFORMATION FOR SEQ ID NO: 1785

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella terrigena*

40 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785

	GCCTGAAACC	GGTCCAGCGG	CGCATCGTTT	ATGCGATGTC	CGAACTGGGT	50
45	CTGAACGCCA	CCGCTAAATT	CAAAAAATCC	GCGCGCACCG	TCGGCGACGT	100
	GCTGGGTAAA	TATACCCGC	ACGGCGATAG	CGCCTGCTAT	GAGGCGATGG	150
	TGCTGATGGC	GCAGCCGTTT	TCTTACCGCT	ACCCGCTGGT	GGACGGTCAG	200
	GGCAACTGGG	GCGCCCCGGA	CGATCCCAA	TCCTTCGCCG	CGATGCGTTA	250
	TACCGAATCC	CGCCTGTCAA	AGTATGCGGA	GCTGCTGCTG	GGCGAGCTGG	300
50	GTCAGGGAAC	CGTTGACTGG	GTACCTAACT	TTGACGGTAC	GATGCAGGAG	350
	CCGAAAATGC	TGCCTGCGCG	TTTGCCGAAT	ATTCTGCTCA	ACGGCACCAC	400
	CGGTATCGCC	GTGGGGATGG	CCACCGATAT	TCCGCCGCAC	AACCTGCGCG	450
	AAGTGCCCAA	AGCGGCCATC	ACCCTGATTG	AAAAGCCGCA	GACCTCGCTC	500

GACGAACTGC	TGGATATCGT	TCACGGGCCG	GACTACCCCA	CCGAAGCTGA	550
AATCATCACC	CCGCGCGCCG	AGATCCGCAA	AATCTATCAG	AACGGTCGCG	600
GCTCGGTTTCG	CATGCGTGCG	GTGTGGAAAA	AAGAGGACGG	CGCGGTGGTG	650
ATTAGCGCCC	TGCCGCAT				668

5

2) INFORMATION FOR SEQ ID NO: 1786

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 7064

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786

CATTACGTTC	TAACACTCAA	GGACGCGGAA	CATTCTCTAT	GGTGTTTGAC	50
CACTATGAAG	AAGTACCAA	GTCTGTTTCT	GAAGAAATTA	TCAAAAAAAA	100
TAAAGGTGAA	TAA				113

25

30 2) INFORMATION FOR SEQ ID NO: 1787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787

AACGTCATTA	CGTTCTAACA	CTCAAGGACG	CGGAACATTC	TCTATGGTGT	50
TTGACCACTA	TGAAGAAGTA	CCAAAGTCTG	TTTCTGAAGA	AATTATCAA	100
AAAAATAAAG	GTGAATAA				118

45

50

2) INFORMATION FOR SEQ ID NO: 1788

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788

15	GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT	50
	GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA	100
	AAAAAATAA AGGTGAATAA	120

20

2) INFORMATION FOR SEQ ID NO: 1789

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789

	AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT	50
	TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA	100
	AAAAATAAAG GTGAATAA	118

40

2) INFORMATION FOR SEQ ID NO: 1790

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790

5 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1791

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
(B) STRAIN: NRRL B-617

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791

GCAACGTCAT TACGTTCTAA CACGCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATCA 100
30 AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1792

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792

50 CGTCATTACG TTCTAACACT CAAGGACGCG GAACATTCTC TATGGTGTTT 50
GACCACTATG AAGAAGTACC AAAGTCTGTT TCTGAAGAAA TTATCAAAAA 100
AAATAAAGGT GAATAA 116

2) INFORMATION FOR SEQ ID NO: 1793

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793

GCAACGTCAT	TACGTTCTAA	CACTCAAGGA	CGCGGAACAT	TCTCTATGGT	50
GTTTGACCAC	TATGAAGAAG	TACCAAAGTC	TGTTTCTGAA	GAAATTATCA	100
AAAAAAATAA	AGGTGAATAA				120

2) INFORMATION FOR SEQ ID NO: 1794

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794

CACTCAAGGA	CGCGGAACAT	TCTCTATGGT	GTTTGATCAC	TATGAAGAAG	50
TACCAAAGTC	TGTTTCTGAA	GAAATTATCA	AAAAAAATAA	AGGTGAATAA	100

2) INFORMATION FOR SEQ ID NO: 1795

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795

GCAACGGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCTGAA GAAATTATTA 100
AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1796

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
20 (ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus mycoides*
25 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796

GCGACAGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
30 ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATTA 100
AAAAAAATAA AGGCGAATAA 120

35 2) INFORMATION FOR SEQ ID NO: 1797

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
45 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797

50 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1798

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCCATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1801

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
(B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACTTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100

CTAAGGAGGA ATTTAGA

117

5 2) INFORMATION FOR SEQ ID NO: 1803

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803

20 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

25

2) INFORMATION FOR SEQ ID NO: 1804

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM *Bacillus cereus*
(B) STRAIN: ATCC 49064

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCACCTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
45 CTAAGGAGGA ATTTAGA 117

50

2) INFORMATION FOR SEQ ID NO: 1805

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814

10	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
	CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
	GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
15	GTCACGCTGA	CTATGT				266

2) INFORMATION FOR SEQ ID NO: 1815

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815

35	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
	CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
	GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
40	GTCACGCTGA	CTATGTTAA				269

2) INFORMATION FOR SEQ ID NO: 1816

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
- (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805

TTGATTTT	TA	TCAATTG	TTC	GAGTATA	ACT	ACTTATG	TAA	GCTTAGA	AAAG	50
TGGGACG	TAA	GTTTCG	CTTT	CTAGTCT	AAA	TATAAA	AATAA	CCTATA	TAAA	100
CTAAGG	GAGGA	ATT	TTAGA							117

2) INFORMATION FOR SEQ ID NO: 1806

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806

TTGATTTT	TA	TCGATTG	TTC	AAGTATA	ACT	ACTTATG	TAA	GCTTAGA	AAAG	50
TGGGACG	TAA	GTTTCA	CTTT	CTAGTCT	AAA	TATAAA	AATAA	CCTATA	TAAA	100
CTAAGG	GAGGA	ATT	TTAGA							117

2) INFORMATION FOR SEQ ID NO: 1807

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807

5 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1808

10

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808

25 TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

30

2) INFORMATION FOR SEQ ID NO: 1809

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAG 117

50

2) INFORMATION FOR SEQ ID NO: 1810

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810

15 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GACGCTGCTC CAGAAGAAAG AGAGCGCGGA ATCACAATCT CAACTGCACA 200
 20 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

25 2) INFORMATION FOR SEQ ID NO: 1811

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811

40 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 45 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

50 2) INFORMATION FOR SEQ ID NO: 1812

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTGCT	GCGATCACTA	100
15 CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
GTCACGCTGA	CTATGTTAAA				270

20

2) INFORMATION FOR SEQ ID NO: 1813

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTGCT	GCGATCACTA	100
40 CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GACGCTGCTC	CAGAAGAAAG	AGAGCGCGGA	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
GTCATGCTGA	CTATGTTAAA	AACATGAT			278

45

2) INFORMATION FOR SEQ ID NO: 1814

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 266 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTG GCGATCACTA 100
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
10 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
GTCACGCTGA CTATGTTA 268

15

2) INFORMATION FOR SEQ ID NO: 1817

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 278 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTG GCGATCACTA 100
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
35 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
GTCACGCTGA CTATGTAAA AACATGAT 278

40

2) INFORMATION FOR SEQ ID NO: 1818

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818

```

5  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
   CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
   CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG      250
   GTCACGCTGA CTATGTTA          268
10

```

2) INFORMATION FOR SEQ ID NO: 1819

```

15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 278 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
   (ii) MOLECULE TYPE: Genomic DNA

   (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Bacillus anthracis
25  (B) STRAIN: CIP 9444

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819

```

30  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
   CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
   CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG      250
   GTCACGCTGA CTATGTTAAA AACATGAT          278
35

```

2) INFORMATION FOR SEQ ID NO: 1820

```

40  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 278 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
45
   (ii) MOLECULE TYPE: Genomic DNA

   (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Bacillus pseudomyoides
50  (B) STRAIN: NRRL B-617

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820

```

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGACCAAATC      150
GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
5  CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTATGTTAAA AACATGAT      278

```

10 2) INFORMATION FOR SEQ ID NO: 1821

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 263 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Bacillus cereus
(B) STRAIN: ATCC 49064

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821

```

25 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCAcA      200
30 CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTA      263

```

35 2) INFORMATION FOR SEQ ID NO: 1822

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 1668 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Streptococcus oralis
(B) STRAIN: ATCC 35037

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822

```

50 CAATCGAAGT ACAACGTTCT CTTGCGGTAT TGGACGGTGC GGTTACTGTT      50
CTTGACTCAC AATCAGGTGT TGAGCCTCAA ACTGAAACAG TTTGGCGTCA      100
AGCAACTGAG TACGGAGTTC CACGTATCGT ATTTGCTAAC AAAATGGACA      150

```

	AAATCGGTGC	TGACTTCCTT	TACTCAGTAA	GCACACTTCA	CGACCGTCTT	200
	CAAGCAAACG	CACACCCAAT	CCAATTGCCA	ATCGGTGCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGATA	TTCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGGTT	GAAGCAGTCG	CTGAAACTGA	400
	TGAAGACTTG	ATGATGAAAT	ACCTTGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGCTATCCGT	AAAGCAACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GTTCTGCCTT	CAAGAACAAG	GGTGTTCAAT	TGATGCTTGA	550
	TGCGGTTATC	GACTACCTTC	CAAGCCCACT	TGATATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGACGAA	650
	GAGCCATTTC	CAGCTCTTGC	CTTCAAGATC	ATGACGGACC	CATTTGTAGG	700
	TCGTTTGACA	TTCTTCCGTG	TATACTCARG	TGTTCTCCAA	TCARGKTCTT	750
	ACGTATTGAA	CACATCTAAA	GGTAAACGTG	AACGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CTAACAGCCG	TCAAGAAATT	GACACTGTTT	ACTCAGGTGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TYCAACTGGT	GACTCATTGM	900
	CAGATGAAAA	AGCTAAAATC	ATCCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGATAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCAGGTAT	GGGTGAGCTT	1100
20	CACTTGGAACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTGGAAGC	1150
	GAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCTGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	TCTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	CGCGGCTTCA	CTTGCCCTTA	1500
	AAGAAGCTGC	TAAGTCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACCATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTC	TGCTTACG				1668

35 2) INFORMATION FOR SEQ ID NO: 1823

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823

50	AGACCTGCGT	TCACAAACAC	AGGGTCGTGC	TTCTTACTCT	ATGGAGTTCT	50
	TGAAGTACAA	CGAAGCGCCA	AACAACGTTG	CTACAGCAAT	CATTGAAGCT	100
	CGTAAGGCTA	GATAA				115

2) INFORMATION FOR SEQ ID NO: 1824

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*
(B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824

CTGCGTTCAC TGACCAAGGT CGTGCACTTT ACTCCATGGA ATTCCTGAAG 50
TATGATGACG CGCCAAACAA CGTAGCTCAG GCCGTAATCG AAGCTCGCGG 100
TAAATAA 107

2) INFORMATION FOR SEQ ID NO: 1825

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825

TTACTCCATG GAGTTCCTGA AGTATGATGA TGCGCCGAAC AACGTTGCTC 50
AGGCCGTAAT CGAAGCCCGT GGTAAATAA 79

2) INFORMATION FOR SEQ ID NO: 1826

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

5. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826

CAGCTGCGTT CTCTGACCAA AGGTCGTGCA TCATACACTA TGGAAATTCCT 50
GAAGTATGAT GATGCGCCAA ACAACGTTGC TCAGGCCGTT ATTGAAGCCC 100
GTGGTAAGTA A 111

10

2) INFORMATION FOR SEQ ID NO: 1827

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
(B) STRAIN: ATCC 8071

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827

GATTTGCGCT CTGCAACTCA TGGGCGTGCT TCGTACTCCA TGGAGTTCTT 50
30 GAAGTACTCT GATGCACCGC AAAACATTGC GAAAGCGATT ATTGAATCTC 100
GTAGCTAA 108

35 2) INFORMATION FOR SEQ ID NO: 1828

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828

50

CTCAGCTGCG TTCTCTGACC AAAGGTCGTG CATCTTACTC CATGGAATTC 50
CTGAAGTATG ATGATGCGCC TAACAACGTT GCTCAGGCCG TTATTGAAGC 100
TCGTGGCAAA TAA 113

2) INFORMATION FOR SEQ ID NO: 1829

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829

GCCGCAGGGT TAAACCAAA GTCCCGTGCT CTCTCCTGAA GGGGAGAGCA 50
CTATAGTAAG GAATATAGCC 70

2) INFORMATION FOR SEQ ID NO: 1830

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
(B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830

GCCTCGGGTA AACTTATAT CCCAGTCCCC CTCGTATAGA GGGGGATAGA 50
GTAAAGGAAG ATAATC 66

2) INFORMATION FOR SEQ ID NO: 1831

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831

TCCACAGGAT TAAACCCAG GTTTAAACCT AAGTCCCGTG CTCTCTCCTC 50
AGGGGAGAGC ACAATAGTAA GGAATATAGC C 81

2) INFORMATION FOR SEQ ID NO: 1832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832

GCTACTAGTT TAAACATTG ATCCCGTGCT CTCTCTATGA AGGGAGAGCA 50
CAAGAGTAAG GAATAAAGCC 70

2) INFORMATION FOR SEQ ID NO: 1833

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
(B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833

TTTCCAGTTA CGACATAAAT GTTATTATGG TCCAGCTTTG ACTGGACTAT 50
TCTGAAAAGA AAGGAATATA TC 72

2) INFORMATION FOR SEQ ID NO: 1834

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834

50
 GCCCCGGGTT TTAAAAACA TTGATCCCGT GCTCTCTCCA GAAGGGGAGA 50
 GCGCAACAGT AAGGAATATA GCC 73

2) INFORMATION FOR SEQ ID NO: 1835

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
 (B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835

CTGCAGCTGA TGGTCCTATG CCACAAACTA GAGAGCACAT CCTTCTATCA 50
 CGCCAAGTAG GTGTTCCATA TATCGTTGTA TTTATGAATA AAGCAGATAT 100
 GGTTGATGAT GCTGAACTTT TAGAATTGGT TGAAATGGAA ATTAGAGAAT 150
 40 TATTAAGCTC TTATGATTTT CCAGGTGATG ACACACCTAT TATTTTCAGGT 200
 TCTGCTTTAA AAGCTCTTGA AGAAGCAAAA GCTGGACAAG ATGGCGAATG 250
 GTCAGCGAAA ATTATGGATC TTATGGCTGC TGTGATAGC TATATTCCAA 300
 CTCCAACCTCG TGACACTGAA AAAGATTTCT TAATGCCAAT TGAAGATGTT 350
 TTCTCAATTT CAGGTCGTGG TACTGTTGTT ACAGGTAGAA TTGAAAAAGG 400
 45 TATTGTAAAA GTTGGTGATA CTATAGAAAT CGTTGGTATT AAAGATACTC 450
 AAACAACAAC TGTAACCTGGC GTTGAAATGT TTAGAAAAGA AATGGACCAA 500
 GGTGAAGCAG GGGATAATGT TGGTGTCTT CTTCGTGGTA CAAAAAAGA 550
 AGAAGTTATC CGCGGTATGG TTCTTGCTAA ACCAAAATCA ATTACTCCAC 600
 ATACTGATTT CGAAGCTGAA GTTTATATCC TAAATAAAGA TGAGGGTGGT 650
 50 AGACATACTC CATTCTTTAA TAACTATAGA CCGCAATTCT ATGTAAGAAC 700
 AACAGATGTA ACAGGTCTA TTAAATTAGC TGATGGCGTT GAAATGGTTA 750
 TGCCTGGTGA AAATGTAAGA ATTACTGTAA GCTTGATTGC ACCAG 795

2) INFORMATION FOR SEQ ID NO: 1836

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836

15 GCCATACTAG TTGTTTCTGC AGCTGATGGC CCAATGCCAC AACTAGAGA 50
 GCACATTTTG CTATCTCGTC AAGTTGGTGT TCCATATATA GTTGTTTTTA 100
 TGAACAAAGC TGATATGGTA GATGACGCAG AGTTGCTAGA ATTAGTTGAA 150
 20 ATGGAGATCA GAGAGTTATT AAGCGAATAT GACTTCCCTG GTGATGATAC 200
 TCCTATTATA AGCGGATCAG CACTTCAAGC TCTTGAAGAA GCTAAAGCTG 250
 GTAATGATGG CGAATGGTCA GCTAAGATTA TGGATCTTAT GGCTGCTGTT 300
 GATAGCTACA TACCAACTCC AGTTCGTGCT ACTGATAAAG ATTTCTTAAT 350
 GCCGATTGAA GACGTATTCT CAATTTCTGG CCGTGGTACT GTTGTTACTG 400
 25 GTAGAATTGA AAAAGGTATA GTTAAAGTTG GTGATACTAT CGAAATCGTA 450
 GGTATTAGAG ATACACAAAC TACAACAGTT ACCGGCGTTG AAATGTTTAG 500
 AAAAGAAATG GATCAAGGCG AGGCTGGTGA TAACGTTGGT GTTCTTTTAC 550
 GCGGTACAAA GAAAGAAGAC GTTGAAAGAG GTATGGTTCT TTGTAAGCCA 600
 AAATCAATTA CTCCTCATA TAAATTTGAG GGAGAAGTTT ATATCTTGAC 650
 30 TAAGGAAGAG GCGGGTAGAC ATACTCCATT CTTCAACAAC TATAGACCAC 700
 AATTTTATGT AAGAACAACA GATGTTACTG GATCAATCAC TCTTCCAGAG 750
 GGTACTGAGA TGGTTATGCC TGGTGATAAC TTAAAAATCA CTGTTGAGTT 800
 AATCAACCCA GTTGCTC 817

2) INFORMATION FOR SEQ ID NO: 1837

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837

CCATACTAGT TGTTTCTGCA GCTGATGGCC CAATGCCACA AACTAGAGAG 50

	CACATTTTGC	TATCTCGTCA	AGTTGGTGTT	CCATATATAG	TTGTTTTTAT	100
	GAACAAAGCT	GATATGGTAG	ATGACGCAGA	GTTGCTAGAA	TTAGTTGAAA	150
	TGGAGATCAG	AGAGTTATTA	AGCGAATATG	ACTTCCCTGG	TGATGATACT	200
	CCTATTATAA	GCGGATCAGC	ACTTCAAGCT	CTTGAAGAAG	CTAAAGCTGG	250
5	TAATGATGGC	GAATGGTCAG	CTAAGATTAT	GGATCTTATG	GCTGCTGTTG	300
	ATAGCTACAT	ACCAACTCCA	GTTCGTGCTA	CTGATAAAGA	TTTCTTAATG	350
	CCGATTGAAG	ACGTATTCTC	GATTTCTGGC	CGTGGTACTG	TTGTTACTGG	400
	TAGAATTGAA	AAAGGTATAG	TTAAAGTTGG	TGATACTATC	GAAATCGTAG	450
	GTATTAGAGA	TACACAAACT	ACAACAGTTA	CCGGCGTTGA	AATGTTTAGA	500
10	AAAGAAATGG	ATCAAGGCGA	GGCTGGTGAT	AACGTTGGTG	TTCTTTTACG	550
	CGGTACAAAG	AAAGAAGACG	TTGAAAGAGG	TATGGTTCTT	TGTAAGCCAA	600
	AATCAATTAC	TCCTCATACT	AAATTTGAGG	GAGAAGTTTA	TATCTTGACT	650
	AAGGAAGAGG	GCGGTAGACA	TACTCCATTC	TTCAACAACT	ATAGACCACA	700
	ATTTTATGTA	AGAACAACAG	ATGTTACTGG	ATCAATCACT	CTTCCAGAGG	750
15	GTACTGAGAT	GGTTATGCCT	GGTGATAACT	TAAAAATCAC	TGTTAGTT	798

2) INFORMATION FOR SEQ ID NO: 1838

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*
- (B) STRAIN: ATCC 33320

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838

35	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
	TATCGGCCAC	GTTGACCATG	GTAAACTAC	TCTGACTGCA	GCAATCACTA	100
	CCGTTCTGGC	TAAACCTAC	GGCGGTTCTG	CACGCGCATT	CGACCAGATC	150
	GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
	CGTTGAATAT	GACACCCCGA	CTCGTCACTA	CGCGCACGTT	GACTGCCCAG	250
40	GGCACGCCGA	CTACGTTAAA	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCGATGC	CACAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATTC	ATGATCGTGT	400
	TCATGAACAA	ATGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGATTTCC	CGGGCGACGA	500
45	CATCCCAGTG	GTTCTGTGGT	CAGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	TAAATCATC	GAGCTGGCTG	GTCACCTGGA	TAAGTACATC	600
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCC	ATCTCCGGCC	GTGGTACTGT	TGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	TAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAT	750
50	ACCGTGAAAT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATTAAAC	850
	GTGAAGATAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCTATCAAG	900
	CCGCACACTC	AGTTCGAATC	AGAAGTTTAT	ATCCTGTCCA	AAGATGAAGG	950

CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	1050
GTAATGCCGG	GCGACAACAT	TCAAATGGTT	GTTACCCTGA	TCCACCCAAT	1100
CGCAATGGAC	GACGGT				1116

5

2) INFORMATION FOR SEQ ID NO: 1839

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
25 TATCGGCCAC	GTTGACCATG	GTAAAACTAC	TCTGACCGCT	GCAATCACTA	100
CCGTTCTGGC	TAAACCTAC	GGTGGTGCTG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCGG	250
GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
30 GCGCGGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	350
TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	400
TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	450
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CGGGCGACGA	500
CACTCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCTCTGGAA	GGCGACGCTG	550
35 AGTGGAATC	TAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	600
CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	650
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	700
GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	750
ACTGCTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
40 CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	850
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	900
CCGCACACCA	AGTTCGAATC	TGAAGTTTAT	ATCCTGTCCA	AAGACGAAGG	950
CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	1050
45 GTTATGCCGG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCGAT	1100
CGCGATGGA					1109

50 2) INFORMATION FOR SEQ ID NO: 1840

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
- (B) STRAIN: ATCC 14029

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840

	GTGTCTAAAG	AAAAATTTGA	ACGTACTAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAAACTAC	CCTGACTGCA	GCTATCACTA	100
15	CCGTACTGTC	TAAAGTATAC	GGTGGTCAGG	CTCGTGCAAT	CGATCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTAGAGTAC	GACACCCCAA	CTCGTCACTA	CGCGCACGTT	GACTGCCCCAG	250
	GTCACGCCGA	CTACGTGAAG	AACATGATCA	CTGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTAGTAGC	TGCGACTGAC	GGCCCAATGC	CTCAGACTCG	350
20	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	450
	GAAATGGAAG	TACGTGAGCT	GCTGTCTCAG	TACGACTTCC	CAGGCGACGA	500
	TACTCCAGTT	GTTCGCGGTT	CTGCACTGAA	AGCGCTGGAA	GGCGATGCTC	550
	AGTGGGAAGA	GAAGATTGTT	GAAGTGGCAG	GCTACCTGGA	CAGCTACATC	600
25	CCTGAGCCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATCTCCGGCC	GTGGTACTGT	AGTAACTGGT	CGTGTAGAGC	700
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	750
	ACTACCAAGA	CTACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGCTGCTGGA	800
	CGAAGGTCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	850
30	GTGATGACGT	AGAGCGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCAATCAAC	900
	CCACACACCA	ACTTTGTAGC	AGAAGTTTAT	ATTCTGTCCA	AAGATGAAGG	950
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050
	GTAATGCCAG	GTGACAACAT	TCAAATGGTT	GTTACCCTGA	TTGCACCAAT	1100
35	CGCGATGG					1108

2) INFORMATION FOR SEQ ID NO: 1841

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841

	TGGCAAAAGC	TAAATTTGAA	CGTATTAAGC	CTCACGTAAA	CGTGGGCACC	50
	ATTGGTCACG	TTGACCATGG	TAAAACCACT	CTGACTGCAG	CTATCTCTCA	100
	CGTACTGGCT	AAGACCTACG	GTGGCGAAGC	TAAAGACTTC	TCTCAAATCG	150
5	ATAACGCTCC	AGAAGAGCGT	GAGCGCGGTA	TTACCATCAA	TACCTCTCAC	200
	ATCGAATATG	ACACGCCATC	ACGCCACTAC	GCCCACGTAG	ACTGCCCAGG	250
	CCACGCTGAC	TATGTTAAAA	ACATGATCAC	TGGTGCTGCA	CAGATGGACG	300
	GCGCGATTCT	GGTAGTCGCT	TCAACAGACG	GTCCAATGCC	ACAGACTCGT	350
	GAGCACATCC	TGCTTTCTCG	TCAGGTTGGC	GTACCATTCA	TCATCGTATT	400
10	CATGAACAAA	TGTGACATGG	TAGATGACGA	AGAGCTGTTA	GAGCTAGTTG	450
	AGATGGAAGT	GCGTGAAGT	TTATCAGAA	ACGATTTCCC	AGGTGATGAC	500
	TTACCGGTAA	TCCAAGGTT	AGCTCTGAAA	GCGCTAGAAG	GCGAGCCAGA	550
	GTGGGAAGCA	AAAATCCTTG	AATTAGCAGC	GCGCTGGAT	TCTTACATTC	600
	CAGAACCACA	ACGTGACATC	GATAAGCCGT	TCCTACTGCC	AATCGAAGAC	650
15	GTATTCTCAA	TTTCAGGCCG	TGGTACAGTA	GTAACAGGTC	GTGTTGAGCG	700
	TGGTATTGTA	CGCGTAGGCG	ACGAAGTTGA	AATCGTTGGT	GTACGTGCGA	750
	CAACTAAGAC	AACGTGTA	GGTGTAGAAA	TGTTCCGTAA	ACTGCTTGAC	800
	GAAGGTCGTG	CAGGTGAGAA	CTGTGGTATT	TTGTTACGTG	GTACTAAGCG	850
	TGATGACGTA	GAACGTGGTC	AAGTATTAGC	GAAGCCAGGT	TCAATCAACC	900
20	CACACACTAC	TTTTGAATCA	GAAGTTTACG	TACTGTCAA	AGAAGAAGGT	950
	GGTCGTCACA	CGCCATTCTT	CAAAGGCTAC	CGTCCACAGT	TCTACTTCCG	1000
	TACAACTGAC	GTAACCGGTA	CTATCGAACT	GCCAGAAGGC	GTAGAGATGG	1050
	TAATGCCAGG	CGATAACATC	AAGATGGTAG	TGACACTGAT	TTGCCCAATC	1100
	GCGATGG					1107
25						

2) INFORMATION FOR SEQ ID NO: 1842

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1116 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Obesumbacterium proteus*
 - (B) STRAIN: ATCC 12841
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1842

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
45	AATCGGCCAC	GTTGACCACG	GTAAAACTAC	CCTGACTGCT	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CACGTGCATT	CGACCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
	GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
50	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAGCTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CAGGCAATGA	500

	TACTCCAATC	ATCCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCGTA	GAAGTGGCTG	AAACTCTGGA	TTCTTACATC	600
	CCAGAACCAG	AACGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTTACCGGT	CGTGTAGAGC	700
5	GCGGTATCGT	TAAAGTTGGT	GAAGAAGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTTAAAT	CAACTTGATC	CGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	800
	CGAAGGTCGT	GCAGGCGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	850
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAA	900
	CCACACACCA	AGTTCGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
10	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTGGAAATG	1050
	GTAATGCCAG	GCGATAACAT	CAAATGATC	GTTACCCTGA	TCCACCCAAT	1100
	CGCAATGGAC	GATGGT				1116

15

2) INFORMATION FOR SEQ ID NO: 1843

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1129 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAAACAAC	TCTGACTGCT	GCTATCACCA	100
35	GCGTTTTAGC	TAAAACTTAT	GGCGGTAACG	CTCGTGCATT	CGATCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCACGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAGTAT	GATACTCCTG	CTCGCCACTA	CGCACACGTA	GAAGTCCCAG	250
	GACACGCCGA	CTATGTGAAA	AACATGATCA	CCGGTGCTGC	TCAAATGGAC	300
	GGCGCGATCT	TAGTTGTTGC	GGCAACTGAT	GGTCCTATGC	CACAGACTCG	350
40	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAACTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAGCT	TCTTTCTGCT	TATGATTTCC	CTGGTGACGA	500
	TACTCCAGTT	GTTGCTGGTT	CTGCGCTGAA	AGCGTTAGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCATT	GAATTAGCCG	GATATCTGGA	TAGCTACATC	600
45	CCAGAGCCAG	AGCGTGCGAT	TGACCGTCCG	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATTTTCAGGCC	GTGGTACAGT	TGTTACCGGT	CGTGTAGAGC	700
	GCGGAATCGT	TAAAGTCGGT	GAAGCCGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTACAAA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGTTACTTGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	850
50	GTGAAGAAAT	CGAACGCGGT	CAAGTACTGG	CTAAGCCAGG	TTCAATCAAC	900
	CCGCACACCA	ACTTTGTATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050

GTGATGCCTG GTGACAACAT TCAGATGACT GTAACCTCTGA TTGCACCAAT 1100
CGCGATGGAC GAAGGTTTAC GCTTCGCTA 1129

5

2) INFORMATION FOR SEQ ID NO: 1844

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
(B) STRAIN: ATCC 49175

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844

ATATTCATAA TGCATTACAA GTTGTGAAAA CAACAAGTGA CGGAAGTGAA 50
AAGACTGTTA CATTGGAAAC TGCTGTAGAA TTAGGGGATG GTGCAGTTCG 100
TACGATTGCC ATGGAATCTA CAGATGGTTT GCAACGTGGC ATGAAAGTAG 150
25 TGGACTTAGG ACGCACAAAT AGCGTTCCTG TGGGACCTGA AACATTAGGT 200
CGTGTATTCA ACGTTTTAGG AGATACAATC GACTTGAAAG AACCATTCCC 250
AGAAGACTTT ACAAGACATG AAATCCATAA ACCAGCACCA AAATTTGAAG 300
AATTAAACAG TCAATATGAA ATTCTACAAA CAGGGATTAA AGTTATTGAC 350
CTTTTAGCAC CTTATCTTAA AGGTGGTAAA ATCGGTTTAT TCGGTGGTGC 400
30 CGGTGTAGGG AAAACCGTAT TAATTCAAGA ATTAATTCAT AATATCGCTG 450
AAGAACTTGG TGGTATTTCA GTATTTACAG GGGTAGGGGA ACGTACTCGT 500
GAAGGGAATG ACCTTTACCA TGAAATGCAA GAATCAGGCG TATCTGCTAA 550
AACAGCGATG GTGTTTGGGC AAATGAACGA ACCACCAGGA GCTCGTATGC 600
GTGTAGCACT AACAGGGTTA ACTATTGCGG AATACTTCCG TGATATGGAA 650
35 AAACAAGACG TGCTTTTATT CATCGATAAC ATTTATCGTT TCACGCAAGC 700
AGGTTTCAGAA GTGTCAGCGT TACTTGGTCG TATGCCTTCT GCCGTAGGGT 750
ATCAACCAAC ATTAGCGACA GAAATGGGTC AATTACAAGA ACGTATCAGT 800
TCAACTAAAG 810

40

2) INFORMATION FOR SEQ ID NO: 1845

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 815 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*

(B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845

5	TGCTCTGCCA	GAAATTAACA	ACGCCCTCCT	CACCGAAGTA	GACCTCTCCG	50
	GCCAAGGCGA	AGGCGAAAGC	GTTCTCAAGA	TGACTCTTGA	GGTTGCTCAG	100
	CACCTCGGCG	ATAACATCGT	CCGTACCATC	GCCATGAAGC	CAACCGACGG	150
	TCTGGTTCGC	GGCGCCACCG	TTATCGATAC	CGGCGCCCCA	ATCACCCTGC	200
	CAGTTGGCGA	CGCAACTAAA	GGTCATGTTT	TCAACGTGAC	CGGTGATGTC	250
10	CTAAACTTGG	GCGAAGGCGA	AACCCTTGAC	GTCAAGGAAC	GGTGGCCAAT	300
	CCACCGCAAG	GCTCCACAGT	TCGACGAACT	CGAACCGGAA	ACCAAGATGT	350
	TCGAAACAGG	CATCAAGGTG	ATCGATCTCC	TCACCCCAT	CGTACAGGGC	400
	GGCAAGATCG	GTCTGTTTGG	CGGTGCTGGT	GTTGGTAAGA	CCGTTCTTAT	450
	CCAGGAAATG	ATCCAGCGTG	TTGCACAGGA	TCATGGCGGT	GTGTCCGTGT	500
15	TCGCGGGTGT	GGGTGAACGT	ACCCGTGAAG	GTAACGATCT	TATCCACGAA	550
	ATGGAAGATG	CGGGCGTTCT	TGATAAGACC	GCGCTTGTGT	TCGGCCAGAT	600
	GGATGAACCG	CCAGGGGGTTC	GTTTGCGTAT	TGCACTTTCC	GGCCTGACCA	650
	TGGCGGAATA	CTTCCGTGAC	GTGCAAAACC	AGGACGTGCT	TTTGTTCATC	700
	GATAACATCT	TCCGCTTCAC	CCAGGCAGGT	TCGGAAGTGT	CCACGTTGCT	750
20	TGGCCGTATG	CCATCAGCAG	TGGGCTACCA	GCCGACCTTG	GCAGATKAAA	800
	TGGGCGCATT	GCAGG				815

25 2) INFORMATION FOR SEQ ID NO: 1846

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846

40	ACCTTCCTCC	TATCTTGAAG	GCCCTGGAGG	TCCAAAACCA	CAGCTCTCGY	50
	TTAGTTTTAG	AGGTGTCCCA	GCATTTGGGT	GAAAACACCG	TTCGTACTAT	100
	TGCTATGGAC	GGTACTGAAG	GATTGGTTCG	TGGTCAAAAT	GTCGTAGATA	150
	CCGGATATCC	TATTAGAGTT	CCTGTGCGTC	CTGAATGTTT	GGGTCGTATC	200
45	ATGAACGTTA	TTGGCGAGCC	TGTTGATGAG	CGCGGYCCTA	TCAAGACCAA	250
	GAAGCTTGCA	CCCATCCACG	CTTCTCCCCC	CGAGTTCGTY	GACCAATCCA	300
	CCACCCCCGA	AATCTTGGAG	ACTGGTATTA	AGGTTGTCGA	TTTGTGCGCC	350
	CCTTACGCTC	GTGGTGGTAA	GATCGGTCTT	TTCGGTGGTG	CCGGTGTGCG	400
	TAAGACTGTG	TTTATCCAGG	AGTTGATYAA	CAACGTTGCC	AAGGCCACG	450
50	GTGGTTACTC	CGTGTTGCTC	GGTGTTGGTG	AGCGTACTCG	TGAGGGTAAC	500
	GATTTGTACC	ACGAGATGAT	TCAAACCTGGT	GTCATCAAGC	TTGATGGCCA	550
	ATCCAAGGCT	GCCCTTGTCT	ACGGMCAAAT	GAACGAGCCC	CCAGGTGCTC	600
	GTGCCCGMGT	CGCTTTGACC	GGTCTTACCG	TTGCTGAATA	CTTCCGTGAT	650

	GAGGAAGGHC	AAGATGTGTT	GCTCTTCATT	GACAAACATTT	TCCGTTTCAC	700
	CCAAGCTGGT	TCTGAAGTGT	CYGCCTTGTT	GGGTCGTATC	CCCTCCGCTG	750
	TCGGTTACCA	ACCCACCTTG	GCCACCGATA	TGGGTGTCAT	GCAAGAGCGT	800
	ATTACCACCA	CCAAGAAGGG	TTCCATTACC	TCTGTCCAGG	CCATTTACGT	850
5	CCCTGCTGAT	GATTTGACCG	ATCCCCTCTCC	TGCCACTACT	TTTGCCCATC	900
	TTGACGCCAC	CACCGTGTTG	TCTCGTTCCA	TCTCTGAGTT	GGGTATTAC	950
	CCCGCTGTCG	ATCCCCTCGA	CTCCAAGTCT	CGTATGTTGG	ATCCYCGTAT	1000
	TGTCGGTGAA	GAGCACTACG	ACATCGCCAC	TGGTGTTCAG	AAGATTCTCC	1050
	ARTCTTACAA	GTCTCTCCAG	GAT			1073

10

2) INFORMATION FOR SEQ ID NO: 1847

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
- (B) STRAIN: ATCC 56220

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TGCCTCACCC	TTTGGGTATT	50
30	TTGCGAATAC	TAATTATAGT	AGAACAACAT	TGCCAAGGCT	CACGGTG GTT	100
	ACTCTGTCTT	CACTGGTGTC	GGTGAACGTA	CTCGTGAGGG	TAACGATTTG	150
	TACCACGAAA	TGCAGGAAAC	TGGTGTCATT	CAGCTCGAGG	GTGAATCCAA	200
	GGTCGCCCTC	GTGTTCCGTC	AGATGAACGA	GCCCCCTGGT	GCCCGTGCCC	250
	GTGTCGCTCT	TACTGGTTTG	ACCATTGCCG	AGTACTTCCG	TGACGAGGAG	300
35	GGTCAAGATG	TGCTTCTCTT	CATTGACAAC	ATTTTCCGTT	TCACTCAGGC	350
	CGGTTCTGAG	GTGTCTGCCC	TTTTGGGTCG	TATCCCCTCT	GCCGTCGGTT	400
	ACCAGCCCAC	TCTCGCCGTC	GACATGGGTG	TCATGCAGGA	GCGTATTACC	450
	ACCACCACCA	AGGGTTCCAT	CACCTCCGTC			480

40

2) INFORMATION FOR SEQ ID NO: 1848

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848

5	TGTCTTCATT	CAGGAGTTGA	TTGTACGTCC	CTTCCTCTCT	ACAAATGACG	50
	GGCGAGGAAA	ATTTTGGCT	TTTTCTAATA	GTCGTTATA	GAACAACATT	100
	GCCAAAGCCC	ACGGTGGTTA	CTCCGTTTTT	ACTGGTGTCG	GCGAGCGGAC	150
	CCGTGAAGGA	AACGATTTGT	ACCACGAGAT	GCAGGAAACC	CGTGTTATCC	200
	AGCTCGATGG	CGAGTCTAAG	GTCGCACTCG	TCTTCGGTCA	GATGAACGAG	250
10	CCCCCGGAG	CCCGTGCCCG	TGTTGCCCTC	ACTGGCCTGA	CCATTGCTGA	300
	ATATTTCCGT	GACGAGGAAG	GTCAAGACGG	TATGTATTCA	TATAAATTAC	350
	TCCGGGCAAA	TTGACTCAGA	ACCGCACTCA	CTCACACATA	TATTAGTGCT	400
	TCTCTTTATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	TCCGAAGTGT	450
	CCGCCCTGCT	TGGTCGTATT	CCCTCCGCCG	TCGGTTACCA	ACCCACTCTC	500
15	GCCGTCGACA	TGGGTGGTAT	GCAGGAACGT	ATCACAACCA	CCACCAAGGG	550
	CTCCATTACC	TYCGTG				566

20 2) INFORMATION FOR SEQ ID NO: 1849

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 817 bases
	(B) TYPE: Nucleic acid
25	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Campylobacter coli</i>
	(B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849

35	AATGAAGCCA	TTGTTGTAAA	TTTTGAAAGT	GAAGGC AAAA	AACAAAAACT	50
	TGTTTTAGAA	GTAGCAGCAC	ACTTGGGCGA	TAATAGAGTT	AGAACTATTG	100
	CTATGGATAT	GACAGATGGC	TTGGTAAGAG	GACTTAAAGC	AGAAGCTTTG	150
	GGTGCTCCTA	TTAGCGTTCC	TGTGGGTGAA	AAAGTTT TAG	GAAGAATTTT	200
40	TAATGTTACG	GGAGATTTGA	TCGATGAAGG	TGAAGAAATT	TCTTTTGATA	250
	AAAAATGGGC	AATTCATAGA	GATCCACCAG	CTTTTGAAGA	TCAAAGCACA	300
	AAAAGTGAGA	TTTTTGAAAC	AGGGATTAAA	GTTGTGGATT	TACTTGCTCC	350
	TTATGCAAAA	GGTGGTAAAG	TAGGTCTTTT	TGGTGGTGCA	GGTGTGGTA	400
	AAACTGTTAT	TATTATGGAG	CTTATT CACA	ATGTTGCATT	TAAACATAGC	450
45	GGCTATTCTG	TATTTGCAGG	TGTAGGTGAG	AGAACTCGTG	AAGGAAATGA	500
	CCTTTATAAT	GAAATGAAAG	AAAGTAATGT	TTTAGACAAA	GTTGCTCTAT	550
	GTTATGGACA	AATGAATGAA	CCACCAGGGG	CAAGAAATCG	TATTGCTTTA	600
	ACAGGTTTAA	CAATGGCTGA	GTATTTT TAGA	GATGAAATGG	GTCTTGATGT	650
	GCTTATGTTT	ATTGATAATA	TCTTTAGATT	TTCACAATCA	GGTTCTGAAA	700
50	TGTCAGCACT	TTTAGGAAGA	ATTCCATCAG	CTGTGGGTTA	TCAACCAACC	750
	CTAGCAAGTG	AAATGGGTAA	ATTCCAAGAA	AGAATTACTT	CAACTAAAAA	800
	AGGATCAATT	ACTTCAG				817

2) INFORMATION FOR SEQ ID NO: 1850

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850

```

AAGGCAACAC GCATAAACTT ATTTTAGAGA CTGCTGCACA CCTTGGAGAT      50
AATCGTGTA  GAACATATCGC TATGGATATG AGCGAAGGAC TTACAAGAGG      100
GTTAGATGCT ATAGCGCTTG GGTCGCCTAT CAGTGTCCTT GTTGGAGAAA      150
AAGTTTTTAGG AAGAATATTC AACGTAATTG GTGATCTTAT AGACGAAGGC      200
GAAGAAGAAA AATTTGATAA AAAATGGTCG ATTCATAGAG ATCCGCCGGC      250
ATTTGAAGAT CAAAGCACAA AAAGTGAAAT TTTTGAAACA GGTATAAAAG      300
TCGTAGATCT TTTGGCTCCT TATGCAAAAG GCGGTAAAGT TGGACTATTT      350
GGCGGTGCCG GCGTTGGTAA AACAGTTATC ATTATGGAAC TTATCCACAA      400
CGTTGCATTC AAACACAGCG GCTATTCGGT ATTTGCCGGT GTCGGTGAAA      450
GAACAAGAGA GGGTAACGAT CTTTATAATG AAATGAAAGA ATCCGGCGTT      500
TTGGATAAAG TTGCCCTTATG TTATGGACAA ATGAATGAAC CGCCGGGTGC      550
AAGAAACCGT ATAGCGCTTA CTGGTCTTAC AATGGCTGAG TATTTTCGTG      600
ACGAGATGGG ACTAGATGTT CTTATGTTTA TCGATAACAT CTTCCGTTTC      650
TCACAATCAG GCTCAGAGAT GTCGGCTCTT CTTGGACGTA TCCCAAGTGC      700
GGTTGGTTAT CAACCAACGT TAGCTAGCGA AATGGGAAGA CTTCAAGAAA      750
GAATCACATC AACTAAAAAA GGTTC                                     775

```

2) INFORMATION FOR SEQ ID NO: 1851

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851

```

CGAAGCTATT GAAGTAAATT TTACAGTAGA AGGCAACACG CATAAACTTA      50
TTTTAGAGAC TGCTGCACAC CTTGGAGATA ATCGTGTAAG AACTATCGCT      100

```

	ATGGATATGA	GCGAAGGACT	TACAAGAGGG	TTAGATGCTA	TAGCGCTTGG	150
	GTCGCCTATC	AGTGTTCCTG	TTGGAGAAAA	AGTTTTAGGA	AGAATATTCA	200
	ACGTAATTGG	TGATCTTATA	GACGAAGGCG	AAGAAGAAAA	ATTTGATAAA	250
	AAATGGTCGA	TTCATAGAGA	TCCGCCGGCA	TTTGAAGATC	AAAGCACAAA	300
5	AAGTGAAATT	TTTGAAACAG	GTATAAAAGT	CGTAGATCTT	TTGGCTCCTT	350
	ATGCAAAAGG	CGGTAAAGTT	GGACTATTTG	GCGGTGCCGG	CGTTGGTAAA	400
	ACAGTTATCA	TTATGGAAC	TATCCACAAC	GTTGCATTCA	AACACAGCGG	450
	CTATTCGGTA	TTTGCCGGTG	TCGGTGAAAG	AACAAGAGAG	GGTAACGATC	500
	TTTATAATGA	AATGAAAGAA	TCCGGCGTTT	TGGATAAAGT	TGCCTTATGT	550
10	TATGGACAAA	TGAATGAACC	GCCGGGTGCA	AGAAACCGTA	TAGCGCTTAC	600
	TGGTCTTACA	ATGGCTGAGT	ATTTTCGTGA	CGAGATGGGA	CTAGATGTTC	650
	TTATGTTTAT	CGATAACATC	TTCCGTTTCT	CACAATCAGG	CTCAGAGATG	700
	TCGGCTCTTC	TTGGACGTAT	CCCAAGTGCG	GTTGGTTATC	AACCAACGTT	750
	AGCTAGCGAA	ATGGGAAGAC	TTCAAGAAAG	AATCACATCA	ACT	793

2) INFORMATION FOR SEQ ID NO: 1852

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter gracilis*
- (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852

	GGACTATTTA	CCGAAGATTA	ACGAAGCTAT	CGAGGTTAAA	TTTGACGTCG	50
35	AGGGCGCTCA	TCGCAGGCTG	ATCCTAGAGG	TAGCCGCGCA	CCTTGAGAGAC	100
	AATCGCGTCC	GCACGATCGC	TATGGATATG	AGCGATGGAC	TTAGGCGAGG	150
	GCTTGAGGCC	GTCGCTTTGG	GCGCGCCTAT	TACGGTGCCCT	GTGGGCGAGA	200
	AAGTTTTGGG	TAGAATTTTT	AATGTTACGG	GCGATCTGAT	CGACGAAGGC	250
	GAGGATGAAA	AATTTGAAAC	CCGCTGGTCG	ATCCACAGAG	ATCCGCCTAG	300
40	CTTTGAAAAT	CAAAGCACGA	AGAGTGAAAT	TTTTGAAACC	GGCATTAAAGG	350
	TAGTCGATCT	GCTCGCCCCT	TATGCAAAGG	GCGGTAAGGT	AGGACTATTC	400
	GGCGGTGCTG	GCGTCGGTAA	GACCGTCATC	ATCATGGAAC	TGATTCAACA	450
	CGTCGCTTTC	AAACACAGCG	GCTACTCCGT	ATTTGCGGGT	GTCGGCGAGC	500
	GAACGAGAGA	GGGAAACGAC	CTTTATAACG	AGATGAAAGA	ATCGGGCGTT	550
45	TTGGATAAAG	TCGCCTTGAC	CTATGGTCAG	ATGAACGAAC	CGCCGGGAGC	600
	GAGAAACCGT	ATCGCGCTAA	CCGTCCTTAC	GATGGCCGAG	TATTTCCGCG	650
	ACGAGCTAGG	GCTTGACGTT	TTGATGTTTA	TTGATAATAT	CTTCCGCTTC	700
	TCGCAGTCGG	GTTCGGAGAT	GTCCGCGCTT	TTAGGACGAA	TTCCGTCCGC	750
	GGTCGGTTAT	CAGCCTACGC	TTGCCAGCGA	AATGGGTAAA	TTACAGGAGC	800
50	GCATTACTTC	TACTAAGAAG	GGCTC			825

2) INFORMATION FOR SEQ ID NO: 1853

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853

	TTTACCTCAA	ATTAATGAAG	CAATTGTTGT	AAATTTTGAA	AGCGAAGGAA	50
	AAAAACATAA	ACTTGTTTTA	GAAGTAGCAG	CTCATTTAGG	AGATAATAGA	100
	GTTAGAATA	TTGCTATGGA	TATGACAGAT	GGTTTGGTAA	GGGGCTTAAA	150
20	AGCTGAGGCT	TTAGGTGCTC	CTATTAGTGT	TCCTGTTGGT	GAGAAAGTTT	200
	TAGGAAGAAT	TTTCAATGTT	ACTGGAGATT	TGATCGATGA	AGGTGAAGAA	250
	ATTTCTTTTG	ATAAAAAATG	GGCAATTCAT	AGAGATCCGC	CAGCTTTTGA	300
	AGATCAAAGC	ACAAAAAGTG	AGATTTTGA	AACAGGGATT	AAAGTTGTAG	350
	ATTTGCTTGC	TCCTTATGCA	AAAGGTGGTA	AAGTAGGTCT	TTTTGGTGGT	400
25	GCAGGTGTTG	GTAAAACGT	TATTATTATG	GAGCTTATTC	ACAATGTTGC	450
	ATTTAAGCAT	AGCGGCTATT	CTGTATTTGC	AGGTGTGGGT	GAGAGAAGTC	500
	GTGAAGGAAA	TGACCTTTAT	AATGAAATGA	AAGAAAGTAA	TGTTTTAGAC	550
	AAAGTTGCTC	TATGTTATGG	ACAAATGAAT	GAACCACCAG	GAGCAAGAAA	600
	TCGTATTGCT	TTAACAGGTT	TAACAATGGC	TGAGTATTTT	AGAGATGAAA	650
30	TGGGTCTTGA	TGTGCTTATG	TTTATTGATA	ATATCTTTAG	ATTTTCACAA	700
	TCAGGTTCTG	AAATGTCAGC	ACTTTTAGGA	AGAATTCCAT	CAGCTGTGGG	750
	TTATCAACCA	ACCCTAGCAA	GTGAAATGGG	TAAATTCCAA	GAAAGAATTA	800
	CTTCAACTAA	AAAAGGCT				818

2) INFORMATION FOR SEQ ID NO: 1854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
 (B) STRAIN: ATCC 43198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854

	ATTACCTGAT	ATCAACAACG	CCTTATTGGT	CTATAAAAAT	GATGAACAAA	50
--	------------	------------	------------	------------	------------	----

	AAAGTAAAAT	TGTGCTAGAA	GCTGCCTTAG	AATTAGGTGA	TGGCATCATT	100
	CGTACAATTG	CCATGGAATC	AACGGATGGT	TTACAACGTG	GGATGGAAGT	150
	TGTCGATACT	GGTAAACCAA	TTTCAGTTCC	AGTTGGTAAA	GAAACGCTAG	200
	GACGTGTCTT	TAACGTTTTA	GGGGATACGA	TTGATATGCA	AGAACCATTT	250
5	GCACAAGATG	CAGATCGTTC	TGCAATTCAT	AAAGCTGCAC	CAAAATTTGA	300
	AGACTTAAGT	ACAAGTACTG	AAATTTTAGA	AACAGGGATT	AAAGTTATCG	350
	ACTTATTAGC	ACCATATTTA	AAAGGTGGTA	AAGTCGGTCT	ATTCGGGGGT	400
	GCCGGAGTAG	GTAAAACCGT	TTTAATCCAA	GAATTAATCC	ATAATATTGC	450
	ACAAGAACAT	GGTGGGATTT	CTGTATTTAC	CGGTGTTGGT	GAACGTACAC	500
10	GTGAAGGAAA	TGACTTGTAT	CATGAAATGC	GTGATTCAGG	AGTTATTGAA	550
	AAAAC TGCCA	TGGTGT TTGG	TCAAATGAAC	GAACCACCTG	GAGCTCGTAT	600
	GCGTGTTGCT	TTAACTGGGT	TAACGATTGC	TGAATATTTT	CGTGATGTAG	650
	AAGGACAAGA	TGTGTTGCTA	TTTATTGATA	ACATCTTCCG	TTTCACTCAA	700
	GCGGGTTCTG	AAGTATCAGC	CTTGCTTGGT	CGTATGCCAT	CTGCCGTGGG	750
15	TTATCAACCT	ACATTGGCTA	CAGAAATGGG	TCAATTACAA	GAACGTATCA	800
	CTTCAACTAA	GAAGGGCTCT	ATCACTTCTA			830

20 2) INFORMATION FOR SEQ ID NO: 1855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855

35	TCTTTACCAG	ATATCAATAA	TGCGCTTATT	GTCTATAAAA	ATGATGAACA	50
	AAAAAGTAAA	ATCGTGCTTG	AAGCTGCTTT	AGAGCTAGGA	GATGGCATT A	100
	TTCGTACGAT	TGCAATGGAA	TCAACTGATG	GATTGCAACG	TGGAATGGAA	150
	GTTTTTCGATA	CAGGTAAGCC	AATTTTCAGTA	CCAGTAGGTC	GTGAAACATT	200
40	AGGTCGTGTA	TTTAATGTTT	TAGGTGATAC	CATTGATACG	CAAGAAGCTT	250
	TTCCTGCTGA	TGCGAATCGT	GATGCGATT C	ATAAATCAGC	TCCAGCTTTT	300
	GAAGAATTAA	GTACAAGTAC	TGAAATCCTA	GAAACAGGGA	TTAAAGTTAT	350
	CGACTTACTA	GCACCATACT	TAAAAGGTGG	GAAAGTTGGT	CTATTCCGGT	400
	GTGCCGGTGT	AGGTAAAACC	GTATTAATTC	AAGAATTAAT	TCATAATATC	450
45	GCCCAAGAAC	ATGGGGGTAT	TTCAGTATTT	ACCGGTGTTG	GTGAACGTAC	500
	ACGTGAAGGA	AATGACTTGT	ATCACGAAAT	GCGTGATTCA	GGCGTTATCG	550
	AAAAAACTGC	TATGGTGTTT	GGGCAAATGA	ACGAACCACC	TGGAGCACGT	600
	ATGCGTGTTG	CGCTAACTGG	ACTAACTATT	GCGGAATACT	TCCGTGATGT	650
	TGAAGGCCAA	GACGTATTGC	TATTTATTGA	TAATATCTTC	CGTTTTACTC	700
50	AAGCAGGTTT	TGAAGTTTCT	GCCTTACTTG	GTCGTATGCC	TTCTGCGGTA	750
	GGTTATCAAC	CTACTTTGGC	TACTGAAATG	GGTCAATTGC	AAGAACGGAT	800
	TACATCAACG	AAGAAAGGTT	CGA			823

2) INFORMATION FOR SEQ ID NO: 1856

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856

TTACCAGACA	TTAATAATGC	CTTGGTTGTC	TATAAAAATG	ACGAACAAAA	50
AACCAAGATT	GTATTAGAAG	CTGCCTTAGA	ACTAGGAGAT	GGTGTGATTC	100
GAAGTATCGC	CATGGAATCT	ACTGATGGCT	TACAACGGGG	AATGGAAGTT	150
GTCGATACTG	GCAGTTCCAT	TTCTGTACCG	GTAGGAAAAG	AAACATTGGG	200
TCGTGTATTT	AACGTTTTAG	GAAATACAAT	TGACTTAGAA	GAACCTTTTC	250
CAGCGGATGC	TAAACGTAGT	GGTATCCATA	AAAAAGCGCC	TGATTTTGAT	300
GAATTAAGCA	CTAGTACAGA	AATTTTAGAA	ACAGGGATTA	AAGTTATTGA	350
CCTATTAGCC	CCTTATTTAA	AAGGTGGTAA	AGTCGGATTA	TTCGGTGGTG	400
CCGGAGTTGG	TAAACCGTT	TTAATTCAAG	AATTAATTCA	TAATATTGCC	450
CAAGAACATG	GTGGGATTTC	TGTTTTTACT	GGTGTGGTG	AAAGAACACG	500
TGAAGGTAAT	GACTTGTATT	ATGAAATGAA	AGAATCTGGC	GTTATCGAAA	550
AAACTGCCAT	GGTATTTGGT	CAAATGAATG	AGCCACCTGG	TGCCCCGGATG	600
CGGGTTGCTT	TAACCGGACT	TACCATTGCG	GAATACTTCC	GGGACGTTGA	650
AGGACAAGAT	GTATTGCTCT	TTATCGATAA	TATTTTCCGT	TTTACCCAAG	700
CTGGTTCAGA	AGTATCTGCC	TTATTAGGAC	GGATGCCCTC	TGCCGTTGGT	750
TATCAACCAA	CTTTGGCTAC	TGAAATGGGA	CAACTTCAAG	AACGGATTAC	800
CTCAACGAAA	AAAGGTTCTA	TTACAT			826

2) INFORMATION FOR SEQ ID NO: 1857

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857

TCCTTACCAG	ACATCAACAA	TGCGTTGATT	GTTTACAAAA	AAAATAAAAC	50
------------	------------	------------	------------	------------	----

	AAAAGTTGTT	CTTGAAGCTG	CTTTGGAAC	TGGTGATGGT	GTTATCCGCA	100
	CGATCTCTAT	GGAATCAACA	GATGGCTTGC	AACGTGGAAT	GGAAGTTGTC	150
	GATACAGGCA	AACCAATCTC	AGTTCCCGTT	GGTAAAGAAA	CTTTAGGTCTG	200
	TGTGTTTAAAC	GTATTAGGTG	AAACAATCGA	CAAAGAAGCG	CCTTTTCCAG	250
5	AAGATGCAGT	AAAAAGCGGT	ATTCATAAAA	AAGCGCCGGC	TTTTGAAGAA	300
	CTTAGTACCA	GTAATGAAAT	TTTAGAAACA	GGGATCAAAG	TTATCGACTT	350
	ATTAGCTCCT	TACTTAAAGG	GTGGTAAAGT	CGGACTATTT	GGTGGTGCCG	400
	GTGTTGGTAA	AACCGTCTTG	ATCCAAGAAT	TGATTCATAA	TATCGCCCAA	450
	GAACACGGTG	GTATTTTCACT	GTTTACGGGT	GTTGGTGAAC	GTACTCGTGA	500
10	AGGGAACGAC	CTTTATTATG	AAATGAAGGA	ATCAGGCGTT	ATTGAGAAAA	550
	CTGCCATGGT	GTTTGGACAA	ATGAACGAGC	CGCCAGGTGC	GCGTATGCGT	600
	GTTGCCTTGA	CTGGTTTGAC	ATTGGCTGAA	TATTTCCGAG	ATGAAGAAGG	650
	ACAAGATGTG	CTGTTGTTTA	TCGACAACAT	CTTCCGTTTC	ACTCAAGCCG	700
	GTTCTGAAGT	TTCTGCCTTG	CTTGGCCGGA	TGCCTTCAGC	CGTTGGCTAC	750
15	CAACCAACTT	TGGCAACTGA	AATGGGTCAA	TTGCAAGAAC	GAATCACTTC	800
	AACGAAGAAG	GGCT				814

20 2) INFORMATION FOR SEQ ID NO: 1858

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858

35	CGCATTAGTT	GTTTATAAAA	ATGATGAGCA	AAAATCAAAA	GTTGTTCTTG	50
	AAGCAGCATT	AGAATTAGGT	GACGGTGTGA	TCCGTACGAT	CGCAATGGAA	100
	TCGACGGATG	GACTACAACG	TGGAATGGAA	GTCATCGACA	CAAGCAAAGC	150
	GATCTCTGTA	CCAGTTGGAA	CAGAAACATT	AGGTCGTGTG	TTCAACGTGT	200
40	TAGGTGAAAC	AATCGATTTG	GAAGCACCAT	TTCCAGAGGA	TGCCCCAAGA	250
	AGCGAGATCC	ACAAGAAAGC	ACCAAATTTT	GATGAATTAA	GCACAAGTAC	300
	AGAGATTCTT	GAAACTGGGA	TCAAAGTCAT	TGACTTATTA	GCACCTTATT	350
	TAAAGGTGG	GAAAGTTGGA	TTGTTTGGGG	GTGCCGGTGT	TGGTAAAACC	400
	GTACTGATCC	AAGAATTGAT	CCATAATATC	GCCCAAGAAC	ATGGGGGAAT	450
45	CTCAGTGTTT	ACCGGTGTAG	GGGAACGTAC	CCGTGAAGGA	AACGATCTGT	500
	ATTACGAAAT	GAAAGATTCA	GGCGTAATCG	AAAAAACAGC	GATGGTGTTT	550
	GGACAAATGA	ATGAGCCACC	AGGTGCTCGT	ATGCGTGTCT	CACTAACTGG	600
	ATTGACGATT	GCGGAATATT	TCCGTGATGT	CGAAGGACAA	GACGTGCTCT	650
	TATTTATTGA	TAATATTTTC	CGTTTCACCC	AAGCAGGTTC	AGAAGTATCT	700
50	GCCTTACTAG	GACGTATGCC	ATCAGCGGTT	GGTTATCAAC	CAACCTTAGC	750
	GACTGAAATG	GGACAACTCC	AAGAACGGAT	CACTTCAACG	A	791

2) INFORMATION FOR SEQ ID NO: 1859

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859

TCCTTACCAG	ACATCAACAA	TGCGTTGATT	GTTTATAAAA	AAGATAAAAC	50
AAAAGTTGTT	CTTGAAGCTG	CTTTGGAAC	TGGTGATGGT	GTTATTCGCA	100
CAATCGCCAT	GGAATCAACG	GATGGATTAC	AACGTGGAAT	GGAAGTTGTC	150
GATACTGGCA	AGCCTATTTT	TGTTCCAGTA	GGAAAAGAAA	CTCTAGGTCG	200
TGTATTTAAT	GTATTAGGTG	AAACAATCGA	CAAGGAAGCG	CCTTTTCCAG	250
AAGATGCAGA	AAAAAGTGGT	ATTCAACAAG	AAGCACCAAC	TTTCGAAGAA	300
CTTAGCACAA	GTAATGAGAT	CTTAGAAACA	GGAATCAAAG	TTATTGACTT	350
GTTAGCTCCT	TACTTAAAAG	GTGGTAAAGT	TGGATTATTT	GGTGGTGCCG	400
GTGTTGGTAA	AACAGTCTTG	ATTCAAGAGC	TAATTCATAA	TATCGCTCAA	450
GAACATGGTG	GTATTTCTGT	GTTTACTGGT	GTTGGTGAAC	GTACTCGTGA	500
AGGGAACGAC	CTTTATTATG	AAATGAAAGA	TTCTGGTGTT	ATTGAGAAAA	550
CTGCTATGGT	GTTCCGGTCAA	ATGAACGAGC	CGCCAGGTGC	ACGTATGCGT	600
GTTGCCTTAA	CTGGTTTAAAC	CTTAGCCGAA	TACTTCCGTG	ATGAAGAAGG	650
ACAAGATGTG	TTGCTATTTA	TTGACAACAT	TTTCCGTTTC	ACTCAAGCCG	700
GATCAGAAGT	TTCTGCCTTA	CTTGGCCGTA	TGCCGTCAGC	AGTTGGTTAC	750
CAACCGACTT	TAGCAACTGA	AATGGGTCAA	TTACAAGAAC	GTATTACGTC	800
GACGAAAAAA	GGTTCAA				817

2) INFORMATION FOR SEQ ID NO: 1860

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Globicatella sanguis*
 (B) STRAIN: ATCC 51173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860

CCTGACATTC	ATAATGCATT	AATTGTAACG	AACGCTGATA	TGGCGGATGT	50
------------	------------	------------	------------	------------	----

	AATGCAAGAA	AATATTTTCGG	ATGAAGAAAA	ATTATTAACC	TTAGAAGTTG	100
	CACTGGATTT	AGGTCATGGA	ATGGTCCGGA	CAATTGCGAT	GGAATCAACC	150
	GATGGTTTGG	AACGCGGCAT	GACAGTTGTG	GATTATTTAA	CACCGATTAA	200
	AGTGCCAGTA	GGCGAAGCCA	CTTTAGGTAG	AGTATTCAAT	GTTTTAGGTG	250
5	AGACAATTGA	TGAACTAGAA	CCGGTTGGCG	ACGATGTTGA	ACTCAAAAGT	300
	ATTCATCGTG	AAGCCCCTAA	ATATGAGGAC	TTAGATAATA	GTTTTTCATGT	350
	TTTAGAAACC	GGAATTAAGG	TCATCGATTT	ATTAGCTCCT	TATATTAAAG	400
	GGGGAAAAAT	CGGTTTATTC	GGTGGTGCCG	GAGTGGGTAA	AACGGTCTTA	450
	ATTCAAGAAT	TAATTCATAA	TATTGCAGAA	CAATTAGGAG	GTATCTCAGT	500
10	TTTCACTGGG	GTTGGAGAAC	GTACCCGTGA	AGGGAATGAC	CTCGTTTTTG	550
	AAATGCGAGA	GTCAGGTGTA	AGCAAGAAGA	CGGCCATGGT	TTTCGGTCAA	600
	ATGAATGAAC	CACCTGGAGC	ACGTATGCGT	GTTGTCTTAA	CAGGACTTAC	650
	AATGGCGGAA	TATTTCCGTG	ACGAATTGAA	ACAAGACGTC	TTATTATTTA	700
	TTGATAATAT	TTATCGTTTT	ACTCAAGCAG	GTTCCGAAGT	GTCAGCCTTA	750
15	TTAGGTCGTA	TGCCTTCAGC	AGTAGGGTAT	CAACCAACTT	TAGCAAGTGA	800
	AATGGGACAA	ATGCAAGAAC	GTATTACGTC	WACGAAGCRC	GGTTCCATTA	850
	CA					852

20

2) INFORMATION FOR SEQ ID NO: 1861

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus garvieae*
- (B) STRAIN: ATCC 49156

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861

	GCGCGACTCT	TCCTGAGATT	AATAACGCAC	TCATCGTTTA	CAAAGATGTA	50
	GACGGCGTTA	AAACTAAAAT	CGTCCTTGAA	GTGGCGTTGG	AACTTGGTGA	100
	TGGTGCCGTA	CGTACCATCG	CTATGGAATC	AACTGATGGC	TTGACACGTG	150
40	GACTTGAAGT	TCTCGATACA	GGTAAAGCAA	TCAGCGTACC	TGTTGGTCAA	200
	GAAACACTTG	GACGTGTCTT	CAATGTACTT	GGAGATGCTA	TTGATGGAGG	250
	GGAAGCATTT	GCTGAAAATG	CAGAACGCAG	CCCTATCCAT	AAAAAAGCCC	300
	CATCTTTTGA	TGAACTTTCA	ACAGCAAATG	AAATTCTGGT	GACAGGGATT	350
	AAAGTTATTG	ACTTGCTTGC	CCCATACCTT	AAAGGTGGTA	AGATTGGGTT	400
45	GTTCCGGTGGT	GCCGGAGTTG	GTAAAACCGT	CCTTATCCAA	GAGTTGATTC	450
	ACAATATTGC	CCAAGAACAC	GGTGGTATTT	CCGTATTTAC	TGGTGTTGGG	500
	GAACGTACAC	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AAGAATCAGG	550
	CGTTATCGAA	AAAACAGCCA	TGGTCTTCGG	TCAAATGAAT	GAACCACCTG	600
	GAGCACGTAT	GCGTGTTGCT	CTTACTGGTT	TGACAATTGC	TGAATATTTT	650
50	CGTGATGTAG	AAAACAAGA	CGTTTTGCTT	TTCATTGATA	ATATCTTCCG	700
	TTTCAACCAA	GCCGGTTCAG	AAGTATCTGC	CCTCTTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	TTACCAACCT	ACGCTTGCAA	CTGAAATGGG	TCAACTTCAA	800
	GAACGTATCA	CTTCAACAAA	ACAAGGTT			828

2) INFORMATION FOR SEQ ID NO: 1862

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis*
 (B) STRAIN: ATCC 11454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862

AATTGCCTGA	RATTAACAAT	GCCTTGATTG	TCTACAAAGA	TGTCAATGGC	50
CTAAAAACAA	AAATTACTCT	TGAAGTTGCT	TTGGAACCTG	GTGATGGTGC	100
AGTTCGTACA	ATCGCTATGG	AATCTACTGA	TGGCTTGACT	CGTGGACTTG	150
AAGTCCTTGA	TACAGGTAAA	GCAGTCAGCG	TTCCTGTTGG	GGAAGCCACT	200
CTTGGTCGTG	TTTTTAACGT	TCTTGGTGAT	GTTATTGACG	GTGGGGAAGA	250
ATTTGCTGCT	GATGCAGAAC	GTAATCCTAT	CCATAAAAAA	GCTCCAACAT	300
TTGACGAATT	GTCAACTGCA	AACGAAGTTC	TCGTAACCTG	GATTAAAGTT	350
GTCGATTTGC	TTGCACCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
TGGTGCCGGA	GTTGGTAAAA	CCGTCCTTAT	TCAAGAATTG	ATTCACAACA	450
TCGCCCAAGA	ACACGGAGGT	ATTTCTGTGT	TTACCGGTGT	TGGGGAACGT	500
ACTCGTGAAG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
TGAAAAAACT	GCCATGGTCT	TTGGTCAAAT	GAATGAACCA	CCAGGAGCAC	600
GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TTGCTGAATA	TTTCCGTGAT	650
GTTCAAGGTC	AAGACGTACT	GCTTTTCATT	GACAACATCT	TCCGTTTCAC	700
ACAAGCTGGT	TCAGAAGTTT	CTGCCCTTTT	GGGACGTATG	CCTTCTGCCG	750
TTGGTTACCA	ACCAACACTT	GCTACTGAAA	TGGGGCAATT	GCAAGAACGT	800
ATCACTTCTA	CTAAGAAGGG	TTCTGTTA			828

2) INFORMATION FOR SEQ ID NO: 1863

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863

CTTACCTGAA	ATCTACAACG	CCCTAGTTAT	TGAATATAAA	TCTGATGCAG	50
------------	------------	------------	------------	------------	----

	AAGAAGCACC	AACTAGCCAA	CTTACTTTAG	AAGTAGCCAT	TCAATTAGGT	100
	GATGACGTTG	TTCGTACAAT	TGCAATGGCA	TCAACTGATG	GTGTTCAAAG	150
	AGGTATGGAA	GTTATTGATA	CTGGGAGCCC	AATCACAGTT	CCAGTTGGTA	200
	CAGTAACACT	TGGTCGTGTA	TTTAACGTAT	TAGGAAACAC	TATCGATTTG	250
5	GATGAGCCAC	TTCCAAGCGA	TATCAAGCGT	AATAAAATTC	ACCGTGAAGC	300
	ACCAACATTT	GACCAATTAG	CAACAACACT	TGAAATTCTT	GAAACAGGAA	350
	TAAAAGTTGT	AGACTTGCTA	GCCCCATATT	TAAAAGGTGG	TAAAATTGGT	400
	TTGTTTCGGCG	GAGCGGGTGT	TGGTAAAACC	GTTTTAATCC	AAGAACTTAT	450
	TCATAATATC	GCTCAAGAAC	ATGGTGGTAT	TTCTGTGTTC	GCTGGTGTTC	500
10	GAGAACGTAC	TCGTGAAGGG	AACGATCTTT	ACTTTGAAAT	GAAAGACTCT	550
	GGTGTAATTG	AAAAAACTGC	CATGGTATTC	GGTCAAATGA	ACGAACCACC	600
	AGGTGCTCGT	ATGCGTGTAG	CTTTAACAGG	TCTTACAATC	GCTGAATATT	650
	TCCGTGATGA	AGAACACCAA	GATGTACTTC	TATTCATTGA	TAATATTTTC	700
	CGCTTTACTC	AAGCTGGTTC	AGAGGTTTCG	GCTTTACTAG	GTCGTATGCC	750
15	ATCTGCAGTA	GGTTATCAAC	CAACTCTAGC	TACCGAAATG	GGACAATTAC	800
	AAGAACGTAT	TACTTCTACT	AATGT			825

20 2) INFORMATION FOR SEQ ID NO: 1864

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864

35	GTCATATTCC	AGAGCTTTAT	GACGCTCTGG	AGGTAAAGGG	CGATGGTAAG	50
	CATCGTTTCA	ACCTAGTTCT	TGAGGTTCAA	CAGCAGATTG	GCGGTGGTGT	100
	GGTACGCTGC	ATTGCCATGG	GTTCTTCTGA	CGGTTTGAGC	AGAGGAATTG	150
	AGGCTGTAAA	TACTGGTGCC	GGTGTTAAGG	TTCCAGTTGG	TCGTGAGACC	200
40	CTAGGACGTA	TTATGAACGT	TTTAGGTCAG	CCTGTAGATG	AGAGAGGTCC	250
	TATCGGACAG	AAAGAGGATT	GGGAAATTCA	CCGTCCAGCT	CCTACCTATG	300
	CTGAGCAGTC	ATCAACTACA	GAAATTCTAG	AAACCGGTAT	TAAGGTTATG	350
	GACCTTATCT	GCCCATTTGC	TAAGGGTGGT	AAAGTTGGTC	TGTTCGGTGG	400
	TGCCGGTGTG	GGTAAGACAG	TTAACATGAT	GGAGCTTATC	AATAACATTG	450
45	CTAAGGCTCA	CTCAGGTCTA	TCTGTATTTA	CCGGTGTTGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	CAGGAATCAA	AGGTTATCGA	550
	TAAGGTATCA	ATGATTTACG	GTCAGATGAA	CGAGCCTCCA	GGGAACCGTC	600
	TACGTGTTGC	TCTGACAGGT	CTGACTGTTG	CTGAGAAGTT	CCGTGACGAA	650
	GGTCTGGATG	TGCTTCTGTT	CATCGATAAC	ATCTATCGTT	ATACACTGGC	700
50	TGGTACAGAG	GTATCTGCTC	TGTTAGGCCG	TATGCCTTCA	GCTGTGGGTT	750
	ACCAGCCTAC	ACTGGCTGAG	GAAATGGGTG	TATTACAGGA	GCGTATTGCT	800
	TCAACTAAGA	AAGGTTCTAT	T			821

2) INFORMATION FOR SEQ ID NO: 1865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865

	TGATACTTTA	CCAGATATCA	ATAATGCATT	AGCCGTATAT	AAAAATGATG	50
	AGAACAAGAC	GCGTGTTGTA	TTGGAAGCTA	CTTTAGAACT	TGGAGATGGG	100
	GTAATTCGTG	CCATTTCTAT	GGGGTCTACT	GACGGCTTGC	AACGTGGCAT	150
20	GGAAGTTGTG	GATACACAAG	AACCTATTTT	TGTTCCGGTA	GGAAATGATA	200
	CTTTAGGTCG	TGTATTTAAT	GTGTTAGGAG	AAACAATAGA	TAATCAGGAG	250
	CCATTTCTCTG	AAGATGCTGA	AAAAAGTGGT	ATTCACAAAA	AAGCCCCTAG	300
	TTTTGATGAA	TTAAGTACTA	GTTTCGGAAAT	ATTAGAAACA	GGGATCAAAG	350
	TGATTGATTT	ATTAGAACCT	TATCTAAGAG	GCGGTAAAGT	CGGATTGTTT	400
25	GGAGGCGCCG	GTGTTGGAAA	AACGGTGCTA	ATTCAAGAAT	TGATCAATAA	450
	TGTTGCCCAA	GAACACGGGG	GTATTTCCGT	GTTTAATGGT	GTAGGTGAAC	500
	GTAATCGTGA	AGGTAATGAC	TTGTATTATG	AAATGCAGGA	TTCAGGCGTT	550
	ATCGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	CACCAGGTGC	600
	TCGTATGCGT	GTTGCTTTAA	CTGGCCTAAC	ACTGGCAGAA	TATTTTCGAG	650
30	ATGTTGAAGG	TCAAGACGTA	TTATTATTTA	TTGATAATAT	TTTCCGTTTT	700
	ACACAAGCAG	GTACCGAAGT	TTCCGCTTTA	CTTGGTAGAA	TGCCATCTGC	750
	TGTTGGCTAT	CAACCCACAC	TAGCAACTGA	AATGGGGCAA	CTGCAAGAAC	800
	GGATTACGTC	AACGGATAAG	GG			822

2) INFORMATION FOR SEQ ID NO: 1866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866

	ATCTCCTCAG	GATCKATAGG	ACTTGATATA	GCTCTTGGA	TAGGCGGCGT	50
--	------------	------------	------------	-----------	------------	----

	ACCAAAAGGA	AGAATAGTCG	AAATTTATGG	GCCAGAAAGC	TCTGGTAAAA	100
	CAACTCTTAC	TTTGCATTTA	ATAGCAGAAT	CTCAAAAAGT	CGGCGGAGTT	150
	TGCGCGTTTG	TAGATGCAGA	GCATGCACTT	GATGTAAAT	ATGCTAAAAA	200
	TTTAGGCGTT	GATACGGATA	ACTTATATAT	TTCTCAACCG	GACTTCGGAG	250
5	AGCAAGCTCT	TGATATAGTA	GAAACTCTAG	CTAGAAGCGG	CGCCGTTGAT	300
	CTTATAGTAA	TAGATAGCGT	AGCAGCTYTA	ACACCAAAAA	GCGAAATAGA	350
	AGGCGATATG	GGAGATCAGC	ACGTAGGGCT	GCAAGCAAGA	CTCATGAGTC	400
	AAGCACTTAG	AAAATTAACC	GGAGTTGTCC	ATAAAATGGG	AACTACAGTT	450
	GTATTTATAA	ACCAAATTCG	TATGAAAATC	GGCGCTATGG	GCTATGGCAC	500
10	TCCTGAAACT	ACTACTGGCG	GAAATGCGCT	TAAATTTTAC	GCTTCAGTTA	550
	GACTTGACGT	ACGTAAAATA	GCTACTTTAA	AACAGAGCGA	TGAGCCAATC	600
	GGAAACCGCG	TAAAAGTAAA	AGTAGTAAAA	AACAAAGTCG	CTCCTCCTTT	650
	TAGACAAGCC	GAATTTGATA	TCATGTTTGG	AGAAGGTATC	AGCAAAGAAG	700
	GAGAGATAAT	AGATTACGGC	GTAAAACTTG	ATATTATCGA	TAAAAGCGGC	750
15	GCTTGGTTTA	GCTATGATAA	TTCAAAATTA	GGTCAAGGCA	GAGAAAATCT	800
	AAAAGCGTTT	TTAAAAGA				818

20 2) INFORMATION FOR SEQ ID NO: 1867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867

35	TCTCCTCAGG	ATCKATAGGA	CTTGATATAG	CTCTTGGTAT	AGGCGGCGTA	50
	CCAAAAGGAA	GAATAGTCGA	AATTTATGGG	CCAGAAAGCT	CTGGTAAAAC	100
	AACTCTTACT	TTGCATTTAA	TAGCAGAATC	TCAAAAAGTC	GGCGGAGTTT	150
	GCGCGTTTGT	AGATGCAGAG	CATGCACTTG	ATGTTAAATA	TGCTAAAAAT	200
40	TTAGGCGTTG	ATACGGATAA	CTTATATATT	TCTCAACCGG	ACTTCGGAGA	250
	GCAAGCTCTT	GATATAGTAG	AAACTCTAGC	TAGAAGCGGC	GCCGTTGATC	300
	TTATAGTAAT	AGATAGCGTA	GCAGCTYTAA	CACCAAAAAG	CGAAATAGAA	350
	GGCGATATGG	GAGATCAGCA	CGTAGGGCTG	CAAGCAAGAC	TCATGAGTCA	400
	AGCACTTAGA	AAATTAACCG	GAGTTGTCCA	TAAAATGGGA	ACTACAGTTG	450
45	TATTTATAAA	CCAAATTCGT	ATGAAAATCG	GCGCTATGGG	CTATGGCACT	500
	CCTGAAACTA	CTACTGGCGG	AAATGCGCTT	AAATTTTACG	CTTCAGTTAG	550
	ACTTGACGTA	CGTAAAATAG	CTACTTTAAA	ACAGAGCGAT	GAGCCAATCG	600
	GAAACCGCGT	AAAAGTAAAA	GTAGTAAAAA	ACAAAGTCGC	TCCTCCTTTT	650
	AGACAAGCCG	AATTTGATAT	CATGTTTGGG	GAAGGTATCA	GCAAAGAAGG	700
50	AGAGATAATA	GATTACGGCG	TAAAACCTGA	TATTATCGAT	AAAAGCGGCG	750
	CTTGGTTTAT	CTATGATAAT	TCAAAATTAG	GTCAAGGCAG	AGAAAATCTA	800
	AAAGCGTTTT	TAAA				814

2) INFORMATION FOR SEQ ID NO: 1868

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868

```

GATAGCATAG GCWCAGGTTC AGTTGGACTT GATCTTGCTT TAGGTATAGG      50
CGGTGTTCCA AAAGGAAGAA TTATAGAAAT TTATGGGCTT GAAAGTTCAG      100
GTAAAACTAC TCTAACTCTA CACATTATCG CAGAATGCCA AAAAGCAGGT      150
GGGGTTTGTG CTTTTATCGA TGCAGAACAT GCACTTGATG TGAAATATGC      200
TAAAAATTTA GGTGTAAATA CAGATGATTT GTATGTTTCT CAACCTGATT      250
TTGGAGAGCA AGCCTTAGAA ATTGTAGAAA CTATAGCWAG AAGTGGTGCA      300
GTAGATCTTA TWGTAGTAGA TAGCGTTGCA GCWCTTACCC CAAAAGCAGA      350
AATTGAAGGC GATATGGGCG ATCARCATGT AGGACTTCAA GCAAGACTTA      400
TGTCTCAAGC TCTAAGAAAA CTTACAGGTA TAGTTCATAA AATGAATACC      450
ACAGTAATTT TCATCAACCA AATTCGTATG AAAATCGGTG CTATGGGTTA      500
TGGTACTCCT GAAACCACAA CAGGTGGAAA TGCATTAAAA TTTTATGCTT      550
CTGTGCGTTT AGATGTTAGA AAAGTAGCAA CCTTAAAMCA AAACGWAGAM      600
CCTATAGGAA ACCGCGTTAA AGTAAAAGTA GTTAAAAATA AAGTTGCTCC      650
TCCATTCAGM CAAGCTGAAT TTGATGTGAT GTTTGGAGAG GGTTTAAGCC      700
GTGAAGGTGA ATTGATCGAT TATGGTGTA AACTTGATAT CGTAGATAAA      750
AGTGGTGCGT GGTTTCTTA TAAAGATAAA AACTTGGAC AAGGTAGAGA      800
AAATTCAAAA GCTTTCTTAA AAGA                                     824

```

2) INFORMATION FOR SEQ ID NO: 1869

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869

```

AGAAAGTTCT GGTAACAACAA CGGTTGCACT GCATGCGATT GCAGAAGTTC      50

```


AAAAACATGG	CGGGACGGCA	GCCTTTATTG	ATGCCGAGCA	CGCGTTGGAC	100
CCTCAATACG	CACAACGTCT	AGGTGTAAAC	ATTGATGAAT	TGCTGCTATC	150
ACAACCAGAT	ACTGGGGAAC	AAGGCTTAGA	AATTGCAGAT	GCTTTAGTTT	200
CAAGTGGCGC	AGTCGATATT	ATCGTTATTG	ACTCGGTGGC	CGCGCTAGTC	250
5 CCCC GTGCTG	AAATCGATGG	CGAGATGGGT	GATGCGCACG	TTGGTCTGCA	300
GGCTCGTTTG	ATGTCACAAG	CATTGCGCAA	GCTGTCAGGC	TCTATCAACA	350
AAACAAAGAC	TATCGCCGTC	TTTATTAACC	AAATTCGT		388

2) INFORMATION FOR SEQ ID NO: 1870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870

TGAAAGTTCA	GGTAAAACAA	CAGTTGCACT	ACACGCTATT	GCAGAAGTAC	50
AAAAAAATGG	CGGAACGGCC	GCTTTCATTG	ATGCTGAGCA	TGCGTTAGAT	100
CCGCAATATG	CACAAAAATT	AGGTGTGAAT	ATCGATGAAC	TACTTCTTTC	150
30 ACAGCCTGAC	ACAGGAGAAC	AAGGTCTAGA	GATCGCTGAT	GCTTTAGTAT	200
CAAGTGGGGC	TGTAGATATC	GTAGTAGTCG	ATTCAGTTGC	TGCTTTAGTT	250
CCACGAGCAG	AAATCGACGG	CGAAATGGGT	GACTCACATG	TCGGGTTACA	300
AGCACGTTTG	ATGTCTCAAG	CATTGCGTAA	ACTCTCTGGT	TCGATCAACA	350
35 AAACAAAAAC	AATCGCTATT	TTCATCAACC	AAATCCGT		388

2) INFORMATION FOR SEQ ID NO: 1871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871

```

AGAGAGTTCC GGTA AAAACAA CTGTTGCGCT TCATGCAATT GCGGAAGTAC      50
AAGCACAAGG CGGAACAGCA GCATTTATCG ATGCTGAGCA TGC GTTGGAT      100
CCGGCTTATG CTA AAAACCT AGGTGTAAAT ATTGATGAAT TATTACTATC      150
TCAACCAGAT ACAGGAGAAC AAGCTTTAGA GATTGCTGAA GCTTTAGTTA      200
5 GAAGTGGTGC AGTTGATATG TTAGTAATTG ACTCCGTTGC AGCACTTGTA      250
CCACGTGCTG AAATCGAAGG CGAGATGGGC GATGCTCATG TTGGATTACA      300
AGCACGTTTA ATGTCCAAG CATTGCGTAA ACTTTCTGGT GTTATTAATA      350
AATCAAAAAC CATTGCTATT TTCATTAACC AAATTCGT      388

```

10

2) INFORMATION FOR SEQ ID NO: 1872

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872

```

AGAGTCATCT GGTAAGACAA CGGTTGCCCT TCATGCAGTT GCGCAAGCAC      50
AAAAAGAAGG TGGTATTGCT GCCTTTATCG ATGCGGAACA TGCCCTTGAT      100
30 CCAGCTTATG CTGCGGCCCT TGGTGTCAAC ATTGACGAAT TGCTCTTGTC      150
ACAACCAGAC TCAGGAGAGC AAGGTCTTGA GATTGCAGGA AAATTGATTG      200
ACTCAGGAGC CGTGGATCTT GTCGTAGTCG ACTCAGTTGC GGCCCTTGTC      250
CCTCGTGCGG AAATTGATGG AGATATCGGT GATAGCCACG TTGGTTTGCA      300
GGCTCGTATG ATGAGCCAGG CTATGCGTAA ACTTGGTGCT TCTATCAATA      350
35 AAACCAAAAAC AATTGCCATC TTTATCAACC AATTGCGT      388

```

2) INFORMATION FOR SEQ ID NO: 1873

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873

	GAACATGACG	CCGACTTTTT	CACGCAATTG	GTTGATAAAG	ATGGCAATTG	50
	TTTTGGTTTT	ATTGATAGAA	GCTCCGAGTT	TACGCATGGC	CTGGCTCATC	100
	ATTCGAGCCT	GCAAACCAAC	GTGACTGTCT	CCAATATCCC	CATCAATTTT	150
5	CGCACGAGGT	ACAAGGGCCG	CAACTGAGTC	GATAACGACA	AGGTCAACTG	200
	CACCTGAGTC	AATCAATTTT	CCAGCAATTT	CAAGACCTTG	TTCACCTGAG	250
	TCTGGTTGTG	ACAAGAGCAA	TTCGTCAATA	TTCACACCAA	GGGCTGCAGC	300
	ATAGGCTGGG	TCAAGAGCAT	GTTCCGCATC	GATAAAGGCT	GCAATACCAC	350
	CTTCTTTCTG	TGCTTGCGCA	ACAGCGTGAA	GGGCAACCGT	TGTCTTACCA	400
10	GATGATTCTG	GCGCRTACAY	TTCGATGATA			430

2) INFORMATION FOR SEQ ID NO: 1874

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874

30	TTGTCGTTGT	TGCTGCCTCC	GACGGTCAGA	TGTAGGTGGA	ACATCTTGGG	50
	AAATACGTCG	TAAAACACGT	CGCTTACGTT	TTCGCGAATA	GGCCCCAGAC	100
	TCGTGAGCAT	TTGCTGCTCG	CCCGCCAGGT	TGGTGTCCAG	AAGATCGTTG	150
	TCTTCGTCAA	CAAAATCGAT	GCTATTGATG	ATCCGGAGAT	GCTGGAAGT	200
	GTCGAACTCG	AGATGCGTGA	GCTGCTGAAC	AGCTACGGTT	TCGAGGGTGA	250
35	AGAGACTCCG	ATCATTTTCG	GTTCCGCTCT	CTGTGCTCTC	GAAGGACGCC	300
	GTGACGACAT	CGGTAAAGAC	AGAATTGAGC	AGCTTATGAA	CGCTGTCGAC	350
	ACCTGGATCC	CCACTCCTCA	GCGTGACCTC	GACAAACCTT	TCTTGATGTC	400
	TGTCGAGGAA	GTGTTCTCTA	TCGCCGGCCG	TGGTACCGTG	GCTTCTGGTC	450
	GTGTCGAGCG	TGGTATCTTG	AAGAAGGACT	CTGAGGTGTA	GATTGTTGGA	500
40	GGCTCCTTCG	AACCCAAGAA	GACCAAAGTC	ACCGACATTG	AAACCTTCAA	550
	GAAGAGCTGT	GATGAATCGC	GTGCTGGTGA	CAACTCTGGT	CTCCTCCTGC	600
	GTGGTATCCG	ACGTGAAGAC	GTCAAGCGTG	GTATGGTCAT	TGCTGTTCCC	650
	GGCAGCACCA	AGGCTCACGA	CAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	700
	CGAGGCGGAG	GGTGGTCGTC	GTAAGGCTT	CGGTGCCAAC	TACCGTCCCC	750
45	AAGTCTTCAT	CCGTACTGCA	GGTAAGTTCC	CGCACACCGT	GTCCAGATCT	800
	TCCGAGAGAT	TAGCGATATA	TGCTAATGAT	TCATCAGACG	AGGCTGCTGA	850
	CCTCAGCTTC	CCTGACGGCG	ACCAATCTCG	CAGAGTTATG	CCTGGTGACA	900
	ACGTCGAGAT	GATCCTGAAG	ACCCACCACC	CTGTTGCTGC	TGAGGCT	947

50

2) INFORMATION FOR SEQ ID NO: 1875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875

```

15  GCTGCTTCCG ATGGTCAAAT GTACGTCAAC CTTATATACA CCCTCTGATA      50
    TGACAGAATG TCGCCTAACA GCACGCGTGA ACTAGGCCCC AAACCCGTGA      100
    GCACTTGCTG CTTGCCCCGCC AGGTCGGTGT CCAGAAGATT GTTGTGTTCTG      150
    TCAACAAGGT TGATGCCGTC GATGACCCTG AGATGTTGGA ACTTGTGTTGAG      200
    CTGGAAATGC GTGAGCTTCT CAGCACTTAC GGCTTCGAAG GCGAGGAGAC      250
20  CCCTATCATC TTCGGTTCCG CCCTATGCGC CCTCGAGGGT CGCCGCCCCG      300
    ATATCGGTAC TGAGCGAATT GACAGCCTTC TTGAGGCCGT TGACACCTGG      350
    ATCCCTACCC CTCAGCGTGA CCTGGACAAG CCTTTCCTGA TGTCTGTCGA      400
    GGAGGTCTTC TCCATTGCCG GTCGTGGTAC CGTTGCCTCT GGCCGTGTTG      450
    AGCGTGGTCT CCTTAAGAAG GACAGCGAGG TCGAGATTCT CGGAGGTGGT      500
25  CAGGTCATGA AGACCAAGGT CACTGACATT GAGACATTCA AGAAGCACTG      550
    TGACGAATCC CGTGCTGGTG ACAACTCCGG TCTTCTTCTC CGTGGTATCC      600
    GCCGTGAGGA TGTCAAGCGC GGTATGGTTA TTGCTGCTCC CGCCTCTATC      650
    AAGGCCCACA AGAAGTTCAT GGTCTCCATG TACGTCCTCA CTGAGGCAGA      700
    AGGTGGCCGT CGCAGTGGCT TCGGTGTCAA CTATCGTCCC CAGGCTTACA      750
30  TTCGCACTGC TGGTAAGTTT TCAAAACATT CGACCTCTCG CCTTAGAAGA      800
    AGAATACCTC TAACTTGAT TTAGACGAGG CTTGCGACCT TTCTTTCCCC      850
    GATGGCGACA TGAGCCGCCG TGTCATGCCT GGTGACAACG TGGAATGAT      900
    CCTCAACCTC AACAACCCTG TCG                                923

```

2) INFORMATION FOR SEQ ID NO: 1876

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876

```

CATCATTGTT GTGTCCGCCA CTGATGGTCA AATGCCTCAA ACTCGTGAGC      50

```

	ATTTGTTGTT	GGCTCGCCAA	GTTGGTGTCC	AACACTTGGT	TGTCTTCATC	100
	AACAAGGTTG	ATGCCGTTGA	TGATCCTGAA	ATGTTGGAGT	TGGTCGAGAT	150
	GGAAATGCGT	GATTTGCTTT	CCCAATACGG	TTTCCCCGGA	GACAACGTCC	200
	CCATTATCCA	GGGTTCGCT	CTCTGCGCTC	TTGAGGACCG	CAACCCCGAG	250
5	ATCGGCCGTA	ACGCCATCAT	GAAGTTGATG	GAGGCTGTTG	ATAGCAGCAT	300
	CCCCACCCCT	GCCCGTGATT	TGGACAAACC	TTTCCTCATG	CCCGTTGAAG	350
	ATGTGTTCTC	CATCTCTGGC	CGTGGTACTG	TTGCCACTGG	ACGTGTTGAG	400
	CGTGGTATGG	TCACCAAGGG	TACTGAAGTT	GAAATCGTCG	GTATGGGCGA	450
	GCACTTCAAG	ACCACCTTGA	CCGGTATTGA	AATGTTCCAC	AAGGAATTGG	500
10	ACAAGGGTAT	GGCTGGTGAC	AACATGGGTT	GCTTGCTTCG	TGGTGTCAAG	550
	CGTGAGCAAG	TCCGTCTGGG	TATGGTTATC	TGTGCCCCCG	GATCCGTCAG	600
	GCCACATAAG	AAGTTCATGG	CTCAGCTCTA	CATTCTCACC	AAGGATGAGG	650
	GAGGCCGCCA	CACTCCCTTC	GTCAACAACT	ACCGCCCACA	AATGTTCTTC	700
	AGAACTGTTG	ATGTTACCGC	CATCCTTAAG	CACCCCCCTG	GTACCCCCGA	750
15	TGCTGATGAG	AAGATGGTCA	TGCCCGGAGA	CAACGTTCAA	CTCGAGTGCG	800
	AGCTCTT					807

20 2) INFORMATION FOR SEQ ID NO: 1877

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter gracilis*
 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877

35	AGTTGTTTCT	GCTGCGGATG	GTCCTATGCC	TCAAACCTCGC	GAGCATATCT	50
	TGCTTCTCTG	TCAAGTAGGC	GTTCCATACA	TCGTAGTTTT	CCTAAACAAA	100
	ACCGATATGG	TCGATGATCC	GGATCTTTTA	GAGTTAGTTG	AAGAGGAAGT	150
	TAGAGATCTT	TTAAAAGAGT	ATAAATTCCC	TGGCGACGAA	ACCCCAATCA	200
10	TTAAGGGTTC	TGCTCTTAAG	GCTCTTGAGG	AAGCTAAGGC	CGGACAAGAC	250
	GGCGAATGGT	CTGCAAAGAT	TATGGAGCTT	ATGGACGCGG	TTGATAGCTA	300
	TATTCCAAC	CCTGTTTCGCG	ATACTGATAA	AGATTTCTCT	CTTCCGATCG	350
	AAGATATTTT	CTCGATTTCC	GGTCGCGGTA	CCGTTGTAAC	CGGTAGAATC	400
	GAAAAAGGTA	TCGTAAAGT	TGGTGATACT	ATCGAGATCG	TAGGTATTAA	450
15	ACCTACTCAG	ACTACTACCG	TCACTGGCGT	TGAGATGTTT	AGAAAAGAGA	500
	TGGATCAAGG	TGAAGCCGCG	GATAATGTAG	GTGTTTTATT	GCGCGGTACT	550
	AAGAAAGAGG	AAGTAGAGCG	CGGTATGGTT	TTATGCAAAC	CAAAATCGAT	600
	CACTCCTCAT	ACTAAATTTG	AGGGCGAGGT	TTATATCCTA	ACTAAAGAAG	650
	AAGGCGGACG	CCATACTCCA	TTCTTTAATA	ATTATAGACC	GCAGTTTTAC	700
30	GTTCGTACGA	CAGATGTTAC	CGGTTTCGATT	ACTCTTCCTG	AAGGAACCGA	750
	GATGGTTATG	CCGGGCGACA	ACGTTAAAT	CACCGTTGAG	CTAATCGCTC	800
	CGATCG					806

2) INFORMATION FOR SEQ ID NO: 1878

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878

```

GCTGCAGATG GCCCTATGCC ACAAAC TAGA GAGCACATTC TTCTTTCTCG      50
TCAAGTAGGC GTTCCATATA TTGTTGTTTT TATGAATAAA GCAGATATGG      100
TTGATGATGC TGAACTTTTA GAGTTAGTTG AAATGGAAAT TAGAGAATTA      150
TTAAGCTCTT ATGATTTCCC AGGCGATGAT ACACCTATTA TTTCTGGTTC      200
TGCTTTAAAA GCTCTTGAAG AAGCTAAAGC TGGACAAGAT GGTGAATGGT      250
CAGCAAAAAT TATGGATCTT ATGGCTGCAG TTGATAGCTA TATTCCAAC      300
CCAACTCGTG AACTGAAAA AGACTTCTTG ATGCCAATTG AAGATGTTTT      350
CTCAATTTCA GGTCGTGGTA CTGTTGTAC AGGTAGAATT GAAAAAGGTG      400
TTGTAAAAGT AGGTGATACT ATCGAAATCG TTGGTATTAA AGATACTCAA      450
ACAACAAC TGTAACAGGTGT TGAAATGTTC AGAAAAGAAA TGGATCAAGG      500
CGAAGCAGGA GATAACGTAG GTGTTCTTCT TCGTGGTACT AAAAAAGAAG      550
AAGTTATCCG TGGTATGGTT CTTGCTAAAC CAAAATCAAT TACTCCACAC      600
ACTGACTTCG AAGCTGAAGT TTATATCTTA AATAAAGATG AAGGTGGTAG      650
ACATACTCCA TTCTTTAACA ACTATAGACC ACAGTTTTAT GTAAGAACAA      700
CTGATGTTAC AGGTTTCGATT AAATTAGCTG ATGGTGTTGA AATGGTTATG      750
CCAGGTGAAA ATGTGAGAAT TACTGTAAGC TTGATCGCTC CAGTAGCACT      800
TGAAGA                                         806

```

2) INFORMATION FOR SEQ ID NO: 1879

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879

```

ATGTATGCAA CCGAGAGCAC TCCCGGATCT TGGTTTAAAT GGCAC TAATA      50

```

	TAAGACAGGC	CTCAAAC TCG	AGAGCATTTA	CTTCTCGCCC	GTCAGATCGG	100
	TATCCAAAAA	ATCGTCGTCT	TCGTGAACAA	GGTTGATGCC	ATCGAGGACA	150
	AAGAGATGTT	GGAGCTTGTT	GAATTGGAGA	TGCGTGAAC T	CCTAACCAGC	200
	TACGGTTTCS	AGGGTGAAGA	AACTCCCATC	ATTTTTGGCT	CTGCTCTCTG	250
5	TGCCCTCSAA	GGAAGACAAC	CCGAGATCGG	TGTTACCAAG	ATTGATGAGC	300
	TCTTGCAGGC	CGTCGACACC	TGGATTCCCA	CTCCTCAGCG	TGAGACTGAC	350
	AAGCCCTTCT	TGATGTCCAT	TGAGGAAGTG	TTCTCTATTT	CCGGACGAGG	400
	AACCGTTGTC	TCCGGCCGTG	TGGAGCGTGG	TATCCTCAAG	AAGGACTCCG	450
	AAGTTGAAAT	TGTCGGCGGT	TCGCCCAGAG	CAATCAAAAC	CAAGGTTACC	500
10	GATATCGAAA	CCTTTAAGAA	GTCTTGCGAC	GAGTCTCGCG	CTGGTGATAA	550
	CTCCGGCTTG	CTCCTACGAG	GCGTTAAGCG	TGAAGATATT	AGCCGTGGCA	600
	TGGTCGTCGC	TGTACCAGGA	AGTGTC AAGG	CCCATACTGA	ATTCTTAGTT	650
	TCGCTTTACG	TCCTCACC GA	AGCTGAGGGT	GGGCGCAAAT	CTGGATT CAG	700
	CAGCAAGTAC	CGCCCACAGA	TGTTCA TT CG	CACTGCCGGT	ATGTAATACT	750
15	GTGATAATTT	CGTTGACATG	GTA CTGATTG	AATTCTATAG	ACGAAGCGGC	800
	TCAGCTCAGC	TGGCCCGGAG	AAGATCAAGA	CAAGATGGCT	ATGCCAGGAG	850
	ACAATATCGA	AATGATT TGC	ACCACCTTGC	ACCCAGTTGC	CGCCGA	896

20

2) INFORMATION FOR SEQ ID NO: 1880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880

	CTGGTAGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACYC	GTGAGCACAT	50
	CCTGCTGGGT	CGCCAGGTTG	GCGTGCCATA	CATCATCGTG	TTCTTGAACA	100
	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAGCTGGT	TGAAATGGAA	150
10	GTMCGTGACC	TGCTGTCACA	GTACGACTTC	CCAGGCGACG	ACACGCCAAT	200
	CGTGCRYGGT	TCTGCGCTGA	AAGCGCTGGA	RGGCGAAGCA	GAGTGGGAAG	250
	CGAAGATCAT	CGAACTGGCT	GGCCATCTGG	ATAACTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAACC	GTTCTTGCTG	CCAATTGAAG	ACGTGTTCTC	350
	CATCTCTGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	CGCGGTRTSG	400
15	TTAAAGTGGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	TACCGTGAAA	450
	TCAACCTGTA	CCGGCGTTGA	GATGTTCCGT	AAGCTGCTGG	ACGAAGGCCG	500
	TGCGGGTGAG	AACTGTGGTA	TCCTGCTGCG	CGGTATCAAG	CGCGAAGATA	550
	TCCAGCGTGG	TCAGGT TCTG	GCGAAGCCAG	GCACCATCAA	GCCACACACC	600
	AAGTTCGAGT	CAGAAGTTTA	TATTCTGTCT	AAAGACGAAG	GCGGCCGTCA	650
30	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACCGG	GACTATCGAA	CTGCCAGAAG	GCGTTGAGAT	GGTGATGCCA	750
	GGCGACAACA	TTCAGATGGT	TGTGACCCTG	ATCCACCCGA	TCGCCATG	798

2) INFORMATION FOR SEQ ID NO: 1881

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhimurium
(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881

```
ATCCTGGTTG TTGCTGCGAC TGACGGYCCG ATGCCGCAGA CCCGTGAGCA      50
CATCCTGCTG GTCGTCAGG TAGGCGTTCC GTACATCATC GTGTTTCCTGA     100
ACAAATGCGA CATGGTTGAT GACGAAGAGC TGCTGGAAC TTTGAAATG      150
GAAGTTCGYG AACTGCTGTC TCAGTACGAC TTCCCGGGCG ACGACACTCC     200
GATCGTTCGT GGTTCCTGCTC TGAAAGCGCT GGAAGGCGAC GCAGAGTGGG     250
AAGCGAAAAT CATCGAACTG GCTGGCTTCC TGGATTCTTA CATYCCGGAA     300
CCAGAGCGTG CGATTGACAA GCCGTTTCCTG CTGCCGATCG AAGACGTATT     350
CTCCATCTCC GTCGTTGGTA CCGTTGTAC CGGTCGTGTA GARCGCGGTA     400
TCATCAAAGT GGGCGAAGAA GTTGAAATCG TTGGTATCAA AGAGACTCAG     450
AAGTCTACCT GTACTGGCGT TGAAATGTTT CGCAAACATG TGGACGAAGG     500
CCGTGCCGGT GAGAACGTAG GTGTTCTGCT GCGTGGTATC AAACGTGAAG     550
AAATCGAACG TGGTCAGGTA CTGGCTAAGC CGGGCACCAT CAAGCCGCAC     600
ACCAAGTTCG AATCTGAAGT GTACATTCTG TCCAAAGATG AAGGCGGCCG     650
TCATACTCCG TTCTTCAAAG GCTACCGTCC GCAGTTCTAC TTCCGTACTA     700
CTGACGTGAC TGGCACCATC GAACTGCCGG AAGGCGTAGA GATGGTAATG     750
CCGGGCGACA ACATCAAAT GGTGTGTTACC CTGATCCACC CGATCGCGAT     800
GGACGACGGT                                     810
```

2) INFORMATION FOR SEQ ID NO: 1882

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
(B) STRAIN: BM10711
(C) ACCESSION NUMBER : AF015628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882

	ATGAATTTTT	ATTAGAGGA	GTTTAACTTG	TCTATTCCCG	ATTCAGGTCC	50
	ATACGGTATA	ACTTCATCAG	AAGACGGAAA	GGTATGGTTC	ACACAACATA	100
	AGGCAAACAA	AATCAGCAGT	CTAGATCAGA	GTGGTAGGAT	AAAAGAATTC	150
5	GAAGTTCCTA	CCCCTGATGC	TAAAGTGATG	TGTTTAATTG	TATCTTCACT	200
	TGGAGACATA	TGGTTTACAG	AGAATGGTGC	AAATAAAATC	GGAAAGCTCT	250
	CAAAAAAAGG	TGGCTTTACA	GAATATCCAT	TGCCACAGCC	GGATTCTGGT	300
	CCTTACGGAA	TAACGGAAGG	TCTAAATGGC	GATATATGGT	TTACCCAATT	350
	GAATGGAGAT	CGTATAGGAA	AGTTGACAGC	TGATGGGACT	ATTTATGAAT	400
10	ATGATTTGCC	AAATAAGGGA	TCTTATCCTG	CTTTTATTAC	TTTAGGTTCG	450
	GATAACGCAC	TTTGGTTTAC	GGAGAACCAA	AATAATTCTA	TTGGAAGGAT	500
	TACAAATACA	GGGAAATTAG	AAGAATATCC	TCTACCAACA	AATGCAGCGG	550
	CTCCAGTGGG	TATCACTAGT	GGTAACGATG	GTGCACTCTG	GTTTGTCTGAA	600
	ATTATGGGCA	ACAAAATAGG	TCGAATCACT	ACAATGGTG	AGATTAGCGA	650
15	ATATGATATT	CCAACTCCAA	ACGCACGTCC	ACACGCTATA	ACCGCGGGGA	700
	AAAATAGCGA	AATATGGTTT	ACTGAATGGG	GGGCAAATCA	AATCGGCAGA	750
	ATTACAAACG	ACAAAACAAT	TCAAGAATAT	CAACTTCAA	CAGAAAATGC	800
	GGAACCTCAT	GGTATTACCT	TTGGAAAAGA	TGGATCCGTA	TGGTTTGCAT	850
	TAAAATGTAA	AATTGGGAAG	CTGAATTTGA	ACGAATGA		888

20

2) INFORMATION FOR SEQ ID NO: 1883

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883

35 AGCCGCTTGA GCAAATTAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1884

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884

50

GTATCCCGCA GATAAATCAC CAC

23

2) INFORMATION FOR SEQ ID NO: 1885

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885

AGCGAAAAAC ACCTTGCCGA C

21

2) INFORMATION FOR SEQ ID NO: 1886

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886

GACGCCCGCG CCACCACT

18

2) INFORMATION FOR SEQ ID NO: 1887

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887

GACGCCCGCG ACACCACTA

19

2) INFORMATION FOR SEQ ID NO: 1888

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888

GACGCCCCGCA ACACCACTA

19

10

2) INFORMATION FOR SEQ ID NO: 1889

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889

GTTCGCAACT GCAGCTGCTG

20

25

2) INFORMATION FOR SEQ ID NO: 1890

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890

40

TTCGCAACGG CAGCTGCTG

19

2) INFORMATION FOR SEQ ID NO: 1891

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891

CCGGAGCTGC CGAICGGG

18

5

2) INFORMATION FOR SEQ ID NO: 1892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892

CGGAGCTGCC AARCGGGG

18

20

2) INFORMATION FOR SEQ ID NO: 1893

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893

35 GGAGCTGGCG ARCGGGGT

18

2) INFORMATION FOR SEQ ID NO: 1894

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894

50

GACCGGAGCT AGCGARCG

18

2) INFORMATION FOR SEQ ID NO: 1895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895

CGGAGCTAGC AARCGGGGT

19

2) INFORMATION FOR SEQ ID NO: 1896

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896

GAAACGGAAC TGAATGAGGC G

21

2) INFORMATION FOR SEQ ID NO: 1897

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897

CATTACCATG GGCGATAACA G

21

2) INFORMATION FOR SEQ ID NO: 1898

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898

CCATTACCAT GAGCGATAAC AG

22

10

2) INFORMATION FOR SEQ ID NO: 1899

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: 15571
- (C) ACCESSION NUMBER: AF124984

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899

30	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
35	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
40	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTGCGAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGCGCG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
45	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
	GGCAACGCTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: SLK-47
- (C) ACCESSION NUMBER: Y11069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900

```

15 CTGTTAGCCA CCCTGCCGCT GGCGGTACAC GCCAGCCCGC AGCCGCTTGA      50
   GCAAATTAAA CTAAGCGAAA GCCAGCTGTC GGGCCGCGTA GGCATGATAG      100
   AAATGGATCT GGCCAGCGGC CGCACGCTGA CCGCCTGGCG CGCCGATGAA      150
   CGCTTTCCCA TGATGAGCAC CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT      200
   GGCGCGGGTG GATGCCGGTG ACGAACAGCT GGAGCGAAAG ATCCACTATC      250
20 GCCAGCAGGA TCTGGTGGAC TACTCGCCGG TCAGCGAAAA ACACCTTGCC      300
   GACGGCATGA CGGTCGGCGA ACTCTGCGCC GCCGCCATTA CCATGAGCGA      350
   TAACAGCGCC GCCAATCTGC TACTGGCCAC CGTCGGCGGC CCCGCAGGAT      400
   TGACTGCCTT TTTGCGCCAG ATCGGCGACA ACGTCACCCG CCTTGACCGC      450
   TGGGAAACGG AACTGAATGA GGCGCTTCCC GGCGACGCCG GCGCCACCAC      500
25 TACCCCGGCC AGCATGGCCG CGACCCTGCG CAAGCTGCTG ACCAGCCAGC      550
   GTCTGAGCGC CCGTTCGCAA CGGCAGCTGC TGCAGTGGAT GGTGGACGAT      600
   CGGGTCGCCG GACCGTTGAT CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT      650
   CGCCGATAAG ACCGGAGCTG GCGAGCGGGG TGCGC GCGGG ATTGTCGCCC      700
   TGCTTGGCCC GAATAACAAA GCAGAGCGCA TTGTGGTGAT TTATCTGCGG      750
30 GATACCCCGG CGAGCATGGC CGAGCGAAAT      780

```

2) INFORMATION FOR SEQ ID NO: 1901

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: U92041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901

```

50 ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT      50
   GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA      100
   GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC      150
   CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC      200

```

	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
5	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCCC	GCAACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTTCGCA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
10	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1902

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 861 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: 803

(C) ACCESSION NUMBER: AF164577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902

35	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CAAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
40	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TGCTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
45	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTTCGCA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	CCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
50	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 700603
 (C) ACCESSION NUMBER: AF132290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903

	ATGCGTTATT	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
20	GCCAGCTGTC	GGGCAGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
25	ACTCTGTGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TGCTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTGCGAA	600
30	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	CCAAACGGGG	TGCGCGCGGG	ATTGTGCGCC	TGCTTGGCC	GAATAACAAA	750
	GCAGAGCGGA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
35	GGCAACGCTA	ACCCGGCGGT	GGCCGCGCGC	GTTATCCGGC	TCGTAG	896

2) INFORMATION FOR SEQ ID NO: 1904

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: JC2926
 (C) ACCESSION NUMBER: AF148851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904

	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
5	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
10	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTTCGAA	600
15	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCC	TGCTTGGCC	GAATAACAAA	750
	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
20	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1905

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (C) ACCESSION NUMBER: AF096930

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905

40	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
45	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTAC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
50	GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTTCGAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700

GCAAACGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
GGCAACGCTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1906

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906

20 CCTTATTCCC TTTTGTGCGG

20

2) INFORMATION FOR SEQ ID NO: 1907

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907

35

CACCTATCTC AGCGATCTGT CT

22

40 2) INFORMATION FOR SEQ ID NO: 1908

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908

50

AACAGCGGTA AGATCCTTGA GAG

23

2) INFORMATION FOR SEQ ID NO: 1909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909

ATGACTTGGT TAAGTACTCA CC

22

2) INFORMATION FOR SEQ ID NO: 1910

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910

ATGACTTGGT TGAGTACTCA CC

22

2) INFORMATION FOR SEQ ID NO: 1911

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911

CCATAACCAT GGGTGATAAC AC

22

2) INFORMATION FOR SEQ ID NO: 1912

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid

1000

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

2) INFORMATION FOR SEQ ID NO: 1913

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGGAACC

20

2) INFORMATION FOR SEQ ID NO: 1914

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

CGCCTTGATC GTTGGGAACC

20

2) INFORMATION FOR SEQ ID NO: 1915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

CGTGGGTCTG GCGGTATCAT

20

35

2) INFORMATION FOR SEQ ID NO: 1918

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

GTGGGTCTCA CCGTATCATT G

21

50

2) INFORMATION FOR SEQ ID NO: 1919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1920

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

2) INFORMATION FOR SEQ ID NO: 1921

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

CGTGGGTCTA GCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1922

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTTCCAAT GATTAGCACT TTTA

24

2) INFORMATION FOR SEQ ID NO: 1923

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTTCCAAT GATAAGCACT TTTA

24

2) INFORMATION FOR SEQ ID NO: 1924

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

GTTTTCCAAT GCTGAGCACT TTT

23

2) INFORMATION FOR SEQ ID NO: 1925

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: MC9690-129
 (C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

40	ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCTTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT	200
	GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG	250
45	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG	450
	CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	500
50	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT	600
	TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	700

GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1928

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: HB251
- (C) ACCESSION NUMBER: X57972

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

25	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
30	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTAAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCATTGGG	AACCGGAGCT	500
35	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
40	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

45

2) INFORMATION FOR SEQ ID NO: 1929

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: 26W
 (C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

```

10 ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAGCT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
   GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
15 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
   ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
   CACAACATGG GGGATCATGT AACCCGCCTT GATAGTTGGG AACCGGAGCT      500
20 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
   TGGCAACAAC GTTGCGCAA CTATTAAGT GCGAACTACT TACTCTAGCT      600
   TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
   ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
   GAGCCGGTAA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
25 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
   TATGGATG                                     808
  
```

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

```

45 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
50 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG      250
   CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
  
```

	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
5	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	GGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
10	AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 1931

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: BM2728
 (C) ACCESSION NUMBER: AF104442

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30

	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
35	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
40	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
45	GAGCCGGTGA	GCGTGGGTCT	CTCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932

```

15  ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
    TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
    CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
    AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGCT      200
    GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
20  CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
    GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
    AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
    ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
    CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
25  GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
    TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT      600
    TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
    ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
    GAGCCGGTGA GCGTGGGTCT AGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
30  GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
    TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
    AGCATTGGTA A                                     861
  
```

2) INFORMATION FOR SEQ ID NO: 1933

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
  
```

	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGT	ACATCGAGCT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGGT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGTGC	GGTATTATCC	CGTGTTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
5	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACCCGCCTT	GATCGTCGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
10	TGGCAACAAC	GTTGCGCAAA	CTATTAACTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
15	TATGGATGAA	CGAGATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

20 2) INFORMATION FOR SEQ ID NO: 1934

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35

2) INFORMATION FOR SEQ ID NO: 1935

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- 40 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936

TACCACCCGC ACGGC

2) INFORMATION FOR SEQ ID NO: 1937

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937

CGGAGTCGCC GTCGATG

2) INFORMATION FOR SEQ ID NO: 1938

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938

CCGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G

2) INFORMATION FOR SEQ ID NO: 1939

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5 CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCGGCC GGGTCG 46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT 19

25 2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT 18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942

GACTGGAACA AAGCCTATAA AAAATCA

27

5 2) INFORMATION FOR SEQ ID NO: 1943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20

2) INFORMATION FOR SEQ ID NO: 1944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

2) INFORMATION FOR SEQ ID NO: 1945

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

2) INFORMATION FOR SEQ ID NO: 1946

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946

CGGCGACTTC GCGGTAT

2) INFORMATION FOR SEQ ID NO: 1947

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947

CGGTATACGG CACCATCGT

2) INFORMATION FOR SEQ ID NO: 1948

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948

GCGGTATACA ACACCATCG

2) INFORMATION FOR SEQ ID NO: 1949

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

10

2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 15 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 17 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

CCTGCTATGG AGCGATGGT

19

5

2) INFORMATION FOR SEQ ID NO: 1953

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

2) INFORMATION FOR SEQ ID NO: 1954

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 589 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 13883
- (C) ACCESSION NUMBER: AF052258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

ACACCGGTCA	ACATTGAGGA	AGAGCTTAAG	AACTCTTATC	TGGATTATGC	50
GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	GGATGTCCGA	GATGGCCTGA	100
AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	TGAACGTATT	GGGCAATGAC	150
TGGAACAAAG	CCTATAAAAA	ATCAGCCCGT	GTCGTTGGTG	ACGTAATCGG	200
TAAATACCAC	CCGCACGGCG	ACTCCGCGGT	ATACGACACC	ATCGTGCGTA	250
TGGCGCAGCC	GTTCTCGCTG	CGTTACATGC	TGGTGGACGG	CCAGGGTAAC	300
TTTGGTTCCA	TCGACGGCGA	CTCCGCCGCG	GCGATGCGTT	ATACCGAAAT	350
TCGTCTGGCG	AAAATCGCTC	ATGAGCTGAT	GGCCGATCTT	GAAAAAGAGA	400
CGGTTCGATTT	CGTCGACAAC	TATGACGGTA	CGGAGCGTAT	TCCGGACGTC	450
ATGCCGACCA	AAATTCCTAA	CCTGCTGGTG	AACGGCGCCT	CCGGGATCGC	500
CGTAGGGATG	GCCACCAACA	TACCGCCACA	TAACCTGACG	GAAGTGATTA	550
ACGGCTGTCT	GGCGTATGTT	GACGATGAAG	ACATCAGCA		589

2) INFORMATION FOR SEQ ID NO: 1955

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG TCTGCGCG

38

2) INFORMATION FOR SEQ ID NO: 1956

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

CGGTAAAACC	ACTTTAACTG	CTGCAATCAC	CAAAGTTT	TCTGAAGAAG	50
GTGGTGCAGA	TTTCTTAGAT	TATTCATCTA	TTGATAAAGC	ACCAGAAGAG	100
AGAGCTAGAG	GTATTACCAT	TTCTACTGCT	CATGTTGAAT	ATGAAACTCC	150
AAACAGACAT	TATTCACATG	TTGATTGTCC	AGGTCATCAA	GATTATATTA	200
AGAACATGAT	TACTGGTGCA	GCTCAAATGG	ATGGTGCTAT	TATTGTTGTT	250
GCAGCTACTG	ATGGTCAAAT	GCCACAAACT	AAGGAACATT	TATTATTAGC	300
TAGACAAGTT	GGTGTTCAAC	ATTTAGTTGT	TTTTGTTAAC	AAGTGTGATA	350
CCGTTGATGA	TCCAGAAATG	TTRGAATTAG	TTGAAATGGA	AATGAGAGAA	400
TTATTGACCG	AATATGGATT	YGATGGTGAT	AACACACCAG	TTATTATGGG	450
TTCTGCATTA	ATGGCATTAG	AAGGTAAGAG	ACCAGAAGTT	GGTAAAGAAT	500
CTATTGTTAA	GTTAATGGAA	GCTGTTGATA	CTTGGATTCC	AACTCCACAA	550
AGAGACTTAG	AAAAACCAT	CTTATTACCA	ATTGATGAAG	TTTTCTCTAT	600
TTCTGGTAGA	GGTACTGTTG	TTTCTGGTAC	TGTTGATAGA	GGTACATTAA	650
AGAAGGGTGA	AGAAGTTGAA	ATTGTTGGTG	GTAAAGAAGG	TGTTATTAAG	700
ACTACTGTTA	CCGGTATTGA	AATGTATCAC	AAGGAATTAG	ATCAAGCACA	750
AGCTGGTGAT	ACTCCAGGTA	TTTTGTTAAG	AGGTGTTAAG	AGAGATCAAA	800
TTGCAAGAGG	TCAAATTCTT	GCAAAGCCAG	GWTCTGTTAA	GGCATAACAAG	850
AAGTTCTTAT	CATCATTATA	CATTTTAACA	AAGGAAGAAG	GTGGTAGACA	900
TACTCCATTT	TCTGAAAATT	ACAGACCTCA	AATGTACATT	AGAACTTCCA	950
ATGTTAATGT	TACTTTGAAG	TTCCCAGAAA	CTGAAGAAG		989

2) INFORMATION FOR SEQ ID NO: 1957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: ATCC 22023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

GGTAAGACCA	CCCTTACTGC	CGCCATCACC	AAGTGCCTTG	CTGAGAAGGG	50
AGGTGCCTCG	TTCTTGGA	CTTGGACT	ACAGTGCCAT	CGACAAGGCG	100
GAGCAAGAGG	TATCACCATC	TCCACTGCGC	ACGTTGAGTA	TGAAACTGCC	150
AACAGACACT	ACTCGCACGT	TGACTGTCCA	GGTCACGCTG	ATTACATCAA	200
GAACATGATT	ACCGGTGCTG	CGCAGATGGA	CGGTGCTATC	ATTGTTCGTTG	250
CAGCCACTGA	CGGTCAGATG	CCACAGACCA	GAGAACACTT	GTTGCTTGCC	300
AGACAAGTTG	GTGTCCAGCA	CATTGTTGTC	TTCGTCAACA	AGGTTGACAC	350
CATCGACGAC	CCTGAGATGC	TTGAGCTTGT	TGAAATGGAG	ATGAGAGAGT	400
TGCTTACTTC	GTATGGATTT	GACGGTGATA	ACACCCAGT	TATCATGGGT	450
TCTGCTTTGT	GTGCTTTGGA	AGGCCGTGAG	CCAGAGATTG	GTGCTAAGGC	500
CATTGACAAG	TTGATGGAGG	CCATTGATGA	GTACATCCCA	ACTCCTCAGA	550
GAGACCTGGA	AAAGCCATTC	YTGATGGGTG	TTGAAGACGT	GTTCTCGATC	600
TCTGGTAGAG	GTACCGTTGT	CACRGGCCGT	GTTGAGCGTG	GTAACCTTGAA	650
GAAAGGTGAT	GAAATTGAAC	TTGTTGGCTA	CAACAAGAAC	CCAATCAAGA	700
CCACCGTCAC	CGGTATCGAA	ATGTTCAAGA	AGGAGTTGGA	ATCTGCCATG	750
GCTGGTGACA	ACTGTGGTAT	CTTGTTGCGT	GGTATCAAGA	GAGATGACGT	800
CAAGAGAGGT	ATGGTTGCTG	CTAAGCCAGG	CTCCGTCTCT	GCACACACCA	850
AGTTCCTCGC	TTCTTGTAC	ATCCTGACRA	AGGAGGAAGG	TGGTCGTCAC	900
AGTGCCTTTG	CTGAGAACTA	CAGACCACAG	ATGTTTCATCA	GAACCGGAGA	950
TGTCACCACC	ATCTTGACAT	GGCCAGAGGA	GCACGCTGAC	C	991

2) INFORMATION FOR SEQ ID NO: 1958

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

	CGGTAAGACC	ACTTTGACCG	CCGCCATCAC	CAAGGTGTTG	AGCGCCAAAG	50
	GTGGTGCTTC	CTTCTTGAC	TACGGGTCCA	TCGACAGAGC	CCCTGAGGAG	100
5	AGAGCCAGAG	GTATTACTAT	CTCGACTGCC	CACGTTGAGT	ACGAGACCGA	150
	TAAGAGACAC	TACGCCCACG	TTGATTGCCC	TGGTCACGCT	GATTACATCA	200
	AGAACATGAT	CACTGGTGCC	GCCCAAATGG	ACGGTGCCAT	TATTGTCGTT	250
	GCTGCTTCTG	ATGGCCAAAT	GCCGCAGACC	AGAGAGCACT	TGTTGCTTGC	300
	CAGACAGGTT	GGTGTGCAGA	ACTTGGTTGT	GTTTGTTAAC	AAGGTGGACA	350
10	CCATCGACGA	CCCCGAAATG	TTGGAGTTGG	TGGAGATGGA	AATGAGAGAA	400
	TTGTTGACCC	ACTACGGCTT	TGACGGTGAC	AACACCCCTG	TCATCATGGG	450
	TTCGGCGTTG	TGTGCCTTGG	AAGACAGGCA	GCCTGAGATT	GGCGAGCAAG	500
	CCATCATGAA	GTTGTTGGAC	GCTGTCGACG	AGTACATTCC	CACTCCTCAG	550
	AGAGACTTGG	AGCAACCATT	TTTGATGCCC	GTTGAGGATG	TTTTCTCCAT	600
15	CTCTGGCAGA	GGTACTGTTG	TCACCGGTCG	TGTTGAGAGA	GGCTCATTTGA	650
	AGAAGGGTGA	GGAGATTGAG	ATTGTTGGCG	ACTTCCCCAA	GCCCTTCAAG	700
	ACTACCGTCA	CCGGCATTGA	GATGTTCAAG	AAGGAGTTGG	ATGCCGCGAT	750
	GGCGGGCGAC	AACGCCGGGA	TCTTGTTGAG	AGGTGTCAAG	AGAGACGAGG	800
	TCTCGAGAGG	TATGGTTTTG	GCCAAGCCCG	GTACTGTCAC	TTCGCACACC	850
20	AAGGTGTTGG	CGTCGCTTTA	CATCTTGACC	AAAGAGGAAG	GTGGCCGCCA	900
	CTCGCCCTTT	GGTGAGAACT	ACAAGCCACA	GTTATTTCATC	AGAACCTCCG	950
	ATGTCACTGG	TACTTTGAGG	TTCCCCGCCG	GTGAG		985

25

2) INFORMATION FOR SEQ ID NO: 1959

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 973 bases |
| 30 | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- | | | |
|----|-----|-------------------------------------|
| | (A) | ORGANISM: <i>Candida catenulata</i> |
| | (B) | STRAIN: ATCC 10565 |
| 40 | (C) | ACCESSION NUMBER: |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

	CGGTAAGACC	ACCTTGACTG	CCGCCATCAC	CAAGGTTCTC	TCCGAGAAGG	50
	GTGGTGCCGA	CTTCTTGAC	TACGGTGCCA	TTGACAGAGC	CCCCGAGGAG	100
45	CGTGCCCGTG	GTATCACCAT	CTCCACTGCC	CACGTTGAGT	ACGAGACTGA	150
	CAACCGTCAC	TACGCCCACA	TTGACTGTCC	CGGTCACGCT	GATTACATCA	200
	AGAACATGAT	TACCGGTGCC	GCCCAGATGG	ACGGTGCCAT	TATTGTCCTT	250
	GCTGCTACTG	ACGGTGCCAT	GCCCCAGACC	CGCGAGCACT	TGCTTCTCGC	300
	CCGTCAGGTT	GGTATCCAGG	AATTGGTTGT	GTTTGTGAAC	AAGGTTGACA	350
50	CCATCGACGA	CCCCGAGATG	TTGGAGCTCG	TTGAGATGGA	GATCCGCGAG	400
	TTGTTGTCTG	AGTTCGGTTT	TGACGGTGAC	AACACCCCCG	TCATCATGGG	450
	TTCCGCTTTG	TGCGCTTTGG	AGGGCAAGCA	GCCCCGAGATT	GGTGAGCAGG	500
	CTATCACCAA	GTTGATGGCC	GCCGTTGACG	AGCACATCCC	CACCCCCCAG	550

	CGTGA	CTTGG	AGCAG	CCCTTT	CTTGAT	GCCT	GTTGAG	GGTG	TTTTCT	CTAT	600
	CTCTG	GCCGT	GGTACC	GTGG	TGACTG	GGTAA	GGTTG	CCCCG	GGTGT	CCTCA	650
	AGAAG	GGGTGA	GGAGAT	TGAG	ATTGTT	GGCA	ACTTTG	GACAA	GCCCTA	CAAG	700
	GTGACT	GTTA	CTGGT	ATTGA	GATGTT	CAAG	AAGGAG	TTGG	ACCAGG	CCAT	750
5	GGCTG	GGTGAC	AACGCC	GGTA	TCTTGT	TGCG	TGGTGT	CAAG	CGTGAC	GAGG	800
	TGTCTC	GTGG	TATGG	TTTTG	GCCAAG	CCCCG	GCACTG	TTGT	CTCGCA	CAAG	850
	AAGGTT	TTTTG	CTTCG	CTTTA	CATCTT	GACC	CAGGAG	GAGG	GTGGCC	GTAA	900
	GACCGG	CCTTC	GGCTCC	AACT	ACAAGC	CCCCA	GTTGTT	TCTTG	CGCACT	ACCG	950
	ACGTC	ACTGG	TACCCT	CACC	TTC						973

2) INFORMATION FOR SEQ ID NO: 1960

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*
- (B) STRAIN: ATCC 28870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

	AAGACT	TACCT	TGACTG	CTGC	AATCACC	CAAG	GTCTTAG	CTG	ATCAAG	GTGG	50
30	TGCTG	ATTTC	TTAGAT	TATG	CATCTA	TATGA	CAAGGCT	CCT	GAAGAA	AAGAG	100
	CAAGAG	GTAT	TACTAT	CTCT	ACTGCT	CACG	TTGAGT	ATGA	AACCCCA	AAC	150
	AGACAT	TATT	CTCATG	TCGA	TTGTCCT	GGC	CATCAAG	ATT	ATATTA	AAGAA	200
	TATGAT	TACT	GGTGCT	GCAC	AAATGG	ATGG	TGCTATT	TATT	GTTGTT	GCTG	250
	CTACTG	ATGG	TCAAAT	GCCA	CAAAC	TAAGG	AACATTT	TATT	ATTAGC	AAGA	300
35	CAAGTT	GGTG	TTCAAC	ATTT	AGTTGT	CTTT	GTTAATA	AAAT	GTGAC	ACCAT	350
	TGATG	ACCCA	GAAATG	TTGG	AATTAG	TTGA	AATGGAA	ATG	AGAGAA	CTAT	400
	TGTCTG	AATA	TGGT	TTTTG	AT	GGTGA	TAA	CA	CTCC	AGTTAT	450
	GCATTG	ATGG	CTTTAG	AAGA	CAAGAG	ACCT	GAAGTT	GGTA	AGGAAT	CTAT	500
	TTTAA	AGTTA	ATGGA	AGCYG	TTGAC	ACATG	GATTCCA	ACC	CCAGAG	AAGAG	550
40	ATTTAG	AAAA	ACCAT	TTTTT	TTACCT	TATTG	ATGAAG	TTTT	CTCAAT	CTCT	600
	GGTAG	AGGTA	CTGTC	GTTT	TGGT	ACTG	TG	GAAAG	AGGTA	CTTTGA	650
	GGGTG	AAGAA	GTTGA	AATTG	TTGGT	GGTAA	GGATG	GGTTCT	ATTAAA	ACTA	700
	CTGTCA	CAGG	TATTG	AAATG	TATCACA	CAAGG	AATTAG	ACCA	AGCGCA	AAGCA	750
	GGTGAT	ACTC	CAGGT	ATTTT	ATTAAG	AGGT	GTCAAG	AAGAG	ACCAA	ATCAA	800
45	GAGAGG	TCAA	ATTTT	AGCAA	AGCCAG	ATTC	CGTTA	AAGGCA	TACAAG	AAGT	850
	TCTTGG	CCTT	TATAT	C	TTAACCA	CAAGG	AAGAAG	GTGG	TAGACA	TACA	900
	CCATTCT	CTG	AAAAC	TACAG	ACCACA	AAATG	TACATC	AGAA	CTACCA	ATGT	950
	TAACGT	TACT	TTGAAG	TTCC	CAGAC	ACTGA	AGAAG				985

2) INFORMATION FOR SEQ ID NO: 1961

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961

GCTCAAGGCA GATGGCATTC CC

2) INFORMATION FOR SEQ ID NO: 1962

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962

GGACAAGGCG GTTGCGTTTG AT

2) INFORMATION FOR SEQ ID NO: 1963

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963

CATTCCCGTC TCGCTGACA GT

2) INFORMATION FOR SEQ ID NO: 1964

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5 ATCTGCCTGC CCGTCTTGC 19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmid pGS05
(C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25
ATGAATAAAT CGCTCATCAT TTTCGGCATC GTCAACATAA CCTCGGACAG 50
TTTCTCCGAT GGAGGCCGGT ATCTGGCGCC AGACGCAGCC ATTGCGCAGG 100
CGCGTAAGCT GATGGCCGAG GGGGCAGATG TGATCGACCT CGGTCCGGCA 150
TCCAGCAATC CCGACGCCGC GCCTGTTTCG TCCGACACAG AAATCGCGCG 200
30 TATCGCGCCG GTGCTGGACG CGCTCAAGGC AGATGGCATT CCCGTCTCGC 250
TCGACAGTTA TCAACCCGCG ACGCAAGCCT ATGCCTTGTC GCGTGGTGTG 300
GCCTATCTCA ATGATATTCG CGGTTTTCCA GACGCTGCGT TCTATCCGCA 350
ATTGGCGAAA TCATCTGCCA AACTCGTCGT TATGCATTCG GTGCAAGACG 400
GGCAGGCAGA TCGGCGCGAG GCACCCGCTG GCGACATCAT GGATCACATT 450
35 GCGGCGTTCT TTGACGCGCG CATCGCGGCG CTGACGGGTG CCGGTATCAA 500
ACGCAACCGC CTTGTCCTTG ATCCCGGCAT GGGGTTTTTT CTGGGGGCTG 550
CTCCCGAAAC CTCGCTCTCG GTGCTGGCGC GGTTCGATGA ATTGCGGCTG 600
CGCTTCGATT TGCCGGTGCT TCTGTCTGTT TCGCGCAAAT CCTTTCTGCG 650
CGCGCTCACA GGCCGTGGTC CGGGGGATGT CGGGGCCGCG AACTCGCTG 700
10 CAGAGCTTGC CGCCGCCGCA GGTGGAGCTG ACTTCATCCG CACACACGAG 750
CCGCGCCCCCT TCGCGACGG GCTGGCGGTA TTGGCGGCGC TGAAAGAAAC 800
CGCAAGAATT CGTTAA 816

15 2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG

19

2) INFORMATION FOR SEQ ID NO: 1967

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

CAGCAATAAG TAATCCAGCG ATG

23

2) INFORMATION FOR SEQ ID NO: 1968

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

GGAGAGATTT CACCGCATAG

20

2) INFORMATION FOR SEQ ID NO: 1969

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1970

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Transposon Tn10
 (C) ACCESSION NUMBER: J01830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

ATGAATAGTT	CGACAAAGAT	CGCATTGGTA	ATTACGTTAC	TCGATGCCAT	50
GGGGATTGGC	CTTATCATGC	CAGTCTTGCC	AACGTTATTA	CGTGAATTTA	100
TTGCTTCGGA	AGATATCGCT	AACCACTTTG	GCGTATTGCT	TGCACTTTAT	150
GCGTTAATGC	AGGTTATCTT	TGCTCCTTGG	CTTGGA AAAA	TGTCTGACCG	200
ATTTGGTCGG	CGCCCAGTGC	TGTTGTTGTC	ATTAATAGGC	GCATCGCTGG	250
ATTACTTATT	GCTGGCTTTT	TCAAGTGC GC	TTTGGATGCT	GTATTTAGGC	300
CGTTTGCTTT	CAGGGATCAC	AGGAGCTACT	GGGGCTGTCG	CGGCATCGGT	350
CATTGCCGAT	ACCACCTCAG	CTTCTCAACG	CGTGAAGTGG	TTCGGTTGGT	400
TAGGGGCAAG	TTTTGGGCTT	GGTTTAATAG	CGGGGCCTAT	TATTGGTGGT	450
TTTGCAGGAG	AGATTTCACC	GCATAGTCCC	TTTTTTATCG	CTGCGTTGCT	500
AAATATTGTC	ACTTTCCTTG	TGGTTATGTT	TTGGTTCCGT	GAAACCAAAA	550
ATACACGTGA	TAATACAGAT	ACCGAAGTAG	GGGTTGAGAC	GCAATCGAAT	600
TCGGTATACA	TCACTTTATT	TAAAACGATG	CCCATTTTGT	TGATTATTTA	650
TTTTTCAGCG	CAATTGATAG	GCCAAATTCC	CGCAACGGTG	TGGGTGCTAT	700
TTACCGAAAA	TCGTTTTTGA	TGGAATAGCA	TGATGGTTGG	CTTTTCATTA	750
GCGGGTCTTG	GTCTTTTACA	CTCAGTATTC	CAAGCCTTTG	TGGCAGGAAG	800
AATAGCCACT	AAATGGGGCG	AAAAAACGGC	AGTACTGCTC	GAATTTATTG	850
CAGATAGTAG	TGCATTTGCC	TTTTTAGCGT	TTATATCTGA	AGGTTGGTTA	900
GATTTCCCTG	TTTTAATTTT	ATTGGCTGGT	GGTGGGATCG	CTTTACCTGC	950
ATTACAGGGA	GTGATGTCTA	TCCAAACAAA	GAGTCATGAG	CAAGGTGCTT	1000
TACAGGGATT	ATTGGTGAGC	CTTACCAATG	CAACCGGTGT	TATTGGCCCA	1050
TTACTGTTTA	CTGTTATTTA	TAATCATTCA	CTACCAATTT	GGGATGGCTG	1100
GATTTGGATT	ATTGGTTTAG	CGTTTTACTG	TATTATTATC	CTGCTATCGA	1150
TGACCTTCAT	GTTAACCCTT	CAAGCTCAGG	GGAGTAAACA	GGAGACAAGT	1200
GCTTAG					1206

2) INFORMATION FOR SEQ ID NO: 1971

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

5 CYGACTGYGC CATCCTYATC A

21

2) INFORMATION FOR SEQ ID NO: 1972

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

20 MGICAGCTCA TYITTGCWKS C

21

2) INFORMATION FOR SEQ ID NO: 1973

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50 ACAAGGGITG GRMSAAGGAG AC

22

2) INFORMATION FOR SEQ ID NO: 1975

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

TGRCCRGGGT GGTTRAGGAC G

21

2) INFORMATION FOR SEQ ID NO: 1976

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

GATGGAYTCY GTYAAITGGG A

21

2) INFORMATION FOR SEQ ID NO: 1977

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

GATGGAYTCY GTYAARTGGG A

21

2) INFORMATION FOR SEQ ID NO: 1978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

CATCITGYAA TGGYAATCTY AAT

23

10

2) INFORMATION FOR SEQ ID NO: 1979

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

CATCYTGYAA TGGYAASCTY AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1980

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40 TCRATGGCIT CIAIRAGRGY YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35 CYGAYTGCGC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50

CYGAYTGYGC YATYCTSATC A

21

2) INFORMATION FOR SEQ ID NO: 1985

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: M1-106
 (C) ACCESSION NUMBER: U81804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
20	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTCTT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCTA	250
	AGTACCAGGT	TACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTGC	350
25	CACCGGTATC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCTGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGT	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
30	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCCGGTGTT	TCCAAGGGTA	AGACCCTTCT	CGAGGCCATC	GACGCCAGTA	700
	GGCCCCCTAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTTCGCCCC	ACCAACGTCA	850
35	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTCCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
40	TTGCAAGTTC	TCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTT	CCCAGAAGCC	TCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATTAA	GAGTGTGGAG	AAGTCCGATG	GGAAGAGCGG	CAAGGTTACC	1350
45	AAGGCCGCCG	AGAAGGCTGC	TAAGAAGAAG	TAA		1383

2) INFORMATION FOR SEQ ID NO: 1986

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus neoformans*
(B) STRAIN: B3501
(C) ACCESSION NUMBER: U81803

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
15	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTTCCT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCCA	250
	GGTACCAGGT	CACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTCG	350
20	CACCGGTATC	GGTGAGTTCG	AGGCCGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCCGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGC	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
25	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCTGGTGTT	TCCAGGGGTA	AGACCCTTCT	CGAGGCCATC	AGCGCCAGTA	700
	GGCCCCATAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTGCGCCCC	ACCAACGTCA	850
30	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTTCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
35	CTGCAAGTTT	GCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTG	CCCAGAAGCC	CCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTCGCCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATCAA	GAGCGTGGAC	AAGACCGAGA	AGGGTGGCAA	GGTCACCAAG	1350
40	GCTGCTGAGA	AGGCTGCCAA	GAAGAAGTAA			1380

2) INFORMATION FOR SEQ ID NO: 1987

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(C) ACCESSION NUMBER: X01638

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

```

      ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA      50
      TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
      TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
10    AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
      AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
      AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG      300
      AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
      TGGTGGTGTC GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
15    GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
      GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
      AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
      AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
      GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGCGGAAA AGGAAACCAA      650
20    GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
      AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
      GTTTACAAGA TCGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
      CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTGCCCCCA GCTGGTGTTA      850
      CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
25    GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
      AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG      1000
      GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA      1050
      ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC      1100
      TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA      1150
30    AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC      1200
      AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC      1250
      ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG      1300
      GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTACCAAG      1350
      GCTGCTCAAA AGGCTGCTAA GAAATAA      1377
35

```

2) INFORMATION FOR SEQ ID NO: 1988

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

50 (C) ACCESSION NUMBER: M10992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

```

ATGGGGTAAAG AGAAGTCTCA CATTAACGTT GTCGTTATCG GTCATGTCGA      50
TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
5 AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTTCATCAAG      300
AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
TGGTGGTGTC GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
10 GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGAGGAAA AGGAAACCAA      650
GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
15 AACAAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTTA      850
CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
20 AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG      1000
GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA      1050
ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC      1100
TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA      1150
AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC      1200
25 AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC      1250
ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCTG      1300
GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG      1350
GCTGCTCAAA AGGCTGCTAA GAAATAA      1377

```

30

2) INFORMATION FOR SEQ ID NO: 1989

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 1377 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
(B) STRAIN: ATCC 10895
45 (C) ACCESSION NUMBER: X73978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

```

ATGGGTAAGG AAAAGACTCA CGTTAACGTT GTCGTCATCG GTCACGTCGA      50
50 CTCTGGTAAG TCTACTACCA CCGGTCACTT GATCTACAAG TGTGGTGGTA      100
TTGACAAGAG AACCATCGAG AAGTTCGAGA AGGAGGCTGC CGAGTTGGGT      150
AAGGGTTCTT TCAAGTACGC CTGGGTTTTG GACAAATTGA AGGCTGAGAG      200
AGAGAGAGGT ATCACCATCG ACATTGCGTT GTGGAAGTTC GAGACTCCAA      250

```

	AGTACCACGT	CACTGTCATT	GACGCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
5	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550
	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
10	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
15	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
20	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
	ACCATTGGGT	AGATTCGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCTG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCCAAA	AGGCTGGTAA	GAAATAG			1377

25

2) INFORMATION FOR SEQ ID NO: 1990

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1377 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eremothecium gossypii*
 (C) ACCESSION NUMBER: A29820

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
15	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250
	AGTACCACGT	CACTGTCATT	GACCCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
30	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550

	AGACTGTTCC	ATTTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
5	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
10	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
15	ACCATTGGGT	AGATTCGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCTG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCCAA	AGGCTGGTAA	GAAATAG			1377

20

2) INFORMATION FOR SEQ ID NO: 1991

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus oryzae*
 (B) STRAIN: KBN616
 (C) ACCESSION NUMBER: AB007770

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

	TGGGGTAAGT	TTATCAACCC	GTCGAGTTGT	GTTGCATCTC	AGATCATGGC	50
	TGACAAGTAC	TTTCCTCCTT	ACAGTAAGGA	AGACAAGCAG	CACATCAACA	100
40	TCGTGCTTAT	CGGCCACGTC	GATTCCGGCA	AGTCCACCAC	CACTGGTCAC	150
	TTGATCTACA	AGTGTGGTGG	TATCGACCAG	CGTACCATCG	AGAAGTTCGA	200
	GAAGGAAGCC	GCTGAGCTCG	GTAAGGGTTC	CTTCAAGTAC	GCCTGGGTTC	250
	TTGACAAGCT	CAAGTCCGAG	CGTGAGCGTG	GTATCACCAT	CGATATCGCC	300
	CTCTGGAAGT	TCCAGACCTC	CAAGTATGAG	GTCACCGTCA	TTGGTAAGCA	350
45	TTTGAGTTCC	AACCTACGTT	GCCCAACATT	TACAGTCATC	TAACAAAGTT	400
	CAATAGATGC	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	450
	ACTTCCCAGG	CTGACTGCGC	TATCCTCATC	ATTGCCTCCG	GTAAGTGGTG	500
	ATTGAGGCT	GGTATCTCCA	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	550
	TCGCTTTCAC	CCTCGGTGTC	CGTCAGCTCA	TCGTTGCCCT	CAACAAGATG	600
50	GACACCTGCA	AGTGGTCTCA	GGATCGTTAC	AACGAAATCG	TTAAGGAGAC	650
	TTCCAACCTC	ATCAAGAAGG	TCGGATACAA	CCCCAAGAGC	GTTCTTTTCG	700
	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCACCAAC	750
	TGCCCCTGGT	ACAAGGGCTG	GGAGAAGGAG	ACCAAGGCTG	GCAAGTCCAC	800

	CGGTAAGACC	CTTCTCGAGG	CCATCGATGC	CATCGAGCCC	CCCGTCCGTC	850
	CCACCGACAA	GCCTCTCCGT	CTTCCCCTCC	AGGATGTCTA	CAAGATCTCT	900
	GGTATCGGTA	CTGTGCCCCG	CGGTCGTGTC	GAGACTGGTG	TCATCAAGCC	950
	TGGTATGGTC	GTTACTTTTCG	CTCCTGCCAA	CGTGACCACT	GAAGTCAAGT	1000
5	CCGTTGAAAT	GCACCACCAG	CAGCTCCAGG	CCGGTAACCC	CGGTGACAAC	1050
	GTTGGTTTCA	ACGTCAAGAA	CGTCTCCGTC	AAGGAAGTCC	GCCGTGGTAA	1100
	CGTTGCCGGT	GACTCCAAGA	ACGACCCCCC	TGCTGGCTGC	GATTCCTTCA	1150
	ACGCCCAGGT	CATCGTCCTT	AACCACCCCG	GTCAGGTCGG	CAACGGTTAC	1200
	GCTCCCCTCC	TGGACTGCCA	CACCGCTCAC	ATTGCTTGCA	AGTTCGCTGA	1250
10	GCTCCTTGAG	AAGATTGACC	GCCGTACCGG	TAAATCTGTT	GAGGACAAGC	1300
	CCAAGTTCAT	CAAGTCTGGT	GATGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1350
	AAGCCCATGT	GTGTGGAGTC	TTTCACTGAC	TTCCCCCCTC	TTGGTCGTTT	1400
	CGCTGTCCGT	GACGTAAGTT	TTTCCCTCTT	GACTATCTTC	ACAATTTTTTC	1450
	ACATATTTTC	ACGCCTCGTC	CCACTCTTTT	TCCTCCCTTC	CTCTTTGGTT	1500
15	CCCCTTTTTG	CCTGCAAGTT	CTCTATAGCT	AACATGATGT	CTAGATGCGT	1550
	CAAACGTGTT	CCGTCGGAGT	TATCAAGTCG	GTTGAGAAGA	ACACTGGCGG	1600
	TTCTGGCAAG	GTCACCAAGG	CCGCCCAGAA	GGCTGGCAAG	AAATAA	1646

20

2) INFORMATION FOR SEQ ID NO: 1992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: R106
 (C) ACCESSION NUMBER: U19723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

	ATGGGTAAGG	AAAAGTCCCA	CATCAACGTC	GTCGTTATCG	GCCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
40	TCGACAAGCG	TACCATCGAG	AAGTTCGAGA	AGGAAGCCGC	CGAACTCGGC	150
	AAGGGTTCCT	TCAAGTACGC	CTGGGTCCCTC	GACAAGCTGA	AGTCTGAGCG	200
	TGAGCGTGGT	ATCACTATCG	ATATCGCTCT	GTGGAAGTTC	GAGACCCCCA	250
	AGTACATGGT	CACCGTCATC	GATGCCCCCG	GTCACCGTGA	TTTCATCAAG	300
	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	TGCGCCATTC	TCATCATTTG	350
45	CGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGCCAGACTC	400
	GTGAGCACGC	CCTTCTCGCC	TACACCCCTG	GTGTCAAGCA	GCTCATCGTC	450
	GCTATCAACA	AGATGGACAC	CACCAAGTGG	TCTGAGGCC	GTTACCAGGA	500
	GATCATCAAG	GAGACCTCCG	GTTTCATCAA	GAAGGTCGGC	TACAACCCCA	550
	AGCACGTTCC	CTTTGTCCCC	ATCTCGGGTT	TCAACGGTGA	CAACATGATT	600
50	GAGGTTTCTT	CCAAC TGCCC	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	650
	GGCCAAGGCC	ACTG GTAAGA	CTCTCCTCGA	GGCCATTGAC	GCCATCGACC	700
	CTCCTTCGCG	CCCCACCGAC	AAGCCCCCTC	GTCTTCCCCT	CCAGGATGTC	750
	TACAAGATCG	GTGGTATTGG	CACGGTGCCC	GTCGGCCGTG	TCGAGACCGG	800

	TACCATCAAG	GGTGGTATGG	TCGTACCTT	CGCCCCGCT	GGTGTACCA	850
	CTGAGGTCAA	GTCCGTCGAG	ATGCACCACG	AGCAGCTCTC	CGAGGGTCTC	900
	CCCGGTGACA	ACGTCGGCTT	CAACGTCAAG	AACGTCTCCG	TCAAGGAGAT	950
	CCGTCGTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTT	1000
5	GCGACTCCTT	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	1050
	GGTGCTGGTT	ACGCACCCGT	CCTCGATTGC	CACACTGCCC	ACATCGCCTG	1100
	CAAGTTCTCC	GAGCTTGTTG	AGAAGATTGA	CCGCCGTACC	GGCAAGTCCG	1150
	TTGAGGCCGC	CCCCAAGTTC	ATCAAGTCTG	GTGACGCCGC	CATCGTCAAG	1200
	ATGGTTCCTT	CCAAGCCTAT	GTGTGTTGAG	GCCTTCACTG	ACTACCCTCC	1250
10	TCTCGGTCGT	TTCGCCGTCC	GTGACATGAG	ACAGACCGTC	GCTGTCGGTG	1300
	TCATCAAGTC	CGTCGCCAAG	TCCGACAAGC	AGGGTGCCGG	TAAGGTTACC	1350
	AAGGCCGCTG	TCAAGGCTGG	CAAGAAGTAA			1380

15

2) INFORMATION FOR SEQ ID NO: 1993

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
- (B) STRAIN: 186AS
- (C) ACCESSION NUMBER: U14100

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

	ATGGGTAAGG	AAGACAAGAC	TCACATTAAC	CTCGTCGTCA	TCGGCCACGT	50
	CGATTCGGGC	AAATCTACCA	CCACTGGTCA	TTTGATCTAC	AAATGCGGTG	100
35	GTATTGACAG	CCGTACCATT	GAGAAGTTCG	AAAAGGAAGC	CGAAGAGTTG	150
	GGCAAGAAAT	CCTTCAAATA	TGCGTGGGTC	CTTGACAAAC	TGAAGTCTGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATTGC	CCTCTGGAAA	TTCGAGACTC	250
	CGAAGTACAG	TGTCACTGTC	ATTGATGCTC	CCGGCCATCG	TGACTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GA CTGCGCTA	TCCTCATCAT	350
40	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
	CTCGTGAGCA	CGCTCTGCTT	GCTTTCACCC	TTGGTGTGAG	GCAACTCATC	450
	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTTCAA	500
	CGAAATCATC	AAGGAGGTTT	CCAAC TTCAT	CAAGAAGGTC	GGATATAACC	550
	CCAAGGCTGT	TCCCTTCGTG	CCAATCTCTG	GTTTCGAGGG	TGACAACATG	600
45	ATTGAACCCT	CCCCCAACTG	CACATGGTAC	AAGGGCTGGA	ACAAGGAGAC	650
	TGCCTCTGGC	AAGTCTTCTG	GTAAAACCCT	TCTCGATGCC	ATTGACGCCA	700
	TTGAACCCCC	AACCCGTCCT	ACCGATAAGC	CCCTCCGTCT	TCCCCTCCAG	750
	GATGTGTACA	AAATCTCTGG	TATTGGCACT	GTTCCCGTCG	GACGTGTTGA	800
	GACTGGTGTC	ATCAAGCCCCG	GTATGGTCGT	GACTTTCGCT	CCCTCCAACG	850
50	TCACCACTGA	AGTCAAGTCC	GTGCAAAATG	ACCACCAACA	ACTCCAGGCT	900
	GGTTACCCTG	GCGACAACGT	CGGCTTCAAC	GTCAAGAACG	TTTCAGTCAA	950
	GGAAGTCCGC	CGTGGCAACG	TTGCTGGCGA	CTCCAAAAAT	GATCCCCCTA	1000
	AGGGCTGCGA	ATCCTTCAAT	GCCCAGGTCA	TCGTCCTTAA	CCACCCCGGC	1050

	CAGGTTGGCG	CTGGTTATGC	CCCAGTCCTC	GACTGCCACA	CTGCCCACAT	1100
	TGCTTGCAAG	TTCTCTGAGC	TTATTGAGAA	GATCGACCGC	CGTACCGGAA	1150
	AGTCTGTTGA	GAACAACCCC	AAGTTCATCA	AGTCTGGTGA	TGCTGCTATC	1200
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTGGAGCCCT	TCACTGACTA	1250
5	TCCCCCTCTT	GGACGTTTCG	CTGTCCGTGA	CATGAGACAA	ACCGTCGCTG	1300
	TCGGTGTCAT	CAAGTCCGTC	ATCAAGTCTG	ACAAGACTGC	TGGCAAGGTC	1350
	ACCAAGGCCG	CGCAGAAGGC	CACCAAGAAA	TAA		1383

10

2) INFORMATION FOR SEQ ID NO: 1994

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neurospora crassa*
- (C) ACCESSION NUMBER: D45837

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

	ATGGGCAAGG	AGGACAAGAC	TCACATCAAC	GTCGTCGTTA	TCGGCCACGT	50
	CGATTCCGGC	AAGTCTACCA	CTACCGGTCA	CTTGATCTAC	AAGTGCGGTG	100
	GTATCGACAA	GCGTACCATC	GAGAAGTTCG	AGAAGGAAGC	CGCTGAGCTC	150
30	GGTAAGGGTT	CCTTCAAGTA	TGCCTGGGTT	CTTGACAAGC	TCAAGGCCGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	TTCGAGACTC	250
	CCAAGTACTA	CGTCACCGTC	ATCGATGCC	CCGGTCATCG	TGATTTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GATTGCGCTA	TCCTCATCAT	350
	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
35	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GCAGTCTATT	450
	GTTGCCATCA	ACAAGATGGA	CACCACCCAG	TGGTCCCAGA	CTCGTTTCGA	500
	GGAGATCATC	AAGGAGACCA	AGAACTTCAT	CAAGAAGGTT	GGCTACAACC	550
	CCGCTGGTGT	CGCTTTCGTC	CCCATCTCCG	GCTTCAACGG	CGACAACATG	600
	CTTGAGCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	650
10	CAAGGCCGGC	AAGGCCACTG	GCAAGACCCT	CCTCGAGGCC	ATCGACGCCA	700
	TTGAGCCCCC	CAAGCGTCCT	ACCGACAAGC	CCCTCCGTCT	TCCCCTCCAG	750
	GATGTCTACA	AGATCGGTGG	TATCGGCACA	GTGCCCCTCG	GCCGTATCGA	800
	GACTGGTGTC	CTCAAGCCCG	GTATGGTCGT	TACCTTCGCT	CCTTCCAACG	850
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTTGCTCAG	900
15	GGTGTCCCCG	GTGACAACGT	CGGCTTCAAC	GTGAAGAACG	TTTCCGTCAA	950
	GGATATCCGC	CGTGGTAAACG	TTGCCGGTGA	CTCCAAGAAC	GACCCCCCTG	1000
	CTGGCGCCGC	CTCTTTCACC	GCCCAGGTCA	TCGTTCTCAA	CCACCCCGGT	1050
	CAGGTCGGTG	CCCGCTACGC	CCCCGTCTC	GACTGCCACA	CTGCCCACAT	1100
	TGCCTGCAAG	TTGCGCCGAGC	TCCTCGAGAA	GATCGACCGC	CGTACTGGTA	1150
50	AGGCTGTTGA	GGCCTCCCCC	AAGTTCATCA	AGTCTGGTGA	TGCTGCCATC	1200
	GTCAAGATGA	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACCGACTA	1250
	CCCTCCCCCTC	GGCCGTTTCG	CCGTCCGTGA	CATGCGTCAG	ACCGTCGCCG	1300
	TCGGTGTCAT	CAAGGCCGTC	GACAAGTCCA	CCGCTGCCGC	TGGCAAGGTC	1350

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

5 2) INFORMATION FOR SEQ ID NO: 1995

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira anserina*
 (C) ACCESSION NUMBER: X74799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100
 GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150
 GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200
 25 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTCGAGACCC 250
 CCAAGTACTA TGTCACCGTC ATTGATGCCC CCGGCCATCG TGATTTTCATC 300
 AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT 350
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450
 30 GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGCTTCAA 500
 CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550
 CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG 600
 CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT 650
 CAAGGGTGGC AAGGCCACCG GCAAGACCTT CCTTGAGGCC ATCGACTCCA 700
 35 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
 GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCT GCGGTATCGA 800
 GACTGGTATC CTCAAGCCCC GTATGGTCGT TACCTTCGCT CCTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
 GGTGTTCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950
 40 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000
 TGGGCGCCGC CTCTTTCGAT GCCCAGGTCA TCGTCCCTCAA CCACCCCGGC 1050
 CAGGTCGGTG CTGGTTACGC CCCCGTCCTC GATTGCCACA CTGCCCACAT 1100
 CGCCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA 1150
 AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 45 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250
 CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300
 TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT 1350
 ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA 1383

50

2) INFORMATION FOR SEQ ID NO: 1996

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira curvicolla*
 (B) STRAIN: VLV
 (C) ACCESSION NUMBER: X96614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

```

15 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
   CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG      100
   GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC      150
   GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA      200
20 GCGTGAGCGT GGTATCACCA TTGATATCGC CCTCTGGAAG TTCGAGACCC      250
   CCAAGTACTA TGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTCATC      300
   AAGAACATGA TTAAGGTGAGT TTCCCAGGCC GATTGCGCCA TTCTCATCAT      350
   TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
   CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC      450
25 GTCGCCATCA ACAAGATGGA CACCACCAA TGGTCCGAGG CCCGCTTCAA      500
   CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC      550
   CCAAGACTGT TGCTTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG      600
   CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGGT      650
   CAAGGGTGGC AAGGCTACTG GCAAGACCCT CCTCGAGGCC ATCGACTCCA      700
30 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTTCAG      750
   GACGTTTACA AGATCGGCGG TATCGGCACA GTCCCTGTCG GCCGTATCGA      800
   GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCC CCTTCCAACG      850
   TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTCTGAG      900
   GGTGTCCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA      950
35 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTC     1000
   TTGGCGCCGC TTCTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC     1050
   CAGGTCGGTG CTGGTTACGC CCCCGTCCTC GATTGCCACA CTGCCCACAT     1100
   CGCCTGCAAG TTCGCTGAGC TCCTGCAGAA GATCGATCGC CGTACTGGTA     1150
   AGGCTGTTGA GGAGAGCCCT AAGTTCATCA AGTCTGGTGA TGCTGCCATC     1200
40 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA     1250
   CCCTCCCCTC GGTCGTTTCG CTGTCCGTGA CATGCGTCAG ACCGTCGCTG     1300
   TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTC     1350
   ACCAAGTCCG CTGCCAAGGC TGGTGGCAAG AAATAA                      1386

```

2) INFORMATION FOR SEQ ID NO: 1997

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*
 (B) STRAIN: 000
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

10
 ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGCGGTG 100
 GTATCGACAA GCGTACCATC GAGAAGTTTCG AGAAGGAAGC CGCTGAGCTC 150
 GGCAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA 200
 15 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC 250
 CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTCATC 300
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT 350
 TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC 450
 20 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGG CTCGTTTCGA 500
 GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC 550
 CCGCCACCGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG 600
 CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC 650
 CAAGGCCGGC AAGTCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA 700
 25 TTGAGCAGCC CAAGCGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
 GATGTCTACA AGATCGGCGG TATCGGCACA GTGCCCGTCG GCCGTATCGA 800
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG 900
 GGTGTTCCCG GTGACAACGT CGGCTTCAAC GTGAAGAAGC TTTCCGTCAA 950
 30 GGATATCCGT CGTGGTAACG TTGCCGGTGA CTCCAAGAAG GACCCCCCTG 1000
 TCGGCGCTGC CTCTTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT 1050
 CAGGTCGGTG CCGGCTACGC TCCCGTCCTC GATTGCCACA CTGCCCACAT 1100
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA 1150
 AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 35 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTCGAGGCTT TCACCGACTA 1250
 CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300
 TCGGTGTCAT CAAGGCCGTC GACAAGACCC AGGCTGTCGC TGGCAAGGTC 1350
 ACCAAGTCTG CTGCCAAGGC TGCCAAGAAG TAA 1383

10

2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414

(C) ACCESSION NUMBER: Z23012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5
ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT 50
CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCGGTG 100
GTATCGACAA GCGTACCATT GAGAAGTTCG AGAAGGAAGC CGCCGAAGTC 150
GGCAAGGGTT CCTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA 200
10 GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC 250
CCAAGTACTA TGTCACCGTC ATTGACGCTC CCGGCCACCG TGAATTCATC 300
AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCTA TCCTCATCAT 350
CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC 450
15 GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA 500
GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTTCAACC 550
CCAAGGCCGT TGCTTTCGTC CCCATCTCCG GCTTCAACGG TGACAACATG 600
CTCACCCCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC 650
CAAGGCTGGC AAGTTCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700
20 TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCCTCCAG 750
GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA 800
GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG 850
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
GGCCAGCCTG GTGACAACGT TGGTTTCAAC GTGAAGAACG TTTCCGTCAA 950
25 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000
TGGGCGCCGC TTCTTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGGC 1050
CAGGTCGGTG CCGGCTACGC CCCCGTCCTC GACTGCCACA CTGCCCACAT 1100
TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA 1150
AGGCTACCGA GTCTGCCCCC AAGTTCATCA AGTCTGGTGA CTCCGCCATC 1200
30 GTCAAGATGA TCCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250
CCCTCCCCTG GGTCGTTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG 1300
TCGGTGTCAT CAAGGCCGTC GAGAAGTCCT CTGCCGCCGC CGCCAAGGTC 1350
ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA 1383

35

2) INFORMATION FOR SEQ ID NO: 1999

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

CATGTCAAYA TTGGTACTAT TGGTCATGT

29

50

2) INFORMATION FOR SEQ ID NO: 2000

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000

CCACCYTCIC TCAMGTTGAA RCGTT

2) INFORMATION FOR SEQ ID NO: 2001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001

ACYACITTRA CIGCYGCIAT YAC

2) INFORMATION FOR SEQ ID NO: 2002

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002

CCIGARGARA GAGCIMGWGG T

2) INFORMATION FOR SEQ ID NO: 2003

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

2) INFORMATION FOR SEQ ID NO: 2004

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

GCTGCCTTCG	ACCGTTCTAA	ACCTCATGTC	AACATTGGTA	CTATTGGTCA	50
TGTTGATCAT	GGTAAACTA	CATTGACTGC	TGCTATCACC	AAAGTTTTAG	100
CCGAACAAGG	TGGTGCCAAC	TTCTTGGATT	ATGGTTCTAT	TGATAGAGCT	150
CCAGAAGAAA	GAGCTAGAGG	TATCACTATT	TCCACTGCCC	ACGTTGAATA	200
CGAAACCAAG	AACAGACACT	ATGCCCACGT	TGATTGTCCA	GGACACGCTG	250
ATTATATCAA	AAATATGATT	ACTGGTGCCG	CTCAAATGGA	TGGTGCTATC	300
ATTGTTGTTG	CTGCCACTGA	TGGTCAAATG	CCTCAAACCA	GAGAACATTT	350
GTTATTGGCC	AGACAAGTTG	GTGTTCAAGA	CTTGGTTGTG	TTTGTCAACA	400
AAGTCGATAC	TATTGATGAC	CCTGAAATGT	TGGAATTAGT	CGAAATGGAA	450
ATGAGAGAAT	TGTTATCCAC	CTACGGTTTT	GATGGTGACA	ACACTCCAGT	500
TATTATGGGA	TCTGCTTTAA	TGGCTTTGGA	AGACAAGAAA	CCAGAAATTG	550
GTAAGGAAGC	TATCTTGAAA	TTGTTAGATG	CTGTCGATGA	ACACATTCCA	600
ACTCCATCAA	GAGACTTGGA	ACAACCATT	TTGTTACCAG	TTGAAGACGT	650
GTTCTCCATC	TCCGGTAGAG	GAAGTGTGT	CACTGGTAGA	GTTGAAAGAG	700
GTGTTTTGAA	GAAGGGTGAA	GAAATCGAAA	TTGTTGGTGG	TTTTGACAAA	750
CCTTACAAGA	CTACTGTTAC	CGGTATTGAA	ATGTTCAAAA	AAGAATTAGA	800
CTCTGCTATG	GCTGGTGACA	ACTGTGGTGT	TTTGTTAAGA	GGTGTTAAAA	850
GAGATGAAAT	CAAGAGAGGT	ATGGTTTTGG	CCAAACCAGG	TACTGCTACT	900
TCTCACAAAG	AGTTCTTGGC	TTCCTTGTAT	ATTTTGACTT	CCGAAGAAGG	950
TGGTCGTTCC	ACTCCATTG	GTGAAGGTTA	CAAGCCTCAA	TGCTTCTTCA	1000
GAACTAACGA	TGTCCTACC	ACATTTTCAT	TCCCAGAAGG	AGAAGGTGTT	1050
GATCATTCTC	AAATGATCAT	GCCAGGTGAC	AACATTGAAA	TGGTTGGTGA	1100
ATTGATCAAA	TCTTGTCCAT	TAGAAGTCAA	CCAACGTTTC	AACTTGAGAG	1150
AAGGTGGTAA	AACTGTTGGT	ACTGGTTTGA	TTACCAGAAT	CATCGAATAA	1200
ACAGAATGTG	CACTGTGAAT	AATAAAAAGA	AAAGAGGTAT	ATATAGGTGA	1250
CTTTGTATTT	TGTATTGAAC	AATAAAATTC	TGTAAATAGT	AAGGGCCTCA	1300
GAAGTTTTGA	TTTGATTTAT	GCCATGTGGA	CTTGTAGAGA	TATCCTTCTC	1350
AAACTTCTTG					1360

2) INFORMATION FOR SEQ ID NO: 2005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

AAGCCGCATG	TCAATATTGG	TACTATTGGT	CATGTTGACC	ACGGTAAAAC	50
GACGTTGACG	GCTGCTATTA	CTAAATGCCT	TTCTGATCTT	GGTCAAGCTA	100
GTTTTATGGA	TTATAGTCAA	ATTGACAAGG	CCCCCGAGGA	AAAGGCACGT	150
GGTATTACCA	TTTCATCTGC	CCATGTTGAA	TACGAAACTG	CTAATCGTCA	200
CTATGCCCAT	GTGGATTGTC	CTGGTCACGC	CGATTACATT	AAGAATATGA	250
TTACTGGTGC	TGCTACAATG	GATGGCGCTA	TCATTGTTGT	TTCTGCTACC	300
GATGGTCAAA	TGCCTCAAAC	TCGTGAACAT	TTGCTTCTGG	CTCGTCAAGT	350
CGGTGTAAAG	CAAATTGTTG	TATACATCAA	TAAAGTCGAT	ATGGTCGAGC	400
CTGATATGAT	CGAGCTTGTC	GAAATGGAAA	TGCGTGAGCT	ACTCTCCGAA	450
TACGGATTTG	ATGGTGACAA	TACTCCAATT	GTTAGCGGCA	GTGCTTTATG	500
TGCCTTAGAG	GGTCGTGAGC	CTGAGATTGG	TCTCAATAGT	ATTACTAAAT	550
TGATGGAAGC	TGTTGATAGT	TATATTACTC	TTCCTGAAAG	AAAAACGGAT	600
GTCCCTTTCT	TGATGGCCAT	CGAGGACGTT	TTTTCAATTT	CAGGTCGCGG	650
AACTGTAGTC	ACTGGCCGTG	TCGAGCGCGG	TACTTTAAAG	AAGGGTGCTG	700
AAATCGAAAT	CGTCGGTTAT	GGTAGCCATT	TAAAGACTAC	CGTTACTGGA	750
ATTGAAATGT	TCAAAAAGCA	GCTTGATGCC	GCCGTTGCCG	GTGACAATTG	800
TGGCCTTTTA	CTTCGTTCTA	TCAAGCGAGA	GCAATTAAAA	CGTGGAATGA	850
TTGTCGCTCA	ACCAGGAACC	GTTGCTCCTC	ATCAGAAATT	CAAGGCATCA	900
TTCTATATTT	TGACAAAAGA	GGAAGGAGGT	CGTCGTACCG	GTTTCGTTGA	950
CAAGTATCGT	CCCCAACTGT	ACAGTCGTAC	TTCCGACGTT	ACTGTCGAAC	1000
TTACCCACCC	TGATCCTAAC	GACTCAGACA	AAATGGTTAT	GCCTGGAGAC	1050
AATGTCGAGA	TGATCTGTAC	GCTTATTCAC	CCCATTGTCA	TCGAAAAAGG	1100
ACAACGCTTC	ACAGTTCGTG	AGGGTGGAAG	CACTGTAGGC	ACAGCTTTGG	1150
TTACTGAACT	TTTGGATTAG	TGCATTTATG	AACTTATTGG	CTTTAAAAAT	1200
TTTGTCATGCT	GAATACCAAT	ATTATGTCCC	TTCTCAGAAT	TCTATAACTA	1250
CAGTGTCATT	ATTGTAATAA	GACTTTTGCA	TCCATTGACA	ATGGTATTTG	1300
ATACTTTTAT	AGTTTCTACT	ATTGTTAGCC	AAAGTTATAA	AA	1342

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: KMK107
 (C) ACCESSION NUMBER: AF027199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

ATGAGTATTC	AACATTTTCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
CTGAAGATCA	GTTGGGTGCA	CGAGTGGGT	ACATCGAACT	GGATCTCAAC	150
AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
GAGCACTTTT	AAAGTTCTGC	TATGTGGTGC	GGTATTATCC	CGTGTTGACG	250
CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
GTTAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCTGCCA	400
ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGACG	CCTGCAGCAA	550
TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	GCGAACTACT	TACTCTAGCT	600
TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
GAGCCAGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 2011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: CLSis L-491
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
TTGCTTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
CTGAAGATCA	GTTGGGTGCA	CGAGTGGGT	ACATCGAGCT	GGATCTCAAC	150
AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
GAGCACTTTT	AAAGTTCTGC	TATGTGGTGC	GGTATTATCC	CGTGTTGACG	250
CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
CACAACATGG	GGGATCATGT	AACCCGCCTT	GATCGTTGGG	AACCGGAGCT	500
GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	GCGAACTACT	TACTCTAGCT	600

TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
GAGCCAGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ATGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 2012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCGCGGATTA TTAAACCGCC CTTCCGCGG-MR-HEG-ATGTCAGAGG GATAGATCCA 49

2) INFORMATION FOR SEQ ID NO: 2013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

AGCTTAAGAA	CTCTTATCTG	GATTACGCGA	TGTCGGTCAT	TGTTGGCCGT	50
GCGCTGCCGG	ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	100
TTACGCCATG	AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	150
CAGCCCGTGT	CGTGGGTGAC	GTGATCGGTA	AATATCACCC	GCATGGTGAT	200
ACTGCCGTCT	ATGACACTAT	CGTCCGTATG	GCACAGCCAT	TCTCACTGCG	250
ATACATGCTG	GTAGATGGTC	AAGGTAACCT	CGGTTCTGTC	GATGGCGACT	300
CCGCCGCAGC	GATGCGTTAT	ACGGAAATCC	GTATGTCGAA	AATCGCCCAT	350
GAG					353

2) INFORMATION FOR SEQ ID NO: 2014

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

1048

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

AGCTCCTATC	TGGATTATGC	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	50
AGATGTCCGA	GATGGCCTGA	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	100
TGAACGTACT	AGGCAATGAC	TGGAACAAAG	CCTATAAAAA	ATCTGCCCGT	150
GTCGTTGGTG	ACGTAATCGG	TAAATACCAT	CCCCATGGTG	ACTCGGCGGT	200
CTATGACACG	ATCGTCCGCA	TGGCGCAGCC	ATTCTCGCTG	CGTTATATGC	250
TGGTAGACGG	TCAGGGTAAC	TTCGGTTCTA	TCGACGGCGA	CTCTGCGGCG	300
GCAATGCGTT	ATACGGAAAT	CCGTCTGGCG	AAAATTGCCC	ATGAACTGAT	350
GGCCG					355

2) INFORMATION FOR SEQ ID NO: 2015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

CCAAGAAGCT CAAAACATC TG 22

2) INFORMATION FOR SEQ ID NO: 2016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

TADCCTGTCC AWACAGCCAT 20

2) INFORMATION FOR SEQ ID NO: 2017

(i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020

GTAGCTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2021

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2022

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2023

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAAGTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

1051

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2028

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACAAATCACG

20

2) INFORMATION FOR SEQ ID NO: 2029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

2) INFORMATION FOR SEQ ID NO: 2030

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

2) INFORMATION FOR SEQ ID NO: 2031

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO:2032

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2035

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2036

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACA CTGGTTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2037

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2038

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

19

2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

20

2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

1057

GTTCTTTCTC CGTATCGTC

19

2) INFORMATION FOR SEQ ID NO: 2046

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATTT TTCTATCTAT

20

2) INFORMATION FOR SEQ ID NO: 2047

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- (C) ACCESSION NUMBER: Z49094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTATGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACCTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAATTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900

1058

AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCAC	AAC TTGGTG	TCGTCATCAA	1050
GCAAGTAATG	TTTCATTTCG	TACCAACCAG	GCCGTAGAAA	CCAATCGTGA	1100
CTGGGGATCA	TCAATGAAAC	CAATCACTGA	CTATGCTCCC	GCTTTAGAAT	1150
ATGGAGTCTA	TGACTCTACT	GCTTCTATTG	TACATGATGT	CCCTTATAAC	1200
TATCCTGGCA	CTGATACTCC	ACTCTACAAC	TGGGATCATG	TCTACTTTGG	1250
AAACATTACA	ATCCAGTATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAACACAAC	GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTATCA	CAAACCAATG	1500
TATATCAATA	AAATCGTCTT	TAGTGATGGT	AGCGAAAAAG	AATTTTCTGA	1550
TGCTGGTACA	CGAGCTATGA	AAGAGACTAC	TGCCTATATG	ATGACTGAAA	1600
TGATGAAAAC	TGTTTTAACT	TACGGAACAG	GACGTGGAGC	CTACCTACCA	1650
TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	CTGACGAAGA	1700
AATTGAAAAG	TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GATGAAATGT	1750
TTGTAGGGTA	TACCCGTAAA	TATGCAATGG	CTGTTTGGAC	AGGATACTCA	1800
AATCGTCTAA	CTCCAATCAT	CGGAGATGGT	TTCCTTGTTG	CTGGTAAAGT	1850
CTATCGTTCA	ATGATAACTT	ACCTTTCTGA	AGATGACCAA	CCTGGAGATT	1900
GGACAATGCC	AGATGGCTTG	TATAGAAATG	GAGAATTTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AAC TTCACAG	TCTAACTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2048

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAG	CTCTCACTCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	TTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTTCAGT	AGAACAACAA	GCAACCAAGC	AAGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGGAAC	TATGGAATGC	550

AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGC	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGGCTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	AGGCTATAAC	CTACTCACAA	CTGGGATGGA	TGTCTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATTT	ACAATACAGA	950
CGAATACGTT	GCCTATCCAG	ACGATGAATT	GCAAGTCGCT	TCTACCATTG	1000
TTGATGTTTC	TAACGGTAAA	GTCATTGCC	AGCTAGGAGC	ACGCCATCAG	1050
TCAAGTAATG	TTTCCTTCGG	AATTAACCAA	GCAGTAGAAA	CAAACCGCGA	1100
CTGGGGATCA	ACTATGAAAC	CGATCACAGA	CTATGCTCCT	GCCTTGAGGT	1150
ACGGTGTCTA	CGAGTCAACT	GCCACTATCG	TTCACGATGA	GCCCTATAAC	1200
TACCCTGGGA	CAAATACCCC	TGTTTATAAC	TGGGATAGGG	GCTACTTTGG	1250
CAACATCACC	TTGCAATACG	CCCTGCAACA	ATCGCGAAAC	GTCCCAGCCG	1300
TGGAAACTCT	AAACAAGGTC	GGACTCAACC	GCGCCAAGAC	TTTCCTAAAT	1350
GGTCTCGGAA	TCGACTACCC	AAGTATTCAC	TACTCAAATG	CCATTTCAAG	1400
TAACACAACC	GAATCAGACA	AAAAATATGG	AGCAAGTAGT	GAAAAGATGG	1450
CTGCTGCTTA	CGCTGCCTTT	GCAAATGGTG	GAACCTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	TAGTGATGGG	AGTGAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AAGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGAGT	TATGGAAC	GACGAAATGC	CTATCTTGCT	1650
TGGCTCCCTC	AGGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGACGAGGA	1700
AATTGAAAAC	CACATCAAGA	CCTCTCAATT	TGTAGCACCT	GATGAACAT	1750
TTGCTGGCTA	TACGCGTAAA	TATTCAATGG	CTGTATGGAC	AGGCTATTCT	1800
AACCGTCTGA	CACCACTTGT	AGGCAATGGC	CTTACGGTCG	CTGCCAAAGT	1850
TTACCGCTCT	ATGATGACCT	ACCTGTCTGA	AGGAAGCAAT	CCAGAGGATT	1900
GGAATATACC	AGAGGGGCTC	TACAGAAATG	GAGAATTTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACCTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2049

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAT	CAACTCATTG	CTGACTTGGG	200

TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTACACCA	1050
GCAAGTAAAC	TTTCATTGGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCCG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGCTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGACT	TATGGAAC	GGCGTGGAGC	CTATCTTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAA	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2050

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

CTGTGGGATA	TCTACAACCTC	CGATCAATAC	GTCTCTTACC	CTGACGATGA	50
TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	TTCAAATGGT	AAAGTCATCG	100
CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	ACGTTTCATT	TGGTACCAAC	150
CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	TCTGCTATGA	AACCAATCAC	200
CGATTATGCA	CCTGCCATAG	AATACGGTGT	TTATGATTCC	ACTGCAACTA	250
TGGTTAATGA	TATTCCTTAT	AACTATCCGG	GAACAAGCAC	ACCTGTCTAC	300
AACTGGGATA	GAGCATATTT	CGGTAATATT	ACTCTGCAAT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTC	AAGTAATACA	ACAGAATCTA	ATAAACAAATA	500
CGGAGCAAGT	AGTGAAGAAA	TGGCTGCTGC	TTATGCTGCC	TTTGCAAATG	550
GTGGCACTTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTCAGTGAT	600
GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	700
CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	CTCAAGCTGG	TAAAACAGGA	750
ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	AACCACATCA	AGAACACTGG	800
CTATGTAGCT	CCAGATGAAA	TGTTTGTGTT	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	TAACCTCTAT	CGTTGGAGAT	900
GTTTCCTAG	TTGCAGCTAA	AGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGATGATGA	50
CATGCAAGTA	GCTTCGACTA	TTGTAGATGT	ATCTAATGGT	AACGTTATTG	100
CACAACTTGG	TGCTCGTCAT	CAAGCAAGTA	ATGTTTCATT	CGGCACCAAC	150
CAGGCTGTGG	AGACCAATCG	TGACTGGGGT	TCTTCTATGA	AACCAATCAC	200
TGACTATGCT	CCCGCTTTAG	AATATGGAGT	CTATGACTCT	ACTGCTTCTA	250
TTGTACATGA	TGTTCCCTTAT	AACTATCCTG	GCACTGATAC	TCCAGTCTAC	300
AACTGGGATC	ATGTCTACTT	TGGAAACATT	ACAATCCAGT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTC	AAGTAACACA	ACTGAATCCA	ACAAACAGTA	500
CGGTGCAAGT	AGTGAAGAAA	TGGCTGCTGC	TTATGCCGCC	TTTTCTAATG	550
GTGGTATTTA	CCACAAACCA	ATGTATATCA	ATAAAATCGT	CTTCAGTGAT	600
GGTAGTGAAA	AAGAATTTTC	TGATGCTGGT	ACACGAGCTA	TGAAAGAAAC	650
TACTGCCTAT	ATGATGACCG	AAATGATGAA	AACTGTTTTA	GCTTACGGAA	700
CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	CACAAGCAGG	TAAGACAGGT	750

ACTTCTAACT	ATACTGACGA	CGAAATTGAA	AAGTATATCA	AGAACACTGG	800
CTACGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	TAAGTCCAAT	CGTAGGAGAT	900
GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	50
TTCCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	100
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	150
TCAACAATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	200
ATATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	250
GAACAAGCAC	ACCTGTCTAC	AACTGGGATC	GAGCATATTT	TGGTAATATT	300
ACTCTGCAAT	ATGCCCTTCA	ACAATCACGT	AATGTTACAG	CAGTTGAAAC	350
ATTAAACAAG	GTTGGTTTAT	ATCGAGCCAA	AACTTTCCTA	AATGGCTTAG	400
GTATCGATTA	CCCAAGCATA	CACATATGCTA	ACGCCATTTT	AAGTAATACA	450
ACAGAATCTA	ACAAACATTA	CGGTGCAAGT	AGTGAAAAAA	TGGCTGCTGC	500
TTATGCCGCC	TTTGCTAATG	GTGGTATTTA	CCACAAACCA	ATGTATATCA	550
ATAAAATCGT	CTTTAGTGAT	GGTAGTGAGA	AAGAATTTTC	TGATGCTGGT	600
ACACGAGCTA	TGAAAGAAAC	TACTGCCTAT	ATGATGACCG	AAATGATGAA	650
AACTGTTTTA	GCTTACGGAA	CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	700
CACAAGCAGG	TAAGACAGGT	ACTTCTAACT	ATACTGATGA	CGAAATCGAA	750
AAACATATCA	AGAATACTGG	CTACGTAGCT	CCAGATGAAA	TGTTTGTAGG	800
CTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	850
TAAGTCCAAT	TGTTGGAGAT	GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC	900
TCAATGATAT	CGTATCTATC	AGAAGATGAC	CAACCTGGAG	ATTGGACGAT	950
GCCAGACGGC	CTGTTCCGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1000
GTTCTACGTG	GAACACACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1050
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1100
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1150
CAAATACAAC	CCCTGATCAA	CAAAATCAGA	ATCCTCAACC	AGCAC	1195

2) INFORMATION FOR SEQ ID NO: 2053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 17619

(C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	50
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	100
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	150
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	200
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	250
TCGTTACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	300
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	350
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	400
ACCGCGCCAA	GACTTTCCTA	AATGGTCTCG	GAATCGACTA	CCCAAGTATT	450
CACTACTCAA	ATGCCATTTT	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	500
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	550
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	600
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AAATGATGAA	AACAGTCTTG	AGTTATGGAA	700
CTGGACGAAA	TGCCTATCTT	GCTTGGCTTC	CTCAAGCTGG	TAAAACAGGT	750
ACCTCTAACT	ATACAGATGA	AGAAATTGAA	AAACACATCA	AAAACACTGG	800
CTATGTAGCT	CCAGATGAAA	CGTTTGTTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAC	ACAAACCGTC	TCACACCAAT	TGTGGGGGAT	900
GGCTTCACAG	TTGCTGCCAA	AGTTTACCGC			930

2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: R6

(C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

CGTCGCATTC	TCTACGGAAT	GAATGAATTG	GGTGTGACCC	CAGACAAACC	50
CCATAAAAAA	TCTGCTCGTA	TTACAGGGGA	TGTCATGGGT	AAATACCACC	100
CACACGGGGA	TTCCTCTATT	TATGAAGCCA	TGGTCCGTAT	GGCTCAATGG	150
TGGAGCTACC	GTTACATGCT	TGTAGATGGT	CATGGGAATT	TTGGTTCCAT	200
GGATGGAGAT	AGTGCTGCCG	CTCAACGTTA	TACCGAGGCA	CGTATGAGCA	250
AGATTGCTCT	GGAAATGCTT	CGTGATATCA	ACAAAAATAC	AGTTGATTTC	300
GTTGAT					306

2) INFORMATION FOR SEQ ID NO: 2055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

ATGTCTAACA	TTCAAAACAT	GTCCCTGGAG	GACATCATGG	GAGAGCGCTT	50
TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	CCAGATATTC	100
GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATTC	TATGAATAAG	150
GATAGCAATA	CTTTTGACAA	GAGCTACCGT	AAGTCGGCCA	AGTCAGTCGG	200
GAACATCATG	GGGAATTTCC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	250
CCATGGTTTCG	TATGTCACAG	AACTGGAAAA	ATCGTGAGAT	TCTAGTTGAA	300
ATGCACGGTA	ATAACGGTTC	TATGGACGGA	GATCCTCCTG	CGGCTATGCG	350
TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	CTTCAGGATA	400
TCGAGAAAAA	GACAGTTCCT	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	450
GAACCAACGG	TCTTGCCAGC	AGCCTTTCCA	AACCTCTTGG	TCAATGGTTC	500
GACTGGGATT	TCGGCTGGTT	ATGCCACAGA	CATTCTCC	CATAATTTAG	550
CTGAGGTCAT	AGATGCTGCA	GTTTACATGA	TTGACCACCC	AACTGCAAAG	600
ATTGATAAAC	TCATGGAATT	CTTACCTGGA	CCAGACTTCC	CTACAGGGGC	650
TATTATTCAG	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	ACTGGGAAAG	700
GGCGCGTGGT	TGTTTCGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	750
AAGGAACAAA	TCGTTATTAC	TGAGATTCCT	TATGAAATCA	ATAAGGCCAA	800
TCTAGTCAAG	AAAATCGATG	ATGTTCTGTG	TAATAACAAG	GTAGCTGGGA	850
TTGCTGAGGT	TCGTGATGAG	TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	900
GAACCTAAGA	AAGACGCTAA	TACTGAGCTT	GTTCTCAACT	ACTTATTTAA	950
GTACACCGAC	CTACAAATCA	ACTACAACCT	TAATATGGTG	GCGATTGACA	1000
ATTTACACACC	TCGTCAGGTT	GGGATTGTTT	CAATCCTGTC	TAGCTACATC	1050
GCTCACCGTC	GAGAAGTGAT	TTTGGCGCGT	TCACGCTTTG	ACAAAGAAAA	1100
GGCTGAGAAA	CGTCTCCATA	TCGTGGAAGG	TTTGATTTCG	GTGATTTCTGA	1150
TTTTTGATGA	AGTCATTGCT	CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	1200
GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	TTTACGGAAG	AACAGGCTGA	1250
GGCTATCGTA	ACTTTGCAAC	TGTACCGTTT	GACCAATACC	GATGTGGTTG	1300
TCTTGACAGGA	AGAAGAAGCA	GAGCTTCGTG	AGAAGATTGC	TATGCTGGCG	1350
GCTATTATCG	GTGATGAAAG	GACTATGTAC	AATCTCATGA	AGAAAGAACT	1400
TCGTGAGGTC	AAGAAGAAAT	TTGCAACTCC	TCGTTTGAGT	TCTTTAGAAG	1450
AACTGCGAA	AGCAATTGAG	ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	1500
GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	TACATCAAGC	GTACCAGTCC	1550
ACGTTCCCTT	GCGGCTTCCA	CCTTGGAAGA	AATTGGCAAG	CGTGATGATG	1600
ACCGTTTGAT	TTTTGTTC	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1650
TTTACAAGTC	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	1700
TATTCGTTGG	AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	1750
TTGAAACGAA	TGAAGAAATC	CTTTATGTGG	AAGTACTGGA	TCAGTTTGAC	1800
GATGCGACAA	CCTACTTTGC	AGTGACTCGC	CTTGGTCAAA	TCAAACGGGT	1850

AGAGCGAAAA	GAATTCACCTC	CATGGCGGAC	CTATAGATCT	AAGTCTGTCA	1900
AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTAGC	AGTGGCTCCG	1950
ATTAAACTAG	ATGATGTTGT	CTTGGTTAGT	CAAAATGGTT	ATGCCCTGCG	2000
TTTCAATATC	GAAGAGGTTT	CGGTTGTCTG	TGCTAAGGCA	GCAGGTGTCA	2050
AGGCTATGAA	TTTGAAAGAA	GATGATGTCC	TCCAATCTGG	CTTTATCTGT	2100
AATACTTCGT	CCTTCTACCT	CTTGACCCAG	CGTGGGAAGCT	TGAAACGTGT	2150
TTCTATTGAG	GAAATTCTAG	CAACCAGCCG	TGCCAAACGA	GGATTACAAG	2200
TCTTGCGTGA	GTTGAAAAAC	AAACCGCATC	GTGTCTTCTT	GGCAGGAGCA	2250
GTTGCAGAGC	AAGGATTTGT	TGGCGATTTT	TTCAGTACGG	AAGTGGATGT	2300
GAACGACCAA	ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	2350
GCCGATTGCA	AGACTTGAAC	TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	2400
ATTTCTGACA	CGATTTCAAG	TGAAGAAGTT	TTTGACGCTT	ATCTTCAGGA	2450
AGTAGTTACT	GAAGATAAAT	AA			2472

2) INFORMATION FOR SEQ ID NO: 2056

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATTGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGCAC	CAACCAAGCT	GTGGAAACCA	ATCGTGAAGT	GGGTTCAACA	200
ATGAAACCAA	TCACAGACTA	TGCTCCTGCC	TTGGAATACG	GTGTCTACGA	250
TTCAACTGCT	ACTATCGTTC	ACGATGAGCC	CTATAACTAT	CCTGGGACAG	300
ATACCCCTGT	CTATAACTGG	GATAGGGGCT	ACTTTGGCAA	TATCACCTTG	350
CAATACGCCC	TGCAACAATC	GCGAAACGTC	CCAGCCGTGG	AAACACTAAA	400
CAAGGTCGGG	CTCAACCGCG	CCAAGACTTT	TCTAAATGGT	CTCGGAATCG	450
ACTACCCAAG	TATTCACCTA	TCAAATGCCA	TTTCAAGTAA	CACAACCGAG	500
TCAGACAAAA	AATATGGAGC	AAGTAGTGAA	AAGATGGCTG	CTGCTTACGC	550
TGCCTTTGCA	AATGGTGGAA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTTAG	TGATGGAAGT	GAAAAAGAGT	TCTCTAATGT	CGGAACCTCG	650
GCCATGAAAG	AAACGACTGC	TTACATGATG	ACAGAAATGA	TGAAAACAGT	700
CTTGACGTAC	GGAATTGGTC	GTGGTGCCCT	CCTGCCTTGG	CTTCCTCAAG	750
CTGGTAAAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AACTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TATGGACAGG	CTATTCTAAC	CGTCTGACAC	900
CACTTGTAGG	CGATGGCCTT	ACGGTCGCTG	CCAAGGTTTA	CCGCTCTATG	950
ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATAACCAGA	1000
GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTACACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TC				1212

2) INFORMATION FOR SEQ ID NO: 2057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

ATGTAGACCA	AGAAGCTCAA	AAACATCTGT	GGGATATTTA	CAATACAGAC	50
GAATACGTTG	CCTATCCAGA	CGATGAATTG	CAAGTCGCTT	CTACCATTGT	100
TGATGTTTCT	AACGGGAAAG	TTATTGCTCA	GTTAGGTTCT	CGTCACCAAT	150
CAAGCAATGT	TTCCTTCGGA	ATCAACCAAG	CTGTTGAAAC	CAACCGTGAC	200
TGGGGTTCTG	CCATGAAGCC	AATCACAGAC	TATGCTCCTG	CCTTAGAGTA	250
TGACATCTAC	GACTCAACTG	CTTCGATTGT	ACATGATGTT	CCTTATAACT	300
ATCCAGGTAC	TGATACTCCC	CTCTACAACT	GGGATAAAGT	CTACTTTGGA	350
AATATTACAA	TCCAGTATGC	ACTTCAACAG	TCACGTAATG	TCACAGCCGT	400
TGAGACTTTG	AATAAGGTCG	GTCTAGATAG	AGCTAAAACC	TTTCTTAATG	450
GTCTTGGTAT	CGACTATCCA	AGCATGCATT	ATGCAAACGC	CATTTCAAGT	500
AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	AGAAAATGGC	550
TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	AAACCAATGT	600
ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	ATACGCTGAT	650
CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	TGACAGAAAT	700
GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	TATCTCCCTT	750
GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATAC	AGATGATGAA	800
ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCTCCAG	ACGAAATGTT	850
TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	GGTATGGACA	GGTTACTCAA	900
ACCGCCTGAC	TCCTATCGTT	GGTGATGGCT	TCTATGTTGC	AGCTAAGGTT	950
TACCGTTCAA	TGATGACTTA	TCTGTCTGAG	GATAACAACC	CTGGCGACTG	1000
GACTATGCCA	GAAGGTCTCT	ATCGAAGTGG	TGAGTTCGTC	TTTAAAAAAG	1050
GTGCTCGTTC	TGCATGGACT	GCTCCTGCTC	CGCAACAGGC	CCCAACACCA	1100
GAAAGTTCGA	GCTCGACATC	AGAAAGTTCA	ACTTCACAGT	CAAGCTCAAC	1150
TACTCCAAGC	ACGAATAATA	GTGCAAACAA	TAATACCAAT	AACCAGCAAC	1200
CAAATACAAC	GCCTGGTCAA	CAAAACCAGA	ACCAAAATCA	GA	1242

2) INFORMATION FOR SEQ ID NO: 2058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	AATACGTTGC	50
CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	GATGTTTCTA	100
ACGGGAAAGT	TATTGCTCAG	TTAGGTTCTC	GTCACCAATC	AAGCAATGTT	150
TCCTTCGGAA	TCAACCAAGC	TGTTGAAACC	AACCGTGACT	GGGGTTCTGC	200
CATGAAGCCA	ATCACAGACT	ATGCTCCTGC	CTTAGAGTAT	GACATCTACG	250
ACTCAACTGC	TTCGATTGTA	CATGATGTTT	CTTATAACTA	TCCAGGTACT	300
GATACTCCCC	TCTACAACTG	GGATAAAGTC	TACTTTGGAA	ATATTACAAT	350
CCAGTATGCA	CTTCAACAGT	CACGTAATGT	CACAGCCGTT	GAGACTTTGA	400
ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TTCTTAATGG	TCTTGGTATC	450
GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	ATACGACTGA	500
GTCAAACAAA	AAGTACGGAG	CAAGTAGTGA	GAAAATGGCT	GCTGCTTACG	550
CTGCTTTTGC	TAACGGTGGT	ATCTACCATA	AACCAATGTA	TATCAACAAA	600
ATCGTCTTTA	GCGATGGTAG	CTCAAAAGAA	TACGCTGATC	CTGGTACTCG	650
TGCCATGAAA	GAGACGACCG	CCTATATGAT	GACAGAAATG	ATGAAGACTG	700
TCTTGGCATA	CGGAACGGGT	CGTGGTGCTT	ATCTCCCTTG	GCTACCTCAA	750
GCTGGTAAGA	CTGGTACATC	AAACTATACA	GATGATGAAA	TTGAAAACATA	800
CATCAAAAAT	ACTGGTTATG	TAGCTCCAGA	CGAAATGTTT	GTTGGTTATA	850
CTCGCAAATA	TTCAATGGCG	GTATGGACAG	GTTACTCAAA	CCGCCTGACT	900
CCTATCGTTG	GTGATGGCTT	CTATGTTGCA	GCTAAGGTTT	ACCGTTCAAT	950
GATGACTTAT	CTGTCTGAGG	ATAACAACCC	TGGCGACTGG	ACTATGCCAG	1000
AAGGTCTCTA	TCGAAGTGGT	GAGTTCGTCT	TTAAAAAAGG	TGCTCGTTCT	1050
GCATGGACTG	CTCCTGCTCC	GCAACAGGCC	CCAACACCAG	AAAGTTCGAG	1100
CTCGACATCA	GAAAGTTCAA	CTTCACAGTC	AAGCTCAACT	ACTCCAAGCA	1150
CGAATAATAG	TGCAAACAAT	AATACCAATA	ACCAGCAACC	AAATACAACG	1200
CCTGGTCAAC	AAAACCAGAA	CCAAA			1225

2) INFORMATION FOR SEQ ID NO: 2059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

TGGCTACTTT	GGAAACATTA	CAGTCCAGTA	TGCTCTTCAA	CAATCACGAA	50
ATGTCACAGC	CGTTGAGACT	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	100
ACCTTCCTCA	ATGGACTTGG	TATCGATTAT	CCAAGCATGC	TTTATGCAAA	150
CGCCATTTCA	AGTAACACAA	CTGAATCCAA	CAAAAAGTAC	GGAGCAAGTA	200
GTGAAAAAAT	GGCCGCTGCC	TACGCAGCTT	TTGCTAATGG	TGGTACTTAC	250
CACAAACCAA	TGTATATCAA	TAAAATCGTC	TTTAGTGATG	GTAGTGAAAA	300
AGAATTTTCT	GATGCCGGTA	CTCGGGCTAT	GAAAGAACT	ACTGCCTATA	350

TGATGACCGA	AATGATGAAA	ACTGTCTTAT	TATACGGAAC	CGGACGTGGA	400
GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	450
TACTGACGAA	GAAATTGAAA	AGTATATCAA	GAATGCTGGT	TACGTAGCTC	500
CAGATGAAAT	GTTTGTTGGT	TATACCCGCA	AATATGCAAT	GGCTGTTTGG	550
ACAG					554

2) INFORMATION FOR SEQ ID NO: 2060

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

CAACTGGGAT	GGATGTCTAC	ACAAATGTAG	ACCAAGAAGC	TCAAAAACAT	50
CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	100
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	150
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	200
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	250
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	300
TCGTTACGGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	350
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	400
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	450
ACCGCGCCAA	GACTTTCCTA	AATGGTCTAG	GAATCGACTA	CCCAAGTATT	500
CACTACTCAA	ATGCCATTTC	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	550
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	600
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	650
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	700
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	750
CTGGACGAAA	TGCCTATCTT	GCTTGGCTCC	CTCAGGCTGG	TAAAACAGGA	800
ACCTCTAACT	ATACAGACGA	GGAAATTGAA	AACCACATCA	AGACCTCTCA	850
ATTTGTAGCA	CCTGATGAAC	TATTTGCTGG	CTATACGCGT	AAATATTCAA	900
TGGCTGTATG	GACAGGCTAT	TCTAACCGTC	TGACACCACT	TGTAGGCAAT	950
GGCCTTACGG	TCGCTGCCAA	AGTTTACCGC	TCTATGATGA	CCTACCTGTC	1000
TGAAGGAAGC	AATCCAGAAG	ATTGGAATAT	ACCAGAGGGG	CTCTACAGAA	1050
ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	GTTCTACGTG	GAGCTCACCT	1100
GCTCCACAAC	AACCCCCATC	AACTGAAAGT	TCAAGCTCAT	CATCAGATAG	1150
TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	AAGCACAAAT	AATAGTACGA	1200
CTACCAATCC	TAACAATAAT	ACGCAACAAT	CAAATACAAC	CCCTGATCA	1249

2) INFORMATION FOR SEQ ID NO: 2061

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

1069

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

GAAGTTGAAC	AGACTGGTCA	CCAAGCTCCT	TCATATCCGC	CAACACTGCA	50
ATTTTCTTGC	CACCTTCATT	GGCTGGAATG	GCAGAGAAAG	TCTCTAAAAT	100
CAGTTTCATA	GCAGTTGGAT	TGGCATTATA	AACATCTGAC	AGGATATCTG	150
CTCCATTGGC	TGCTTTCTTC	CACTCGGTAC	GGTTACGCGT	CAATTCAAGA	200
TGTTGGAAGG	CCAAACGAAT	TTGCTCCTCT	GAAACTCCTT	CTTGCAAGGC	250
AACATAGGAT	GCAATCATAG	CATTTGTGCG	ATTGTACTTG	CCAGTTACTG	300
GCAAATCAAG	GGCTTGCTCT	AAGAAATTGA	CCTTGAAGGT	CAGACTATCT	350
TTGCGCTCAA	CCAAGTCGGT	AATTCCCAGC	TCTGCTCCTT	GACCAAAACG	400
AACCACCTTT	TTATCAGTTG	GCAAATAGTC	CTCTACGATA	GGGTCAGCCG	450
GCGCTAAAAG	CAAGGAACCT	GAAGCCATTC	CGTCTGCAAT	TTGCATTTTT	500
CCTTTAGCAA	TCTCAGAACG	GTCTTTGAAA	AAGGCCAAAT	GAGCTTCTCC	550
AACCAAGGTC	ACGATGGCTG	TATGGACAG			579

2) INFORMATION FOR SEQ ID NO: 2062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCACAAAC	TTGGTGCTCG	TCATCAAGCA	AGTAATGTTT	150
CATTTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	GGGATCATCA	200
ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	GAGTCTATGA	250
CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	CCTGGCACTG	300
ATACTCCACT	CTACAACTGG	GATCATGTCT	ACTTTGGAAA	CATTACAATC	350
CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	CACAACTGAA	500
TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	CTGCCTACGC	550
TGCTTTTGGT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	ATCAATAAAA	600
TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	TGGTACACGA	650
GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	TGAAAACTGT	700
TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	CTTCCACAAG	750

CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AGCTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TTTGGACAGG	ATACTCAAAT	CGTCTAACTC	900
CAATCATCGG	AGATGGTTTC	CTTGTTGCTG	GTAAAGTCTA	TGTTTCAATG	950
ATAACTTACC	TTTCTGAAGA	TGACCAACCT	GGAGATTGGA	CAATGCCAGA	1000
TGGCTTGTAT	AGAAATGGAG	AATTTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTACACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TCAACA				1216

2) INFORMATION FOR SEQ ID NO: 2063

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

AATACGTCTC	TTACCCTGAC	GATGATTTGC	AAGTCGCATC	CACGGTCGTA	50
GATGTTTCAA	ATGGTAAAGT	CATCGCCCAA	CTTGGAGCTC	GTCACCAAGC	100
AAGTAACGTT	TCATTTGGTA	CCAACCAAGC	TGTGGAAACC	AATCGTGACT	150
GGGGTTCAAC	AATGAAACCC	ATCACCGATT	ATGCACCTGC	CATAGAATAC	200
GGTGTATATG	ATTCCACTGC	AACTATGGTT	AATGATATTC	CTTATAACTA	250
TCCGGGAACA	AGCACACCTG	TCTACAACTG	GGATCGAGCA	TATTTTGGTA	300
ATATTACTCT	GCAATATGCC	CTTCAACAAT	CTCGTAACGT	ACCCGCCGTT	350
GAGACACTAA	ACAAGGTTGG	TTTAGATAGA	GCTAAAAGTT	TCCTAAATGG	400
TTTAGGAATC	GACTATCCTG	TAATGCACTA	TTCAAATGCT	ATTTCAAGTA	450
ATACTACCGA	ATCTAGTAAA	CAGTACGGGG	CAAGTAGTGA	AAAAATGGCC	500
ACTGCCTATG	CCGCATTTCG	AAACGGCGGT	ATTTACCACA	AACCAATGTA	550
CATCAATAAG	GTTGTCTTTA	GCGATGGTAG	CGAAAAAGAA	TTTTCTGACC	600
CTGGCACAAG	AGCCATGAAA	GAAACGACTG	CTTACATGAT	GACAGAGATG	650
ATGAAAACAG	TCTGGACTTA	CGGAACTGGT	CGCGGTGCCT	ACCTACCTTG	700
GCTTCCACAA	GCAGGTAAAA	CAGGTACTTC	TAATACTACT	GACGAAGAAA	750
TTGAAAAGTA	TATCAAGAAC	ACTGGTTACG	TAGCTCCAGA	TGAAATGTTT	800
GTAGGGTATA					810

2) INFORMATION FOR SEQ ID NO: 2064

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	TAGATGTTTC	50
AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	GCAAGTAACG	100
TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	CTGGGGATCA	150
ACTATGAAAC	CAATCACAGA	CTATGCTCCT	GCCTTGGAGT	ACGGTGTCTA	200
CGATTCAACT	GCTACTATCG	TTCACGATGA	GCCCTATAAC	TACCCTGGGA	250
CAGATATCCC	TCTCTATAAC	TGGGATCGAG	CATATTTCCG	TAATATTACT	300
CTGCAATATG	CCCTTCAACA	ATCTCGTAAC	GTACCTGCCG	TTGAAACACT	350
AAACAAGGTC	GGTCTAGATA	AGGCTAAAAC	CTTCCTTAAT	GGTCTTGGTA	400
TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	TAATACAACT	450
GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATAG	CTACCGCCTA	500
TGCCGCATTC	GCAAATGGTG	GTATTTACCA	CAAACCAATG	TACATCAATA	550
AAGTTGTCTT	TAGCGATGGT	AGCGAAAAAG	AATTTTCTGA	CCCTGGCACA	600
AGAGCCATGA	AAGAAACGAC	TGCTTACATG	ATGACAGAAA	TGATGAAAAC	650
AGTCTGGACG	TACGGAACGT	GTCGTGGTGC	CTACCTGCCT	TGGCTTCCTC	700
AAGCTGGTAA	AACAGGTACC	TCTAACTATA	CTGACGAAGA	AATTGAAAAG	750
TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GA		782

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA

22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA

22

2) INFORMATION FOR SEQ ID NO: 2067

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

2) INFORMATION FOR SEQ ID NO: 2068

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAC

19

2) INFORMATION FOR SEQ ID NO: 2069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

2) INFORMATION FOR SEQ ID NO: 2070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTTGACCCAC AAGCGCCG

18

2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

GTGCTGGAAG	GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	50
TAGTCCTAGT	CCGAGTCGCC	CGCAAAGTTC	CTCGAATAAC	TCCGTACCCG	100
GAGCGCCAAA	CCGGGTCTCC	TTCGCTAAGC	TGCGCGAACC	ACTTGAGGTT	150
CCGGGACTCC	TTGACGTCCA	GACCGATTCT	TTCGAGTGGC	TGATCGGTTC	200
GCCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AACCCAGTGG	250
GTGGCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC	300
GGGTCGATGT	CGTTGTCTGT	CTCTGACCTT	CGTTTCGACG	ATGTCAAGGC	350
ACCCGTCGAC	GAGTGCAAAG	ACAAGGACAT	GACGTACGCG	GCTCCACTGT	400
TCGTCAACGC	CGAGTTCATC	AACAACAACA	CCGGTGAGAT	CAAGAGTCAG	450
ACGGTGTTCA	TGGGTGACTT	CCCGATGATG	ACCGAGAAGG	GCACGTTTCAT	500
CATCAACGGG	ACCGAGCGTG	TGGTGGTCAG	CCAGCTGGTG	CGGTGCGCCG	550
GGGTGTACTT	CGACGAGACC	ATTGACAAGT	CCACCGACAA	GACGCTGCAC	600
AGCGTCAAGG	TGATCCCGAG	CCGCGGCGCG	TGGCTCGAGT	TTGACGTCGA	650
CAAGCGCGAC	ACCGTCGGCG	TGCGCATCGA	CCGCAAACGC	CGGCAACCCG	700

TCACCGTGCT	GCTCAAGGCG	CTGGGCTGGA	CCAGCGAGCA	GATTGTTCGAG	750
CGGTTCCGGT	TCTCCGAGAT	CATGCGATCG	ACGCTGGAGA	AGGACAACAC	800
CGTCGGCACC	GACGAGGCGC	TGTTGGACAT	CTACCGCAAG	CTGCGTCCGG	850
GCGAGCCCCC	GACCAAAGAG	TCAGCGCAGA	CGCTGTTGGA	AAACTTGTTT	900
TTCAAGGAGA	AGCGCTACGA	CCTGGCCCCG	GTCGGTCGCT	ATAAGGTCAA	950
CAAGAAGCTC	GGGCTGCATG	TCGGCGAGCC	CATCACGTCG	TCGACGCTGA	1000
CCGAAGAAGA	CGTCGTGGCC	ACCATCGAAT	ATCTGGTCCG	CTTGACGAG	1050
GGTCAGACCA	CGATGACCGT	TCCGGGCGGC	GTCGAGGTGC	CGGTGGAAAC	1100
CGACGACATC	GACCACTTCG	GCAACCGCCG	CCTGCGTACG	GTCGGCGAGC	1150
TGATCCAAAA	CCAGATCCGG	GTCGGCATGT	CGCGGATGGA	GCGGGTGGTC	1200
CGGGAGCGGA	TGACCACCCA	GGACGTGGAG	GCGATCACAC	CGCAGACGTT	1250
GATCAACATC	CGGCCGGTGG	TCGCCGCGAT	CAAGGAGTTC	TTCGGCACCA	1300
GCCAGCTGAG	CCAATTCATG	GACCAGAACA	ACCCGCTGTC	GGGGTTGACC	1350
CACAAGCGCC	GACTGTCCGC	GCTGGGGCCC	GGCGGTCTGT	CACGTGAGCG	1400
TGCCGGGCTG	GAGGTCCGCG	ACGTGCACCC	GTCGCACTAC	GGCCGGATGT	1450
GCCCCGATCGA	AACCCCTGAG	GGGCCCAACA	TCGGTCTGAT	CGGCTCGCTG	1500
TCGGTGTACG	CGCGGGTCAA	CCCGTTCCGG	TTCATCGAAA	CGCCGTACCG	1550
CAAGGTGGTC	GACGGCGTGG	TTAGCGACGA	GATCGTGTAC	CTGACCGCCG	1600
ACGAGGAGGA	CCGCCACGTG	GTGGCACAGG	CCAATTCGCC	GATCGATGCG	1650
GACGGTCGCT	TCGTGAGGCC	GCGCGTGCTG	GTCCGCCGCA	AGGCGGGCGA	1700
GGTGGAGTAC	GTGCCCTCGT	CTGAGGTGGA	CTACATGGAC	GTCTCGCCCC	1750
GCCAGATGGT	GTCGGTGGCC	ACCGCGATGA	TTCCCTTCCT	GGAGCACGAC	1800
GACGCCAACC	GTGCCCTCAT	GGGGGCAAAC	ATGCAGCGCC	AGGCGGTGCC	1850
GCTGGTCCGT	AGCGAGGCCC	CGCTGGTGGG	CACCGGGATG	GAGCTGCGCG	1900
CGCGGATCGA	CGCGGCGACG	TCGTGCTCGC	AAGAAAGCGG	CGTCATCGAG	1950
GAGGTGTCGG	CCGACTACAT	CACTGTGATG	CACGACAACG	GCACCCGGCG	2000
TACCTACCGG	ATGCGCAAGT	TTGCCCGGTC	CAACCACGGC	ACTTGCGCCA	2050
ACCAAGTCCC	CATCGTGGAC	GCGGGCGACC	GAGTCGAGGC	CGGTGAGGTG	2100
ATCGCCGACG	GTCCCTGTAC	TGACGACGGC	GAGATGGCGC	TGGGCAAGAA	2150
CCTGCTGGTG	GCCATCATGC	CGTGGGAGGG	CCACAACCTAC	GAGGACGCGA	2200
TCATCCTGTC	CAACCGCCTG	GTCGAAGAGG	ACGTGCTCAC	CTCGATCCAC	2250
ATCGAGGAGC	ATGAGATCGA	TGCTCGCGAC	ACCAAGCTGG	GTGCGGAGGA	2300
GATCACCCGC	GACATCCCGA	ACATCTCCGA	CGAGGTGCTC	GCCGACCTGG	2350
ATGAGCGGGG	CATCGTGC GC	ATCGGTGCCG	AGGTTCGCGA	CGGGGACATC	2400
CTGGTTCGGCA	AGGTCACCCC	GAAGGGTGAG	ACCGAGCTGA	CGCCGGAGGA	2450
GCGGCTGCTG	CGTGCCATCT	TCGGTGAGAA	GGCCCGCGAG	GTGCGCGACA	2500
CTTCGCTGAA	GGTGCCGCAC	GGCGAATCCG	GCAAGGTGAT	CGGCATTTCG	2550
GTGTTTTTCCC	GCGAGGACGA	GGACGAGTTG	CCGGCCGGTG	TCAACGAGCT	2600
GGTGCGTGTG	TATGTGGCTC	AGAAACGCAA	GATCTCCGAC	GGTGACAAGC	2650
TGGCCGGCCG	GCACGGCAAC	AAGGGCGTGA	TCGGCAAGAT	CCTGCCGGTT	2700
GAGGACATGC	CGTTCCCTTG	CGACGGCACC	CCGGTGGACA	TTATTTTGA	2750
CACCCACGGC	GTGCCGCGAC	GGATGAACAT	CGGCCAGATT	TTGGAGACCC	2800
ACCTGGGTTG	GTGTGCCCCA	AGCGGCTGGA	AGGTGACGCG	CGCCAAGGGG	2850
GTTCCGGACT	GGGCCGCCAG	GCTGCCCGAC	GAAGTGTCTG	AGGCGCATGC	2900
GAACGCCATT	GTGTCGACGC	CGGTGTTTGA	CGGCGCCAG	GAGGCCGAGC	2950
TGCAGGGCCT	GTTGTGCTGC	ACGCTGCCCC	ACCGCGACGG	TGACGTGCTG	3000
GTCGACGCCG	ACGGCAAGGC	CATGCTCTTC	GACGGGCGCA	GCGGCGAGCC	3050
GTTCCCGTAC	CCGGTCACGG	TTGGCTACAT	GTACATCATG	AAGCTGCACC	3100
ACCTGGTGGA	CGACAAGATC	CACGCCCCGCT	CCACCGGGCC	GTACTCGATG	3150
ATCACCCAGC	AGCCGCTGGG	CGGTAAGGCG	CAGTTCGGTG	GCCAGCGGTT	3200
CGGGGAGATG	GAGTGCTGGG	CCATGCAGGC	CTACGGTGCT	GCCTACACCC	3250
TGCAGGAGCT	GTTGACCATC	AAGTCCGATG	ACACCGTCGG	CCGCGTCAAG	3300
GTGTACGAGG	CGATCGTCAA	GGGTGAGAAC	ATCCCGGAGC	CGGGCATCCC	3350
CGAGTCGTTC	AAGGTGCTGC	TCAAAGAACT	GCAGTCGCTG	TGCCTCAACG	3400
TCGAGGTGCT	ATCGAGTGAC	GGTGCGGCGA	TCGAACTGCG	CGAAGGTGAG	3450
GACGAGGACC	TGGAGCGGGC	CGCGGCCAAC	CTGGGAATCA	ATCTGTCCCG	3500
CAACGAATCC	GCAAGTTTCG	AGGATCTTGC	GTAA		3534

2) INFORMATION FOR SEQ ID NO: 2073

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2074

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2075

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G

41

2) INFORMATION FOR SEQ ID NO: 2076

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1076

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTTCA GATTCACCCA RCGCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

2) INFORMATION FOR SEQ ID NO: 2080

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

2) INFORMATION FOR SEQ ID NO: 2081

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

2) INFORMATION FOR SEQ ID NO: 2082

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

2) INFORMATION FOR SEQ ID NO: 2083

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTCGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACGCGTCAA CACCCGTACA AGTCGTCTTT TGCGCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAAACCTAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTTG CATCACCTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 2087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

2) INFORMATION FOR SEQ ID NO: 2088

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

2) INFORMATION FOR SEQ ID NO: 2089

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAACT TATTGACCTT

20

2) INFORMATION FOR SEQ ID NO: 2090

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAAGTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAACTTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

2) INFORMATION FOR SEQ ID NO: 2094

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTTCT TGACCTACTT TCAA

24

2) INFORMATION FOR SEQ ID NO: 2095

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

2) INFORMATION FOR SEQ ID NO: 2096

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

2) INFORMATION FOR SEQ ID NO: 2097

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1185 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1082

(A) ORGANISM: *Mycoplasma pneumoniae*
 (B) STRAIN: ATCC 29342
 (C) ACCESSION NUMBER: AE000019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

ATGGCAAGAG	AGAAATTTGA	CCGATCTAAA	CCCCACGTTA	ATGTAGGTAC	50
TATTGGCCAC	ATTGACCACG	GTAAAACAAC	TTTAACAGCA	GCTATTTGTA	100
CTGTATTAGC	AAAAGAAGGT	AAATCAGCTG	CTACTCGTTA	CGACCAAATC	150
GATAAGGCTC	CGGAAGAAAA	AGCACGGGGA	ATTACGATTA	ACTCCGCTCA	200
CGTGAGGTAC	TCCTCTGACA	AGCGTCACTA	TGCTCACGTT	GACTGTCCAG	250
GACACGCTGA	CTACATTAAG	AACATGATTA	CTGGTGCTGC	ACAAATGGAT	300
GGTGCCATTC	TAGTAGTTTC	AGCAACTGAC	AGTGTTATGC	CCCAAACCCG	350
TGAACACATT	TTGTTGGCCC	GCCAAGTGGG	TGTGCCACGC	ATGGTAGTGT	400
TCCTAAACAA	GTGTGACATT	GCAACTGATG	AAGAAGTGCA	AGAGTTAGTA	450
GCAGAAGAGG	TACGTGACTT	ATTAACTTCT	TACGGCTTTG	ATGGCAAGAA	500
CACCCCTATT	ATTTATGGTT	CTGCACTTAA	AGCGCTTGAA	GGTGATCCTA	550
AGTGGAAGC	TAAGATCCAT	GATTTAATGA	ATGCAGTTGA	TGAATGGATT	600
CCAACTCCTG	AACGTGAAGT	GGACAAACCC	TTCTTGTTGG	CAATCGAAGA	650
CACCATGACG	ATTACTGGCC	GTGGTACCGT	GGTTACCGGT	CGGGTTGAAC	700
GTGGTGAATT	GAAAGTAGGT	CAAGAAATTG	AAATCGTTGG	TTTACGTCCA	750
ATCCGTAAAG	CAGTTGTTAC	CGGAATCGAA	ATGTTCAAAA	AGGAACTTGA	800
TTCAGCAATG	GCTGGGGACA	ACGCTGGGGT	ATTACTCCGT	GGTGTGGACC	850
GTAAAGAAGT	GGAACGTGGT	CAAGTGTTAG	CTAAACCAGG	TTCGATTAAA	900
CCGCACAAGA	AATTTAAAGC	GGAAATCTAT	GCTTTAAAGA	AGGAAGAAGG	950
TGGTCGTCAC	ACCGGTTTCT	TAAACGGTTA	CCGTCCCCAA	TTCTACTTCC	1000
GTACTACAGA	CGTTACTGGT	TCGATTTCCC	TACCAGAAAA	CACCGAAATG	1050
GTGCTACCAG	GTGACAATAC	CTCGATTACA	GTTGAACTAA	TTGCACCAAT	1100
TGCTTGTGAA	AAAGGTAGTA	AGTTCTCCAT	CCGTGAAGGT	GGTCGAACGG	1150
TTGGTGCTGG	TTCAGTCACG	GAAGTGCTTG	AATAG		1185

2) INFORMATION FOR SEQ ID NO: 2098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

2) INFORMATION FOR SEQ ID NO: 2099

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

CAGCCCGCGA	GCGTAACCTG	GCTGCGATTT	CCGGCGCGGA	TTTTCGCAGT	50
GCGGTTACGC	TCGGAAAGCG	CGGGCCTCGC	CCACGCGGCG	GATGATGTCA	100
GCGGGGTGGT	CCTCGGCGAC	GACCCGAC	ACGATCCACC	CGTAGCGGTG	150
CTGGACTTTC	TCGTGCCGGA	GGATGTCTTT	CCGGTAGTGG	TAGCGACTGG	200
TCAGATGGTG	GTCGCCGTCA	TACTCGGCCG	CGACCTTGAT	GTCTTGCCAG	250
CCCATATCCA	AATGGGCTTC	CGCCCAGCCC	CATTCGTTGC	GCACCGCGAT	300
CTGCGTCTGG	GGGCGCGGAA	AGCCGGCGCG	GATCAACAAC	AAGCGCAGCC	350
AGGTTTCCTT	GGGGGACTGG	GCACCGCCGT	CGACGAGGTC	CAGAGCGGCT	400
CTTGCGGCCT	TCATGCCACG	GCGGCCCGGA	TAGCGCTCGA	TCAGCGGCTC	450
GACGTCGGCC	ACCTTCAAAT	CGGTGGCCTG	TATCAGGGCG	TCGACGGCCG	500
CGACGGCGGG	GTCCAATGGA	AATCGACTGG	TCAGGTCGAG	CGCCGTTTCG	550
TCCGGTGTGG	TCACGCGCAT	GCCCTCGATG	ACGCAGATCT	CGTCGGGCTC	600
GATGCGCTCT	TCCCAGACTT	GCAGCCCCGG	GGCACGGCGG	CGGTTGGTGT	650
CGATGATCGC	GGCGGGAAGA	TCCGCGTCGA	TCCACTTGGC	GCCATGGAAG	700
GCAGAAGCCG	AGTAGCCGGC	CAGCACGCCG	CGGCGGCGCG	AGCGCAGCCA	750
CAGCGCTTTT	GCACGCAATT	GCGCGGTCAG	TTCCACACCC	TGCGGCACGT	800

1084

ACACGTCTTT	ATGTAGCGCG	ACATACCTGC	TGCGCAATTC	GTAGGGCGTC	850
AATACACCCG	CAGCCAGGGC	CTCGCTGCCC	AGAAAGGGAT	CCGTCATGGT	900
CGAAGTGTGC	TGAGTCACAC	CGACAAACGT	CACGAGCGTA	ACCCAGTGC	950
GAAAGTTCCC	GCCGGAAATC	GCAGCCACGT	TACGCTCGTG	GACATACCGA	1000
TTTCGGCCCC	GCCGCGGCGA	GACGATAGGT	TGTCGGGGTG	ACTGCCACAG	1050
CCACTGAAGG	GGCCAAACCC	CCATTCGTAT	CCCGTTCAGT	CCTGGTTACC	1100
GGAGGAAACC	GGGGGATCGG	GCTGGCGATC	GCACAGCGGC	TGGCTGCCGA	1150
CGGCCACAAG	GTGGCCGTCA	CCCACCGTGG	ATCCGGAGCG	CCAAAGGGGC	1200
TGTTTGGCGT	CGAATGTGAC	GTCACCGACA	GCGACGCCGT	CGATCGCGCC	1250
TTCACGGCGG	TAGAAGAGCA	CCAGGGTCCG	GTCGAGGTGC	TGGTGTCCAA	1300
CGCCGGCCTA	TCCGCGGACG	CATTCCCTCAT	GCGGATGACC	GAGGAAAAGT	1350
TCGAGAAGGT	CATCAACGCC	AACCTCACCG	GGGCGTTCCG	GGTGGCTCAA	1400
CGGGCATCGC	GCAGCATGCA	GCGCAACAAA	TTCGGTTCGAA	TGATATTCAT	1450
AGGTTTCGGTC	TCCGGCAGCT	GGGGCATCGG	CAACCAGGCC	AACTACGCAG	1500
CCTCCAAGGC	CGGAGTGATT	GGCATGGCCC	GCTCGATCGC	CCGCGAGCTG	1550
TCGAAGGCAA	ACGTGACCGC	GAATGTGGTG	GCCCCGGGCT	ACATCGACAC	1600
CGATATGACC	CGCGCGCTGG	ATGAGCGGAT	TCAGCAGGGG	GCGCTGCAAT	1650
TTATCCCAGC	GAAGCGGGTC	GGCACCCCCG	CCGAGGTCGC	CGGGGTGGTC	1700
AGCTTCCTGG	CTTCCGAGGA	TGCGAGCTAT	ATCTCCGGTG	CGGTCATCCC	1750
GGTCGACGGC	GGCATGGGTA	TGGGCCACTG	ACACAACACA	AGGACGCACA	1800
TGACAGGACT	GCTGGACGGC	AAACGGATTC	TGGTTAGCGG	AATCATCACC	1850
GACTCGTCGA	TCGCGTTTCA	CATCGCACGG	GTAGCCCAGG	AGCAGGGCGC	1900
CCAGCTGGTG	CTCACCGGGT	TCGACCGGCT	GCGGCTGATT	CAGCGCATCA	1950
CCGACCGGCT	GCCGGCAAAG	GCCCCGCTGC	TCGAACTCGA	CGTGCAAAAC	2000
GAGGAGCACC	TGGCCAGCTT	GGCCGGCCGG	GTGACCGAGG	CGATCGGGGC	2050
GGGCAACAAG	CTCGACGGGG	TGGTGCAATC	GATTGGGTTC	ATGCCGCAGA	2100
CCGGGATGGG	CATCAACCCG	TTCTTCGACG	CGCCCTACGC	GGATGTGTCC	2150
AAGGGCATCC	ACATCTCGGC	GTATTCGTAT	GCTTCGATGG	CCAAGGCGCT	2200
GCTGCCGATC	ATGAACCCCG	GAGGTTCCAT	CGTCGGCATG	GACTTCGACC	2250
CGAGCCGGGC	GATGCCGGCC	TACAACCTGA	TGACGGTCGC	CAAGAGCGCG	2300
TTGGAGTCGG	TCAACAGGTT	CGTGCGCGCG	GAGGCCGGCA	AGTACGGTGT	2350
GCGTTCGAAT	CTCGTTGCCG	CAGGCCCTAT	CCGGACGCTG	GCGATGAGTG	2400
CGATCGTCGG	CGGTGCGCTC	GGCGAGGAGG	CCGGCGCCCA	GATCCAGCTG	2450
CTCGAGGAGG	GCTGGGATCA	GCGCGCTCCG	ATCGGCTGGA	ACATGAAGGA	2500
TGCGACGCCG	GTCGCCAAGA	CGGTGTGCGC	GCTGCTGTCT	GACTGGCTGC	2550
CGGCGACCAC	GGGTGACATC	ATCTACGCCG	ACGGCGGCGC	GCACACCCAA	2600
TTGCTCTAG					2609

2) INFORMATION FOR SEQ ID NO: 2102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

2) INFORMATION FOR SEQ ID NO: 2103

1085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCAGCG GAAATAGTTG GAC

23

2) INFORMATION FOR SEQ ID NO: 2104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CICGAGTC

18

2) INFORMATION FOR SEQ ID NO: 2105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37rv
- (C) ACCESSION NUMBER: U68480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

ATGACACAGT	GCGCGAGCAG	ACGCAAAGC	ACCCCAAATC	GGGCGATTTT	50
GGGGGCTTTT	GCGTCTGCTC	GCGGGACGCG	CTGGGTGGCC	ACCATCGCCG	100
GGCTGATTGG	CTTTGTGTTG	TCGGTGGCGA	CGCCGCTGCT	GCCCGTCGTG	150
CAGACCACCG	CGATGCTCGA	CTGGCCACAG	CGGGGGCAAC	TGGGCAGCGT	200
GACCGCCCCG	CTGATCTCGC	TGACGCCGGT	CGACTTTACC	GCCACCGTGC	250
CGTGCGACGT	GGTGCGCGCC	ATGCCACCCG	CGGGCGGGGT	GGTGCTGGGC	300
ACCGCACCCA	AGCAAGGCAA	GGACGCCAAT	TTGCAGGCGT	TGTTTCGTCT	350
CGTCAGCGCC	CAGCGCGTGG	ACGTCACCGA	CCGCAACGTG	GTGATCTTGT	400
CCGTGCCGCG	CGAGCAGGTG	ACGTCCCCGC	AGTGTC AACG	CATCGAGGTC	450

1086

ACCTCTACCC	ACGCCGGCAC	CTTCGCCAAC	TTCGTCGGGC	TCAAGGACCC	500
GTCGGGCGCG	CCGCTGCGCA	GCGGCTTCCC	CGACCCCAAC	CTGCGCCCCG	550
AGATTGTCGG	GGTGTTTACC	GACCTGACCG	GGCCCCGCGC	GCCCCGGGCTG	600
GCGGTCTCGG	CGACCATCGA	CACCCGGTTC	TCCACCCGGC	CGACCACGCT	650
GAAACTGCTG	GCGATCATCG	GGGCGATCGT	GGCCACCGTC	GTCGCACTGA	700
TCGCGTTGTG	GCGCCTGGAC	CAGTTGGACG	GGCGGGGCTC	AATTGCCCCAG	750
CTCCTCCTCA	GGCCGTTCCG	GCCTGCATCG	TCGCCGGGCG	GCATGCGCCG	800
GCTGATTCCG	GCAAGCTGGC	GCACCTTCAC	CCTGACCGAC	GCCGTGGTGA	850
TATTCGGCTT	CCTGCTCTGG	CATGTCATCG	GCGCGAATTC	GTCGGACGAC	900
GGCTACATCC	TGGGCATGGC	CCGAGTCGCC	GACCACGCCG	GCTACATGTC	950
CAACTATTTT	CGCTGGTTCG	GCAGCCCCGA	GGATCCCTTC	GGCTGGTATT	1000
ACAACCTGCT	GGCGCTGATG	ACCCATGTCA	GCGACGCCAG	TCTGTGGATG	1050
CGCCTGCCAG	ACCTGGCCCG	CGGGCTAGTG	TGCTGGCTGC	TGCTGTGCGG	1100
TGAGGTGCTG	CCCCGCCTCG	GGCCGGCGGT	GGAGGCCAGC	AAACCCGCCT	1150
ACTGGGCGGC	GGCCATGGTC	TTGCTGACCG	CGTGGATGCC	GTTCAACAAC	1200
GGCCTGCGGC	CGGAGGGCAT	CATCGCGCTC	GGCTCGCTGG	TCACCTATGT	1250
GCTGATCGAG	CGGTCCATGC	GGTACAGCCG	GCTCACACCG	GCGGCGCTGG	1300
CCGTCGTTAC	CGCCGCATTC	ACACTGGGTG	TGCAGCCAC	CGGCCTGATC	1350
GCGGTGGCCG	CGCTGGTGGC	CGGCGGCCGC	CCGATGCTGC	GGATCTTGGT	1400
GCGCCGYCAT	CGCCTGGTCG	GCACGTTGCC	GTTGGTGTGC	CCGATGCTGG	1450
CCGCCGGCAC	CGTCATCCTG	ACCGTGGTGT	TCGCCGACCA	GACCCTGTCA	1500
ACGGTGTTGG	AAGCCACCAG	GGTTCGCGCC	AAAATCGGGC	CGAGCCAGGC	1550
GTGGTATACC	GAGAACCTGC	GTTACTACTA	CCTCATCCTG	CCCACCGTCG	1600
ACGGTTCGCT	GTCGCGGCGC	TTCGGCTTTT	TGATCACCGC	GCTATGCCTG	1650
TTCACCGCGG	TGTTTCATCAT	GTTGCGGCGC	AAGCGAATTC	CCAGCGTGGC	1700
CCGCGGACCG	GCGTGGCGGC	TGATGGGCGT	CATCTTCGGC	ACCATGTTCT	1750
TCCTGATGTT	CACGCCACC	AAGTGGGTGC	ACCACTTCGG	GCTGTTCCGC	1800
GCCGTAGGGG	CGGCGATGGC	CGCGCTGACG	ACGGTGTTGG	TATCCCCATC	1850
GGTGCTGCGC	TGGTCGCGCA	ACCGGATGGC	GTTCTTGCGG	GCGTTATTCT	1900
TCCTGCTGGC	GTTGTGTTGG	GCCACCACCA	ACGGCTGGTG	GTATGTCTCC	1950
AGCTACGGTG	TGCCGTTCAA	CAGCGCGATG	CCGAAGATCG	ACGGGATCAC	2000
AGTCAGCACA	ATCTTTTTTC	CCCTGTTTGC	GATCGCCGCC	GGCTATGCGG	2050
CCTGGCTGCA	CTTCGCGCCC	CGCGGCGCCG	GCGAAGGGCG	GCTGATCCGC	2100
GCGCTGACGA	CAGCCCCGGT	ACCGATCGTG	GCCGGTTTCA	TGGCGGCGGT	2150
GTTTCGTCGG	TCCATGGTGG	CCGGGATCGT	GCGACAGTAC	CCGACCTACT	2200
CCAACGGCTG	GTCCAACGTG	CGGGCGTTTG	TCGGCGGCTG	CGGACTGGCC	2250
GACGACGTAC	TCGTGAGGCC	TGATACCAAT	GCGGGTTTCA	TGAAGCCGCT	2300
GGACGGCGAT	TCGGGTTCCT	GGGGCCCCCT	GGGCCCGCTG	GGTGGAGTCA	2350
ACCCGGTCGG	CTTCACGCCC	AACGGCGTAC	CGGAACACAC	GGTGGCCGAG	2400
GCGATCGTGA	TGAAACCCAA	CCAGCCCCGG	ACCGACTACG	ACTGGGATGC	2450
GCCGACCAAG	CTGACGAGTC	CTGGCATCAA	TGGTTCTACG	GTGCCGCTGC	2500
CCTATGGGCT	CGATCCCGCC	CGGGTACCGT	TGGCAGGCAC	CTACACCACC	2550
GGCGCACAGC	AACAGAGCAC	ACTCGTCTCG	GCGTGGTATC	TCCTGCCTAA	2600
GCCGGACGAC	GGGCATCCGC	TGGTCGTGGT	GACCGCCGCG	GGCAAGATCG	2650
CCGGCAACAG	CGTGCTGCAC	GGGTACACCC	CCGGGCAGAC	TGTGGTGCTC	2700
GAATACGCCA	TGCCGGGACC	CGGAGCGCTG	GTACCCGCCG	GGCGGATGGT	2750
GCCCCGACGAC	CTATACGGAG	AGCAGCCCAA	GGCGTGCGCG	AACCTGCGCT	2800
TCGCCCCGAGC	AAAGATGCCC	GCCGATGCCG	TCGCGGTCCG	GGTGGTGGCC	2850
GAGGATCTGT	CGCTGACACC	GGAGGACTGG	ATCGCGGTGA	CCCCGCCGCG	2900
GGTACCGGAC	CTGCGCTCAC	TGCAGGAATA	TGTGGGCTCG	ACGCAGCCGG	2950
TGCTGCTGGA	CTGGGCGGTC	GGTTTGGCCT	TCCCGTGCCA	GCAGCCGATG	3000
CTGCACGCCA	ATGGCATCGC	CGAAATCCCG	AAGTTCCGCA	TCACACCGGA	3050
CTACTCGGCT	AAGAAGCTGG	ACACCGACAC	GTGGGAAGAC	GGCACTAACG	3100
GCGGCCTGCT	CGGGATCACC	GACCTGTTGC	TGCGGGCCCA	CGTCATGGCC	3150
ACCTACCTGT	CCCGCGACTG	GGCCCGCGAT	TGGGGTTCCC	TGCGCAAGTT	3200
CGACACCCTG	GTCGATGCCC	CTCCCGCCCA	GCTCGAGTTG	GGCACCGCGA	3250
CCCGCAGCGG	CCTGTGGTCA	CCGGGCAAGA	TCCGAATTGG	TCCATAG	3297

2) INFORMATION FOR SEQ ID NO: 2106

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C

31

2) INFORMATION FOR SEQ ID NO: 2107

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCACGCTC GC

32

2) INFORMATION FOR SEQ ID NO: 2108

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTGTTTAC AACCCGCCCC C

41

2) INFORMATION FOR SEQ ID NO: 2109

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCGGGCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCGGGCCCTT AACGATTTC ACGAATCTGG ATTCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCGGGCTTGA TGAAGTTTTG GGTTTCCTTG ACAATTGCG CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2114

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2115

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCGGGCTTGA TGATTTCTC GAATCTAGAT TGGGCCCGC

39

2) INFORMATION FOR SEQ ID NO: 2116

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCCG

39